

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 02/086443 A2

- (51) International Patent Classification⁷: **G01N**
- (21) International Application Number: **PCT/US02/12476**
- (22) International Filing Date: **18 April 2002 (18.04.2002)**
- (25) Filing Language: **English**
- (26) Publication Language: **English**
- (30) Priority Data:
- | | | |
|------------|-------------------------------|----|
| 60/284,770 | 18 April 2001 (18.04.2001) | US |
| 60/290,492 | 10 May 2001 (10.05.2001) | US |
| 60/339,245 | 9 November 2001 (09.11.2001) | US |
| 60/350,666 | 13 November 2001 (13.11.2001) | US |
| 60/334,370 | 29 November 2001 (29.11.2001) | US |
| 60/372,246 | 12 April 2002 (12.04.2002) | US |
- (71) Applicant (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **MURRAY, Richard** [US/US]; 22643 Woodbridge Court, Cupertino, CA 95014 (US).
- (74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111-3834 (US).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Declaration under Rule 4.17:**
— of inventorship (Rule 4.17(iv)) for US only
- Published:**
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

WO 02/086443 A2

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

5

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

20

BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (normicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

20

20

25

bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBF-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

5 The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two
10 or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type
15 promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers
20 to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or
25 synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding,
30 duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization.

Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols. A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

"Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, 10 horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, 20 which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such 25 homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, 30 cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

5

Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S.

Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and Ouellette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

5 The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

10 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample
15 source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU
20 data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern
25 encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in
30 or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

15 **Characteristics of lung cancer-associated proteins**

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, salivary producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

10 TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

25 In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

5 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

10 The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

20 Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

25 In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guillermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

25 Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

- 5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more
10 fully outlined below.

- While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be
15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

- 20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

- Substitutions, deletions, insertions or any combination thereof may be used to arrive
25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

- 30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

5 Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

10 Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent
15 Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric
20 molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung
25 cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

30 Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody therefrom may contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

15 In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be
25 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman
Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems
typically automate procedures, including sample and reagent pipetting, liquid dispensing,
timed incubations, and final readings of the microplate in detector(s) appropriate for the
assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide
detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides
technical bulletins describing screening systems for detecting the modulation of gene
transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or
random or directed digests of proteinaceous cellular extracts, may be used. In this way
libraries of proteins may be made for screening in the methods of the invention. Particularly
preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins,
with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g.,
substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30
amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to
about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical
equivalents herein is meant that the nucleic acid or peptide consists of essentially random
sequences of nucleotides and amino acids, respectively. Since these random peptides (or
nucleic acids, discussed below) are often chemically synthesized, they may incorporate a
nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible
combinations over the length of the sequence, thus forming a library of randomized candidate
bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are
5 randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription
20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein
20 or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

 Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Insti. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g.,

Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the
10 sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- In one embodiment, a therapeutically effective dose of a lung cancer protein or
25 modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the
10 molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate
20 and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

25 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to

5 accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the
10 patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be
15 used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can
20 be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present
25 invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for
30 introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques. Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In:
30 Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

5 Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a
10 plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular
15 epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

20 In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or
25 modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As
30 such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
5 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as
described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-
993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A				
	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL 70% SQUAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61 0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, VdJrc Reg	2.68 3.28
10	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96 0.14
	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitter)	0.79 0.07
	101102	L07594	Hs.79059	transforming growth factor; beta receptor	2.55 1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88 0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89 0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59 0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15 0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81 0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31 0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44 0.82
20	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96 0.45
	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27 0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04 0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96 0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81 3.45
25	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95 0.23
	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62 0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9 0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27 0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86 1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27 0.47
	104212	AB002298	Hs.173035	KIAA0300 protein	1.17 0.16
	104691	AA011176	Hs.37744	ESTs	1.08 0.35
	104825	AA035613	Hs.141883	ESTs	0.75 0.27
	104857	AA043219	Hs.19058	ESTs	2.6 3.3
35	104865	AA045136	Hs.22575	ESTs	1.23 0.49
	104989	AA102098	Hs.118615	ESTs	0.63 0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86 0.34
	105847	AA398608	Hs.32241	ESTs	1.32 0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78 0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2 0.47
	106536	AA453997	Hs.23804	ESTs	0.82 0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99 0.07
	106667	AA461086	Hs.16578	ESTs	1.17 0.4
	106773	AA478109	Hs.188833	ESTs	1.46 0.43
45	106797	AA478962	Hs.169943	ESTs	1.18 0.32
	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98 0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidy)	1.05 0.14
	106954	AA496980	Hs.204038	ESTs	1.25 0.33
	107054	AA600150	Hs.14366	ESTs	1.11 0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07 2.58
	107994	AA036811	Hs.165030	ESTs	0.7 0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02 0.48
	108041	AA041552	Hs.61957	ESTs	1.44 0.51
	108087	AA045709	Hs.40545	ESTs	1.98 1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52 0.72
	108435	AA078787	Hs.194101	ESTs	2.53 1.53
	108480	AA081093	Hs.68055	ESTs	1.56 0.48
	109252	AA194830	Hs.85944	ESTs	2.69 3.18
	109550	FD1534	Hs.26981	ESTs	1.19 0.65
60	109613	F03031	Hs.27519	ESTs	1.01 0.29
	109837	H00656	Hs.29792	ESTs	0.81 0.15
	109893	H04768	Hs.30484	ESTs	1.44 0.32
	109984	H09594	Hs.10299	ESTs	0.62 0.14
	110099	H16568	Hs.23748	ESTs	1.01 0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1 0.22
	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26 0.26
	111341	N80935	Hs.22483	ESTs	1.57 0.52
	111510	R07856	Hs.16355	ESTs	3.96 1
	111737	R25410	Hs.9218	ESTs	0.97 0.24
70	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22 0.35
	113238	T62979	Hs.189813	ESTs	2.27 0.45
	113540	T90496	Hs.16757	ESTs	1.06 0.22
	113552	T90889	Hs.16026	ESTs	1.16 0.42
	113606	T93093	Hs.17125	ESTs	1.48 0.7
75	113695	T96965	Hs.17948	ESTs	1.54 0.28
	113946	W84753	Hs.37896	ESTs	1.79 0.72
	114251	Z39898	Hs.21948	ESTs	1.95 0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42 0.13
	115230	AA278300	Hs.182980	ESTs	2.62 0.42
80	115279	AA279760	Hs.63671	ESTs	1.79 0.91
	115566	AA398083	Hs.43977	ESTs	0.86 0.2
	115965	AA446661	Hs.173233	ESTs	0.79 0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29 0.68
	116279	AA486073	Hs.57362	ESTs	2.27 0.78
	117023	H88157	Hs.41105	ESTs	1.36 0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		""yr30g11.s1 Soares fetal liver spleen	1.32	0.53
	119824	W74536	Hs.184	advanced glycosylation end product-specd	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20553	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		""yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
20	125167	W45560	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AA17667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		""HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369387	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486557	Hs.105895	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		""yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
45	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22557	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
55	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78081	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50583	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	0.33
	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylthidrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calcitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
85	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

5	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	101124	L10343	Hs.112341	*Protease inhibitor 3, skin-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	*Melanoma antigen, family A, 2"	1	1
10	101204	L24203	Hs.82237	Alaxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (oomifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
15	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		*Human parathyroid hormone-related peppl	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
20	101759	M80244	Hs.184601	*Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
	101809	M86849		*Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	*Protein tyrosine phosphatase, receptor-	1	1
25	101851	M94250	Hs.82045	Midkine (neurtic growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	*Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	*Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
30	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U66083	Hs.37110	*Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
35	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
40	102963	X15943	Hs.37058	*Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	*Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratifer	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
45	103119	X63629	Hs.2877	*Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
50	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	ST4 Oncofetal antigen	1	3.93
	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		*ESTs, Highly similar to integral membra	0.99	1.8
55	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
60	104978	AA088458	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM1	1.64	2.89
	105012	AA116036	Hs.9329	*Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
65	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
	106012	AA411621	Hs.8695	ESTs; same as BFH67	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
70	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
75	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
80	107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
85	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
	109565	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H58617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
5	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	*Diacylglycerol kinase, zeta (104kD)*	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
15	113970	W86748	Hs.8109	ESTs	1.17	1.73
	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456958	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
45	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
50	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
60	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R06041	Hs.18048	*Melanoma antigen, family A, 10*	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) numb	1.52	2.26
	125972	AA434562	Hs.35408	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
70	126645	A1167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	A1354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	A1204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
	129404	AA172056	Hs.111128	ESTs	1	1
80	129466	L42583		*Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X*	0.98	1.96
85	130385	AA126474	Hs.155223	stannocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	*Human DNA-PK mRNA, partial cds	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.98
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	*Doublecortx; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	*laminin gamma2 chain gene (LINC2), exon	1	1
20	132659	Z75190	Hs.54481	*Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	*Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.55105	*ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	*A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	*SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564I1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	*Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	*Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	***collagen, type XI, alpha 1***	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	*Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
50	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830		AFX control: 28S ribosomal RNA	0.88	1.53
70	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		***Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		***Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
85	100398	D84557	Hs.155462	minichromosome maintenance deficient (ml	1.08	1.9
	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Eptcan, All. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutral)	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	Interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein (cl	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoilin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differentiat	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytotactin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91668	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribulose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
85	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105521	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
15	106103	AA421104	Hs.12094	ESTs	1.04	1.44
	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.8605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to p112 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.s	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase	1.21	1.85
	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.95
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777O23 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
5	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
	122059	AA431737	Hs.98749	EST	1.93	2.33
10	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [H.sapiens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
	123398	AA521265	Hs.105514	ESTs	1	1.93
15	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
20	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	A1382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPLI)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
30	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombinatio	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733	AA328993	Hs.104558	ESTs	1.34	1.94
40	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
	129703	AA401348	Hs.179999	ESTs	0.97	1.63
45	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4-galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral onco	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

5	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DP1; DP11)	0.7	6.21
	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
20	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
45	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chitobiosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenes. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661	23182_1
	100667	26401_3
70		BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668	26401_3
80		L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
85	101332	25130_1
		J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

100780 458_127

100830 4002_1

100906 4312_1

100930 16865_1

102221 3861_1

101809 32963_1

102590 15932_1

101977 29073_1

102781 20812_1

AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983
AA625873 W78031 BE206307 AA550803 AI743147 AI990075 AA948274 AA129533 AI635399 AA605313 AI624669 AW594319 AI221834 AI373434
AA307706 BE550282 AI760457 AI630635 AI221521 AW674314 AW078889 AI933732 AI686969 AI186928 AW074595 AI127486 AI079544
AI910815 AI17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977
AA306247 AA352501 AW403639 F05421 AA224473 AA305321 H93904 AA089512 AW391543 AW402915 AW173382 AW402701 AW403113
H94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AI375913 BE384156 W24652 AA746288 AA568223 BE090591
R33033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW571566 AI128799
AI803319 AL042776 AW074313 AI887722 AI032284 AA447521 AI123885 N29334 AI354911 AW090687 AA236763 AA435535 AA236910
AA047124 AA236734 AW514610 H93467 AA962007 AI446783 AA127259 AI613495 AI686720 AI587374 AA936731 AA702453 AI859757
AA216786 AI251819 AI469227 AA806022 AI092324 N71868 AA968782 AA236919 AA809450 AA227220 AA765284 AI192007 AA768810
AA805794 AA729280 AA806238 AW768817 N71879 AI050686 AA505822 AA668974 AI688160 BE045915 AW466315 AA731314 AA649568
AA834316 AW591901 AW063876 AW294770 AI300266 AI336094 AI560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675
AI457474 AW466316 AA550969 AA630788
BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865
BE396881 BE560031 BE514199 BE560037 BE560454
AC004770 W05005 AA356068 AA094281 H29358 T56781 AW875313 L37374 BE312466 BE311755 BE207106 BE293320 BE018115 AW239090
BE548830 AW247547 AA776062 BE397382 AA486713 T10111 T09340 AW489881 BE547280 AA356003 AW581520 AW875331 AA580720
AW875336 BE276873 BE408229 AW188148 BE255166 BE253761 AW793727 AW373141 AW581548 AA471223 AA305950 BE263976 AA626820
BE257409 AW360962 AA090655 C00312 AI312741 BE407213 AA209352 AW298199 AW248553 AW297794 AW731722 BE300586 AW731972
AW615446 BE301599 AW615520 AA486714 AW440257 AI196516 AA564630 AA618079 AW192592 AW474985 AA604580 AI627461 AA765440
AI680394 AL135548 AI683224 AI581126 AW245096 AW194154 H29274 N70363 AA629758 AA580602 AA862006 AI683841 AI097667 AI928583
AI358774 BE243487 AA620553 AA653297 AA292690 T10110 Z38906 AA908544 AA340930 AI185438 T03328 T28844 AI687010 AI864965
AI872575 BE388740 T56780 AW373138 BE258717 AA699671
AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852
AA446421 AW881866 AI459428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454 AA305698
AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175
AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139 R00722
J04129 NM_002571 AA293088 AA477016 AA046631 T28299 AA476904 AA433955 AA430486 AA495907 AI151391 AA291495 AA402723 W25651
AA705816 AI826712 AW296294 AA293479 AI276581 AW044154 AI080180 AI417985 AI274168 AI474212 AA495908 AA635664 AI092114
AI804952 AA479874 AI597661 AI420511 AA479738 AA421417 AA421247 AA436220 AL047797 M34046 N42277 AA228076 W02698 AW20297
AA434311 AI369971 AA479731 AI865541 AI418020 AA421246 AA452764 AL048051
NM_005769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836
AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA235051 AI129757
AW366451 T34489 D58106 D56351 AI936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349 AA147546
AI952998 AA912579 AI143356 AW902211 R64717 AW157236 AI815242 D45274 AW263991 AA442920 AA129965 AL035713 AI932255 AI949082
AI142826 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419 AW193969 AW673561
AW592609 AI224044 H43943 AA091912 R49632 R48353 AI568409 R48256 AI198046 H27986 H43899 AI678759 AI680310 AI624220 H17052
AA156410 N56062 AI699430 AA664529 T09406 T10459 AA627506 AI379584 N83831 N88633 AW022651 AA971281 AA248036 AI039197
AI914689 AA973825 AL047305 AA129966 AI798369 AW264348 AI445879 AI658759 N67924 AI933507 AI216121 AI333174 T10972 AI376028
AI186756 AI273778 AA610487 AI797946 AA853903 AA903939 AI338587 AI278494 AW627595 AA904019
M68649 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544
AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114 AW264544 AI018136
AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715
AW020066 AI783695 AI589498 AI917637 AW264471 AW384491 AI816732 AW368530 AW368521 AW368463 AA461087 AI341438 AI970613
AI040737 AI418400 AA947181 AA962716 AI280695 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW136766
AI076554 AW511702 N69323 H88912 AA257017 AI952506 H88913 AI912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
R61573 BE005029 X98091 AA297307 BE537267 BE566138 BE566139 F11561 BE564795 BE568776 AW064005 BE566479 BE380035 BE567012
BE568634 BE566568 AA298060 BE566043 BE568813 BE568518 AA283070 BE565414 BE566738 BE568585 BE565667 BE566116 BE566433
U62136 AF049140 BE567057 BE567297 BE567403 BE564316 BE567400 BE568854 BE566588 AA448772 AA071353 AW732642 BE564996
AA297763 AA278550 AA421083 AA298184 AA091007 AA984577 AA205916 N28759 AL031291 C15757 C15761 H02728 BE566410 AA129335
AA419499 N87741 BE379689 BE004824 BE379611 D25874 AA148454 AA323654 AW950311 AA448795 AW494243 AA773386 AA773843
AW020327 BE343580 BE504258 BE549990 BE220200 AI673334 AI202679 AA975515 D61421 AI168688 AA102843 AW246821 AI276203
AI074054 AI633824 AI962927 AI148926 N50969 AI308911 AA410994 AW373025 AA148455 H02620 AA688293 AI246318 N22220 AI917777
AI050054 AI097286 AA663794 AW368662 AW627826 AW078734 AI253060 AA749154 AA832236 AI192358 AW024676 AA448676 AA764891
BE439467 AA661534 AA258061 AI090546 AA995157 AI051011 AA584421 AI026032 AW591338 AW589563 AA776914 AW024684 AA421002
F09219 BE464500 AI383595 AA954244 AA601583 AA737304 AA195549 AA805778 AI055876 AA164942 AW013961 AI672608 AW514211 D59441
AW582574 AA160935 BE566501 BE564612 BE565353 BE568195 BE565447 BE568302 BE566097 BE565470 BE564249 AL036217 AW749424
BE567494 AA102842 AA314761 AV661237 C14211 AA651866 AW798997 AA470605
AF112213 AL050318 T24804 AW248136 BE366341 BE263177 W16677 BE250224 BE563669 BE267405 BE566577 AV651354 AV651292
AI346903 AI539128 AI189171 S83364 AW073849 AI816760 AW073309 AI422690 AA296692 AI860301 AI805446 N77735 AI340328 BE092530
AW028742 BE088442 AA657742 AA742438 AW170086 AI038920 AI432379 N35073 AI936194 AA868655 AA983612 AI077505 BE080433
AI375014 AI126547 AI348244 AI346077 AI748952 N26915 AI753574 AI093341 AI278762 BE092517 N74204 H08158 T58149 AI129303 N58366
AA524456 BE122661 AA542925 AI246120 AI735203 AA706829 AA877544 AI082289 AA926687 N92840 AW249798 AA934763 AW998363
AI128632 N25202 AI240209 AW118892 N80744 R35655 AI342321 AI340141 AW878792 AI857321 H09610 W04601 AW006650 AA126006
AA553675 AI052791 AW059835 AI041906 AA814658 AW002059 AA729483 AI609301 AA994633 AA903651 AI459183 T95072 AW088630
AI126112 AI800091 AI561215 H17502 AW475072 AI819003 AI683272 AI262701 AW793140 T81787 R99586 AI275160 AI310420 AI698929
AA159174 AI827968 F30305 F30309 AA806662 AI091923 AW878722 AA583430 AW571913 AI674584 AA292533 AI079471 AA642325 AA719050
AW793172 AA305476 AW103745 T23459 N79525 AI784438 AA534551 AW193751 AI074360 BE281214 T32229 W25066 W01205 T63086
AW795348 AI361287 AW795353 AW795349 AA594759 AI400295 D11489 AI370689 AA482356 AA485295 W40151 AA564661 AW300745
AI346938 AI374975 AI423782 AW193899 AA612604 AI183409 AA996156 AW366963 AW366977 AI284860 AA846503 AI985064 AA844576
AA737921 AA873274 BE241546 BE241540 AA484058 AW468970 AA127876 AA159120 AW001568 AW795213 AW795258 AW795330 BE250589
BE387572 AA910895 AA161217 BE250380 W31500 T95167 AI719306 AI359224
BE258778 BE281230 BE410044 T33723 AW672694 AW410439 NM_006429 AF026292 T35505 BE542333 T08940 AU076737 AW247471
BE393215 AW328640 BE542408 T32170 BE302544 T31955 BE206898 BE275738 T32570 BE386426 BE298746 BE389937 BE293991 BE315289
BE389578 R34739 R15312 BE279365 BE277756 AL036019 T33725 BE277779 BE302962 AL047294 BE276505 T09070 T33673 BE312580
AW387774 BE257175 AW674367 BE253331 BE270344 BE299831 BE273576 T32062 AI751831 BE618381 AA304899 BE252268 U45364
BE256790 BE207199 BE256209 BE251941 BE250791 BE313955 BE269806 BE543623 BE279212 BE252289 T31699 BE262220 T31669
AA315781 AA192212 N84547 BE292377 BE259631 AA232179 AI133144 T31292 AA315945 BE407301 BE251184 BE409006 AI880158 AI904003
AI904114 AW651768 AW651763 R58247 BE271897 U83843 C05298 BE261609 BE255973 AA351650 N84631 BE263637 AW452910 AA328465
AA324549 AW579525 BE252296 BE257551 AL048332 BE208630 AA359336 AW327897 AA151742 AA305816 BE076862 BE076866 BE263161
AA323785 AA676588 AA626565 AA078917 W87657 R09002 R94021 AA312032 BE276665 AA295608 AW407162 AA329374 AW877912 N27885
AA369256 AA360968 BE250476 N85427 BE265569 AI278639 AI616576 AI691037 AW328583 AI567949 AI983455 AW277732 AI811297 AI571508
AW073674 BE296039 BE467326 AI828796 AI816578 AW511604 AI921213 AW152427 AI795787 AI801618 AW156866 AI628144 AI890339
AW173690 AW511540 BE535620 AA383014 BE301164 AI866596 AW514909 AA658050 AW575243 AA074631 AI093488 AW575408 AW675443
AW615636 AW732207 AW377638 AA321784 AA641629 AA633105 AA527640 AW129146 AW615672 BE394607 AA483902 AW475032 BE378532

AA872808 AA469388 AW105268 BE047301 AW591843 AW410056 AW517153 AI950495 AA746641 AI914878 AA873185 AI696911 AA548625
AA911505 AA148762 AW674535 AI587329 BE328328 AW270348 AA158225 AW117705 AW474997 AW519193 AA614757 AW664383 AI082647
AW590973 AI476711 AA192213 N88741 BE464552 AW072679 AI453708 AA152166 AA805924 AI581078 AI125768 AW173484 AI961980
BE300766 AI199698 AI636792 AW247333 AW272861 AW078818 AA150012 AA551232 AA678821 AW873869 AW768266 AW660315 AA319210
AA814551 AA157994 AA318886 AI582962 AW089224 AI355098 AI343694 AW072598 N21054 AI301249 AA742924 H17917 AW326584
AW248898 AI751830 AA907816 R08898 AW087989 AI828300 AA148596 AI269577 T33426 AA213571 AI973201 AA666279 R49612 AI573183
AW799762 AW410068 AW769666 AI952097 AI475204 D57490 AW517531 BE245270 AW470008 T33427 AW005731 AI795795 BE616141 BE312730
T15747 AA552875 T23644 AW361289 AI758558 BE207435 AA876958 T03361 AA883569 F37533 AA582321 AW082524 R42212 AA973847
T18900 AA086502 AI559867 AI302418 AA948667 AA745670 T08939 T33724 T33722 BE621568 D57489 D25906 BE621151 F16510 C05966
T35127 AA630427 AI933481 AA309426 AI918440 BE651854 BE618866 BE394675 BE296173 AW951687 BE383739 BE616141 BE312730
BE535351 AW080575 BE313330 BE616664 AI354390 AA847315 BE544509 BE515212 BE297833 BE278808 BE544844 AW090178 AI890664
BE546708 AW189943 BE274412 BE382399 BE266392 BE254949 BE280696 BE383237 BE261756 BE257721 BE312683 BE275476 BE514880
BE545314 BE313587 BE384537 BE386691 BE264813 AW592575 AI336332 AI278641 AI795791 BE222662 AW249316 AA314361 AI360612
AW402923 BE266845 AA075945 AA314436 BE384640 AW731769 AW957077 AA552234 AA573560 AW367038 AA313399 AI983873 BE410159
BE263803 BE514339 BE409073 BE281296 BE543396 BE395387 BE088360 BE546946 BE546570 BE390626 AA074638 AA301821 AW845230
AW582379 AI949222 AW029572 AA515843 AW272394 BE250234
C14322 W74050 AI074232 AA595624 BE048955 AI148417 AI583145 AI473460 AI801688 AW573593 AI950741 AI628140 AW467921 R98105
AI149258 AI247584 AI078378 AI139850 AA489411 W27444 R98104 AI033826 AA699589 AI033120 N55544 W88984 AW970771 AA703362
AA099138 AA708792 AA046150 H98981 AI916674 AA953018 AI972749 AI921343 AA909044 AA094751 AI203124 AA582143 AI446654
AW235415 R70377 AA099236 F20703 AA524436 R69484
H04043 D60988 D60337
AI204246 AI204250 AI194050
H83265 T63524 AA304359 AW960551 AI672874 AI749427 AA227777 AW027055 AA971834 T49644 T54122 AI983239 AI808233 T91264 T96544
AI350945 AI709114 R72382 T48788 R48726 AW385418 AI095484 T49645 AA928653 AA570082 AW007545 T57178 AA516413 AA913118 T57112
AA564433 AA774503 AA367671 T59757
W78816 AI720806 AI633854 AI632086 AI668663 N70894 AW571809 AI383592 AI201348 W80715 N91880 AW963101 AA339011
AB033023 BE391906 BE275965 BE277872 BE003882 AA313774 BE019159 BE298024 BE299727 BE300011 BE390277 BE394764 N87550
BE409419 BE408652 BE408197 AL119332 AA622427 AI816265 AA610118 T07318 AA019839 AA634430 BE205794 BE049461 AI042322
AI652711 AI917645 AA630045 AW191969 AI817882 T17271 AI803663 AI095533 H46D19 AW592438 AI624836 BE475552 D51149 AW132058
AA639614 AI925762 AW088153 T17455 AA018640 AW751475 BE300241 AI816255 BE391981 AW408671 AA333910 AW875446 AW875703
AW875926 AW875645 AW875647 AW938037 AL138042 AW892619 BE243018 AW995454 BE246381 BE009082 BE278921 AW957842 AA262454
H30121
W72062 AF088057 W76255 AI827219 AI631461 AW449295 AI354957 AI913803 T62772 AI222040 T62921 T63781
AI678765 H12175 R14664 AI914049 AA955383 H08009 H19418 AW953728 AI358021 AA587361 AI269377 AA369905 AW957113 H27693
AI300474 H73776 W74397 AA579804 AI131018 W72331 AI719085 AA568348 AI859045 AI814819 AI888714 BE467470 AW131268 H19419
H27694 AI342165 AI914155 AA534872 BE018176 R60206 H11647 R45641 AI860466 BE301656 AI125453 AW98120 AA593735 AA879110
AI016404 T35018 AA588397 AW449767 AA470365 BE501139 AA588354 AI337500 AW078532 Z41279 AI125449 AA935725 AA404338
L42583 NM_005554 L42601 BE183076 AI541221 BE140567 L42610 V01516 J00269 AW275792 AW383052 AW380143 AI541102 BE612846
AI541344 AW238368 BE613405 BE615705 BE615301 AW379823 AW794706 AA194806 AA194992 AA583052 AW384024 AW384000 AA641239
AI246504 AI540333 AW238681 AA640939 AI540863 AI608860 AW862564 AW366725 AW366983 AW366870 AA596020 AW794721 AW794511
AI591181 BE182523 AW794644 AW794620 AI935234 AI608903 AI608623 AW797060 AW084935 BE182517 BE182319 AI890082 AW238346
AW797012 BE182522 AW794838 AI608794 AW304289 AA147193 AA595995 AW381128 AW366720 AA583718 AI828416 BE122864 AW368343
AA431080 AW082039 AW380976 AA587144 AA443636 AW872937 AW794448 AW378382 AW085761 AW794718 AW263895 AA583587
AA583991 AA583994 AA586886 AA586880 AW368365 AI814460 AA586991 AI282829 AW378405 AA586721 AI609242 AA431973 AA232959
AI813095 AW263854 AW378391 AW378415 AW378381 AA036990 AW238395 AI285446 BE208219 BE049526 AA583051 AW366711
AI285580 AW082642 AI285712 AA582875 AW591216 AW368719 AW378408 BE122835 AA582976 BE350422 AA418328 AI541454 AI565930
AA583700 AA150575 AW238427 AI287474 AA912658 AA584223 AW238528 C17918 AW136169 AA159847 AI923797 AI609009 BE182479
AI915198 AW378114 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AI872793 AA583981 AI284571
BE182316 BE182507 AA233331 AI824572 AI540586 D29492 BE182931 AA036948 BE551821 D29401 AW378365 C00141 D29181 D29567
AW103359 W95238 AI991663 AA587298 BE184608 AA099833 W95121 W95150 D29584 AI934111 D29455 D29533 AW265380 D29290
AW238463 AA121041 D29204 AA585925 D29441 AW081840 AA587018 D29323 AA582891 BE182433 BE182437 BE185295 BE182434
AW015534 AA314369 AA290715 BE568683 AW629494 D28364 AW995678
AW077114 AA580734 AL041945 AA101515 AA121344 D78130 NM_003129 AA341650 T84166 AF098865 AA130976 BE089553
T66122 AW175590 F05344 AI114760 R12900 AA194871 AA132298 D78129 AA132213 AW948930 AW948919 AA263053 AW946593 AW948840
AA278558 R50895 N26940 N40818 AW021255 AA054851 AA663379 AW948795 AW948893 AA400356 AW948911 N85024 W78844 AI341546
AI760182 AA286763 BE617763 BE617263 AW263690 BE049454 BE617928 AW515038 AW950584 AA601009 AI079194 AA147204 AW083163
AA130981 AI218369 AA604784 AI806257 AI559556 AA232318 AA258065 AI471982 AA687949 AI143944 N30172 AA400196 AI084342
AI221380 AA948469 AI802469 H05720 AA113270 AA158138 AA076231 AI521024 AI810962 AI133616 AA805106 AA101516 R40052 R50778
R43280 T65036 AW131924 AA114251 AA152331 F09650 AA580614 AA558927 C75491 Z38352 AA954595 Q75606 W80742
D56165 M36981 X59965 NM_002512 BE379177 AA314838 BE256445 BE252016 AW248343 AI720933 AW085701 BE386050 BE619742
BE277805 AA147951 AA603113 BE253293 AI246588 AI183405 AI954174 AI126891 AI289101 AI123832 AW129670 AA471268 AW170242 AW873079 AA148011 AI608620
AA482961 AI003658 H43261 AA657978 AI735072 R83138 AA722002 AA626271 AW273877 BE464626 AA071483 AA429973 AA494342
AA620436 AA775597 AA775601 AA826847 AI192585 AA826359 AA411159 AI193419 AI204013 AA705323 AA716255 AI784611
AI128227 AA828464 AI148911 AI493446 AI626084 AI189180 AI721196 AI190618 AA284987 AI128543 AA632064 AI333073 AI278470 AA131688
AI491768 AA937581 AA630065 AA834257 AW249841 AA583742 AI309756 AA961676 AI760860 AA557818 AA954238 H43655 AI302564
AA127545 AI609219 H20426 AI042292 AI056466 AA581836 W47002 AA422057 AA937673 F29757 AA829208 AW327462 AA372098 W02144
AA036805 AA487365 AA961037 AI139946 AA487250 AA737118 AI952504 AI242293 AA650552 AI708401 AI633133 AA630848 AA654317 F24128
AI434165 W46252 AW043879 AI033763 F37228 AA687809 N49087 AA876981 AA506947 AI914572 AI833284 F22253 AA026222 R50166
AI219267 N27095 AA496512 AI784222 AI289904 AA513145 AA528547 AA418700 F36721 AI880700 AI601170 AI862851 AI708633 AA524499
AA642220 AA496628 AI718709 W80579 AI720547 F20718 AA649943 AA588229 N40503 H46029 BE262669 BE391069 BE537538 AI510751
AI905968 AI318611 H46099 AI472604 T60667 AA373087 W32479 AA514034 BE619183 AA134672 AA127544 H26942 BE536689 AW327461
AA422139 AW262357 AW327348 F33510 AI630382 AW827126 F27133 AI335189 AW517599 W80471 AA885814 N89681 BE393173 AA617760
AA584268 AA460537 AA446261 H20425 N64040 AW276801 AA316367 AA071232 BE545409 AA308292 BE274447 AA380861 AA340038
AA341808 AA865579 AI018634 AI766314 AI919302 AA872367 AA991404 AI906961 AA888375 BE621012 AA505388 AA935192 AA290828
R50220 H50814 H44721 AW951723 AA514796 AA418708 AW673377 AA379622 AA977995 AA708224 AA708216 AI318249 AI318233 AA411160
AA026221 AA316774 AA486908 AI500094 AA096362 AW583742 BE536422 BE618653 R70203 AA131732 AA345048 BE562720 T28342
NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376697 AW848723 AW376697 AW848723
AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155
AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584
BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114
BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW086840
BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674
BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA098991 AA131128 AA337270 AA340777 AW384371 AA852212
R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264
AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467

5

10

15

20

25

AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784
AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458
AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470
AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866
AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975
AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI308554 AI686869 AI568892 AW190555 AI571075 AI220573
AA056527 AI471874 AI304772 AW517828 AI915598 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070
AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878
AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633
AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962
AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861
AW860878
100528 45979_1 BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165
AI638794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865
H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044
AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
BE389577 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
100559 2260_1 NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
100576 9986_1 X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
124357 genbank_N22401 N22401
101624 entrez_M55998 M55998
101625 entrez_M57293 M57293
135158 57963_1 AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
25	100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
	100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
30	100138	U83508	Hs.2463	angiotensinogen 1			2.30					
	100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
	100305	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
	100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
	100458	S74019	Hs.247979	Vpre-B	42.40							
35	100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
	100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
	101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
	101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitter)				193.20				
40	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
	101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
	101308	L41390		"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
	101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
45	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
	101397	M26380	Hs.180878	lipoprotein lipase								3.54
	101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
	101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
	101507	X16896	Hs.82112	interleukin 1 receptor; type 1				37.60				
50	101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar			2.54					4.25
	101537	AI469059	Hs.184915	zinc finger protein; Y-linked								
	101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
	101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
	101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
55	101560	AW958272	Hs.83733	intercellular adhesion molecule 2, exon								3.38
	101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
	101605	M37984	Hs.118845	troponin C; slow								3.80
	101621	BE391804	Hs.62661	guanylate binding protein 1; Interferon-	30.20							
	101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
60	101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
	101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
	101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					6.85
	101994	T92248	Hs.2240	uteroglobin								
	102020	AU077315	Hs.154970	transcription factor CP2			2.45					
65	102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
	102112	AW025430	Hs.155591	forkhead box F1	54.60							3.98
	102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.62
	102202	NM_000507	Hs.574	fructose-bisphosphatase 1								
	102241	NM_007351	Hs.268107	Multimerin			2.32					
70	102310	U33839		Accession not listed in Genbank		7.00						
	102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
	102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protein								3.75
	102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
	102636	U67092		"Human ataxia-telangiectasia locus prote			2.40					
75	102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
	102675	U72512	Hs.7771	"Human B-cell receptor associated protei						3.56		
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)								4.51
	102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
	102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
80	103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
	103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
	103098	M85361		Human mRNA for T cell receptor; clone IG					10.00			
	103117	X63578	Hs.295449	parvalbumin		6.00						
	103241	X76223		Hsapiens MAL gene exon 4			2.47					
	103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
85	103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

PCT/US02/12476
5.97

[illegible]

	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
5	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AI798863	Hs.87191	ESTs	2.40				
	109578	F02208	Hs.27214	ESTs	10.00				
10	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
	109650	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs	8.40				
	109724	D59899	Hs.127842	ESTs			29.40		
15	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
	109833	R79864	Hs.29889	ESTs	10.00				
	109837	H00656	Hs.29792	ESTs	6.49				
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs			107.00		
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B				2.22	
	110271	H28985	Hs.31330	ESTs				3.48	
	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
25	110634	R98905	Hs.35992	ESTs			20.00		
	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-				4.15	
	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfamily		3.13			
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33				
30	110971	AI760098	Hs.21411	ESTs			44.60		
	111023	AV655386	Hs.7645	ESTs	32.40				
	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein				3.42	
35	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap				3.91	
	111442	AW449573	Hs.181003	ESTs			33.20		
	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AI741471	Hs.23666	ESTs	46.20				
40	111807	R33508	Hs.18827	ESTs	16.00				
	111862	R37472	Hs.21559	EST				3.91	
	112045	AI372588	Hs.8022	TU3A protein				2.74	
	112057	R43713	Hs.22945	EST				4.92	
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
45	112314	AW206093	Hs.748	ESTs	9.00				
	112324	R55965	Hs.26479	limbic system-associated membrane protei			14.00		
	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H		2.49			
	112380	H63010	Hs.5740	ESTs		2.34			
50	112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!!! ALU SUBFAM	8.00			4.53	
	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9					
	112492	N51620	Hs.28694	ESTs			29.80		
	112541	AF038392	Hs.116674	ESTs				3.62	
	112620	R80552	Hs.29040	ESTs		2.37			
	112623	AW373104	Hs.25094	ESTs		2.26			
55	112867	T03254	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs	6.50				
	112954	AA928953	Hs.6655	ESTs	7.00				
	113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!!! ALU SUBFAM				4.39	
60	113086	AA346839	Hs.209100	DKFZP434C171 protein			10.00	4.47	
	113140	T50405	Hs.175987	ESTs					
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00				
	113257	AI821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
65	113454	AI022166	Hs.16188	ESTs	6.00				
	113502	T89130		ESTs	39.60				
	113552	AI654223	Hs.16026	ESTs					3.88
	113645	T95358	Hs.333181	ESTs				2.58	
	113691	T96935	Hs.17932	EST			38.20		
70	113706	AA004693	Hs.269192	ESTs				3.09	
	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31			
	113924	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
	114035	W92798	Hs.269181	ESTs			13.00		
	114058	AK002016	Hs.114727	ESTs				5.00	
75	114084	AA708035	Hs.12248	ESTs			40.60		
	114121	H05785	Hs.25425	ESTs		2.31			
	114124	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00				
	114275	AW515443	Hs.306117	interleukin 13 receptor; alpha 1	6.00				
	114297	AA149707	Hs.173091	DKFZP434K151 protein			48.80		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H				3.45	
	114449	AA020736		*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
	114452	AI369275	Hs.243010	ESTs, Moderately similar to RTC0_HUMAN G	14.00				
	114609	AA079505		*zm97a5.s1 Stratagene colon HT29 (#93722				3.13	
	114648	AA101056		*zm25b3.s1 Stratagene neuroepithelium NT			35.40		
85	114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy				3.42	
	114762	AA146979	Hs.288464	ESTs	33.00				

	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.268391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs			48.00		
	115566	AI142336	Hs.43977	ESTs			56.20		
10	115683	AF255910	Hs.54650	ESTs; Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.s			33.60		
	115819	AA486620	Hs.41135	Endomucin 2			74.40		
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs			388.80		
	116035	AA621405	Hs.184664	ESTs			33.20		
15	116049	AA454033	Hs.41644	ESTs			45.80		
	116081	AI190071	Hs.55278	ESTs				3.57	
	116082	AB029496	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekdi			30.00		
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20				
	116835	N39230	Hs.38218	ESTs			41.20		
25	116970	AB023179	Hs.9059	KIAA0962 protein			11.00		
	117023	AW070211	Hs.102415	ESTs			91.00		
	117027	AW085208	Hs.130093	ESTs	49.40				
	117036	H88908	Hs.41192	EST			32.60		
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs			30.60		
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
	117543	BE219453	Hs.42722	ESTs		16.00			
35	117567	AW444761	Hs.44565	ESTs				12.00	
	117570	N48649	Hs.44583	ESTs				11.00	
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
	117791	N48325	Hs.93956	EST		9.00			
40	117929	N51075	Hs.47191	ESTs			29.20		
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN		2.40			
	118446	N66361	Hs.269121	ESTs		2.28			
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein			33.00		
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi			52.60		
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
60	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB			33.80		
	119889	W84346	Hs.58671	ESTs			30.03		
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)			36.60		
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs				8.00	
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein			46.60		
	121082	AA398722		ESTs			39.00		
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
	121363	AI287280	Hs.97933	ESTs				12.00	
75	121366	AI743515		ESTs			20.00		
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs			30.20		
	121545	AA412442	Hs.98132	ESTs		2.29			
	121622	AA416931	Hs.126065	ESTs		9.00			
80	121665	AA416556	Hs.98234	ESTs			34.80		
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

	121835	AB033030	Hs.300670	ESTs	2.34				
	121841	AA427794	Hs.104864	ESTs	2.61				
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428559	Hs.98610	ESTs		46.80			
	121950	AA429515		EST		31.40			
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98745	EST				3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST		39.80			
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
	122285	AA436981	Hs.121602	EST				3.14	
15	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemman		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
20	122831	AI857570	Hs.5120	ESTs				3.37	
	122913	AI638774	Hs.105328	ESTs		32.20			
	123049	BE047680	Hs.211869	ESTs		41.80			
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
25	123309	N52937	Hs.102679	ESTs			19.00		
	123455	AA353113	Hs.112497	ESTs		82.80			
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00				
30	123837	AI807243	Hs.112893	ESTs		32.40			
	123844	AA938905	Hs.120017	olfactory receptor, family 7; subfamily		2.63			
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR		70.60			
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs		13.00			
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs		29.40			
	124348	AI796320	Hs.10299	ESTs	17.00				
40	124358	AW070211	Hs.102415	^yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs		30.80			
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph				6.03	
45	124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO		2.50			
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs		37.60			
	125097	AW576389	Hs.335774	ESTs		10.00			
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs				2.79	
	125299	T32982	Hs.102720	ESTs		34.20			
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
55	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00			
	126303	D78841		HUM525A05B Human placenta polyA+ (Tfu)		33.60			
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu		29.80			
	126773	AA648284	Hs.187584	ESTs	39.60				
60	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypotetica	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c		34.40			
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs		29.40			
65	127832	AW976035	Hs.292396	ESTs		37.20			
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs		38.40			
	128101	AA905730	Hs.128254	ESTs	7.33				
	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3)-glycoprotein beta-				2.58	
70	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)		3.09			
	128333	W68800	Hs.12126	ESTs; Weakly similar to LR6 [H.sapiens]		34.40			
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to !!!! ALU SUB		41.60			
	128687	AW271273	Hs.23767	ESTs		87.00			
	128726	AI311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp		9.00			
	128833	W26667	Hs.184581	ESTs				3.76	
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10683	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)		11.00			
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
85	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-11B (h11B3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.11154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement					
	129958	R27496	Hs.1378	annexin A3		87.80			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque		44.60			
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr	2.72				
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		42.20			
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr	2.54				
	130312	AF056195	Hs.15430	DKFZP586G1219 protein		51.60			
	130436	NM_001928	Hs.155597	D component of complement (adipsin)				3.16	
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0758 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfam				3.14	
	131179	AA171388	Hs.184482	DKFZP586D0624 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f				4.03	
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	H15205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs	45.80				
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28				
	131717	X94630	Hs.3107	CD97 antigen					3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein				3.48	
	131861	AL096858	Hs.184245	KIAA0929 protein Msx2 Interacting nuclea	54.00				
55	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrima profile rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2	2.66				
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
	133129	AA428580	Hs.65551	ESTs					5.49
70	133147	AA026533	Hs.66	Interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
75	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74802	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f				3.27	
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80			

	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134677	AA251363	Hs.177711	ESTs		32.20		
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00			
	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05		
5	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki		57.80		
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333383	ficollin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs		31.60		
	135053	AW796190	Hs.93678	ESTs			3.21	
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate	8.00			
	135203	C15737	Hs.269386	ESTs			4.31	
	135236	AI636208	Hs.96901	ESTs	43.00			
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd			6.42	
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
	135388	W27965	Hs.99865	EST	38.80			
20	135402	L12398	Hs.99922	dopamine receptor D4			4.21	

TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108447	43452_7	AA079126
108550	120073_1	AA084867 AA084996
108655	127522_1	AA099960 AA113013
102397	44371_1	U41898
126303	1525933_1	D78841 D78880
125810	1554054_1	H00083 R81062
103627	2615_2	Z48513 Z48512
121366	280401_1	AI743515 AA405617 AW276706
114509	116777_1	AA079505 AA079537
115272	172113_1	AW015947 AA211890 AA279425
108338	112186_1	AA070773 AA070774
108434	114012_1	AA078899 AA078782 AA075788
123802	genbank_AA620448	AA620448
102310	NOT_FOUND_entrez_U33839	U33839
102636	entrez_U67092 U67092	
104776	genbank_AA026349	AA026349
120504	genbank_AA256837	AA256837
113502	genbank_T89130T89130	
108499	genbank_AA083103	AA083103
101308	entrez_L41390 L41390	
108629	genbank_AA102425	AA102425
103098	221_215	M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
103241	entrez_X76223 X76223	
103508	entrez_Y10141 Y10141	
103575	entrez_Z26256 Z26256	
119514	NOT_FOUND_entrez_W37937 W37937	
121082	genbank_AA398722	AA398722
128534	AA464918_at	AA464918
105817	genbank_AA397825	AA397825
121518	genbank_AA412155	AA412155
114449	genbank_AA020736	AA020736
114648	genbank_AA101056	AA101056
121950	genbank_AA429515	AA429515
107723	genbank_AA015967	AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigenelD:	Unigene number					
	Unigene Title:	Unigene gene title					
10	R1:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.					
	R2:	80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas					
	R3:	70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples					
15							
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
20	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
25	134951	BE305081	Hs.169358	hypothetical protein		8.00	
	134799	M36821	Hs.89690	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
	134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8861	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
35	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor			
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
	134182	D52059	Hs.7972	KIAA0871 protein	12.20		
45	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
	133978	AF035718	Hs.78061	transcription factor 21			
	133835	AI677897	Hs.76640	RGC32 protein			
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and colled-body phosphprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
	133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
	133488	AA335295	Hs.74120	adipose specific 2			
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
55	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
60	132836	AB023177	Hs.29900	KIAA0960 protein			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
65	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		
	131751	T96555	Hs.31562	ESTs			1.76
70	131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		
	131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
	131676	AI126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2			
	131536	AA019201	Hs.269210	ESTs		9.40	
	131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
	131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
80	131207	AF104266	Hs.24212	latrophilin			1.75
	131156	AI472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			
	131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
85	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
	130762	D84371	Hs.1898	para-oxonase 1	12.00		

	130657	AW337575	Hs.201591	ESTs		
	130655	AJ831952	Hs.17409	cysteine-rich protein 1 (intestinal)		
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled		1.91
	130555	R69743	Hs.116774	Integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr		6.60
	130259	NM_000328	Hs.153614	refinitis pigmentosa GTPase regulator		1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas		
15	129626	F13272	Hs.111334	ferritin, light polypeptide		
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20	
20	129402	W72062	Hs.11112	ESTs		2.11
	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, lata	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95
25	129210	AL039940	Hs.202949	KIAA1102 protein		
	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol		4.20
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
30	128789	AW368576	Hs.139851	caveolin 2		2.24
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51
35	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00	
	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00
	128458	H55864	Hs.56340	ESTs		
40	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
45	127896	AI669586	Hs.222194	ESTs		7.00
	127859	AA761802	Hs.291559	ESTs	14.00	
	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
50	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	OnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csq2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K		4.67
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13		3.50
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40568	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	H04043		gb:yy45c03.r1 Soares placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
85	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AM22996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidy)		10.60
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
	124578	N58321	Hs.231500	EST	21.43	
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yy37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
	123936	NM_004673	Hs.241519	angiopoietin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
30	123073	AA485061	Hs.105652	ESTs	31.20	
	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs	3.60	
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:z174e03.r1 Soares_testis_NHT Homo sap	14.80	
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST		7.20
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
65	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	trypsin beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis	10.00	
	118901	AW292577	Hs.94445	ESTs	3.96	
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	9.60	
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21339 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_	6.60	
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s	3.80	
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037748	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST		5.00
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence	4.00	
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	20.20	2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen			
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI508657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human			
	116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhml2 protein	18.60		
	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	19.40		
10	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	AI373052	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs		2.00	
40	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN IIII			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI554223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
	113502	T69130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
50	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yp74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.50		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91081	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HTO18 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4		1.75	
	110576	H00659	Hs.37889	ESTs	13.00		
	110369	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothe		3.91	
	109796	A1800515	Hs.12024	ESTs		17.20	
	109688	R41900	Hs.22245	ESTs		9.60	
5	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs		1.89	
	109472	AK001989	Hs.91165	hypothetical protein		6.00	
10	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypothe	11.00		
15	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434i0428			
	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str		1.83	
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp554G112 (fr		3.60	
20	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	A1797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
25	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
30	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
35	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase		1.76	
	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
40	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
	106797	A1768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL		2.05	
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
45	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		2.40	
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5		1.78	
	106562	AL031846	Hs.152151	plakophilin 4		1.76	
50	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot		2.19	
	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
55	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying		1.94	
	105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-		1.75	
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm		2.47	
60	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
65	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
70	104825	AA035613	Hs.141883	ESTs		1.87	
	104781	AA099904	Hs.21610	DKFZP434B203 protein		1.93	
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH	10.20		
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone	4.20		
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein		1.91	
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD		1.80	
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
85	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

5	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		1.76
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		2.15
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		
	102698	M18657	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	A198550	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00
	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
30	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00
40	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24
	100351	D64158				6.20
	100299	D49493				21.20
	100134	AA305746	Hs.2171	growth differentiation factor 10		
	100108	U09577	Hs.49	macrophage scavenger receptor 1		
45	100095	Z97171	Hs.76873	hyaluronoglucosaminidase 2		1.79
	100066		Hs.78454	myocilin, trabecular meshwork inducible	5.40	
					11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
125831	1522905_1	H04043 D60988 D60337
126816	122973_1	AA248234 AA090985
65	126852	136135_1 AA399961 AA128347
	121059	273450_1 AA393283 AA398628
	120637	200885_1 AA811804 AA809404 AA286907 AW977624
	122011	7617_2 AA431082
70	120934	177521_1 AA226198 AA226513 AA383773
	123802	genbank_AA620448 AA620448
	116814	genbank_H50834 H50834
	118329	genbank_N63520 N63520
	104404	H58762_at H58762
75	104776	genbank_AA026349 AA026349
	113502	genbank_T89130 T89130
	101262	entrez_L35854 L35854
	108573	genbank_AA086005 AA086005
	101447	entrez_M21305 M21305
80	124357	genbank_N22401 N22401
	108781	genbank_AA128654 AA128654
	112794	genbank_R97018 R97018
	100351	entrez_D64158 D64158
85	100555	tigr_HT2245 M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigeneID	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	AH58623		gb:tk04g09.x1 NCL CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.86849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	AI989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AL050097	Hs.272531	DKFZP58680319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
40	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:nc97c02.s1 NCI_CGAP_Pr2 Homo sapiens	28.80
	124008	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
50	124839	R55784	Hs.140942	ESTs	21.20
	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

5	130149	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase domain	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4859	cyclin L anti-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
35	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
45	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
40	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
55	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				4.69
	101045	J05614		gb:Human proliferating cell nuclear anti					4.19
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
60	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	oploid receptor, mu 1			6.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
70	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (comifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
80	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
85	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

	101695	M69136	Hs.135626	chymase 1, mast cell	4.79		
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21		
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50		
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino		18.57	4.10
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant			
	101804	M86699	Hs.169840	TTK protein kinase	4.50		
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00		
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56		
10	101842	M93221	Hs.75182	mannose receptor, C type 1		12.80	
	101851	BE260964	Hs.82045	midkine (neurotrophin growth-promoting factor			5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80		
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)	7.40		
15	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12
	102111	L36198	Hs.81884	sulfotransferase family, cytosolic, 2A,		12.00	
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20		
	102154	U17760	Hs.75517	laminin, beta 3 (nclecin (125kD), kallinin	2.62		
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85		
20	102217	AA829978	Hs.301613	JTV1 gene			6.18
	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50		
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15
25	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro		9.33	
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87		
	102368	U39817	Hs.36820	Bloom syndrome	15.91		
30	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20	
	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family			12.00
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50		
	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50		
	102642	AA205847	Hs.23016	G protein-coupled receptor		22.00	
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence	12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50		
40	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50		
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24
	102696	BE540274	Hs.239	forkhead box M1			5.54
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60		
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78
45	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat			4.26
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H		14.40	
	102829	NM_006183	Hs.80962	neurotensin	8.00		
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70	
50	102913	NM_002275	Hs.80342	keratin 15	4.64		
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93		
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol		11.40	
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01		
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90		
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro	9.80		
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05		
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07		
	103185	NM_008825	Hs.74388	transmembrane protein (63kD), endoplasm			5.62
	103192	M22440	Hs.170009	transforming growth factor, alpha	7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00	
65	103316	X83301	Hs.324728	SMA5			9.80
	103375	NM_006982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71		
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00		
	103385	NM_007069	Hs.37189	similar to rat HREV107			11.00
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93		
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98
	103446	X98834	Hs.79971	sal (Drosophila)-like 2		21.40	
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive	13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40	
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02		
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50		
	103558	BE616547	Hs.2785	keratin 17	6.41		
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84
	103587	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	78.50		
80	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51		
	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50		
	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00		
	103847	AF219946	Hs.102237	tubby super-family protein	10.40		
85	103913	AW967500	Hs.133543	ESTs			15.60
	104094	AA418187	Hs.330515	ESTs	6.60		

	104150	AL122044	Hs.331633	hypothetical protein DKFZp556N034		26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80		3.98
	104261	AW248364	Hs.5409	RNA polymerase I subunit			
	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80		
5	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29		
	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21		
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		15.79	
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H		17.40	
10	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp554D016 (fr	6.40		6.55
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr			
	104754	AI206234	Hs.155924	cAMP responsive element modulator		10.00	
	104758	BE560269	Hs.7010	NPD002 protein			4.47
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87		
	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83		
15	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.85		
	105026	AA609485	Hs.124219	hypothetical protein FLJ12934	11.00		
	105076	AI598252	Hs.37810	hypothetical protein MGC14833			5.01
	105132	AA148164	Hs.247280	HBV associated factor			3.99
20	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti		11.00	
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00		
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32		
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00		
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi		10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69		9.20
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8			
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80	
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12		
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82		
30	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00	
	105848	AW954054	Hs.24951	ESTs		7.60	
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha			4.14
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80	
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40	
35	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50		
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00		
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439			3.95
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36			6.04
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20	
40	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso			5.02
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 [6.60		
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa			5.04
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced			7.25
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80	
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75		
	106586	AA243837	Hs.57787	ESTs		10.84	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp556B076 (fr		45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00		
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00		
50	106813	C05766	Hs.181022	CGI-07 protein		11.40	
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00	
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56		
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S			4.27
	107054	AI076459	Hs.15978	KIAA1272 protein		34.80	
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71		
	107098	AI823593	Hs.27688	ESTs		24.80	
	107104	AI076640	Hs.15243	nucleolar protein 1 (120kD)			7.05
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20	
60	107203	D20426	Hs.41639	programmed cell death 2		7.60	
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50		
	107284	NM_005529	Hs.187958	solute carrier family 6 (neurotransmitte	2.71		
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71	
	107516	X57152	Hs.99853	fibrillarin			4.33
65	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)			4.00
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80		
	107851	AA022953	Hs.61172	EST		8.00	
	107901	L42612	Hs.335952	keratin 6B	3.40		
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88		
70	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50		
	108015	AW298357	Hs.49927	protein kinase NYD-SP15			23.40
	108056	AA043675	Hs.62633	ESTs			12.80
	108075	AI667370	Hs.139709	hypothetical protein FLJ12572			12.80
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00		
75	108296	N31256	Hs.161623	ESTs	6.60		
	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937			11.80
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer			11.80
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			20.80
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40		
80	108573	AA086005		gb:z184c04.s1 Stratagene colon (937204)			25.40
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60		
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285			14.60
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00		
	108699	AA121514	Hs.70832	ESTs			10.00
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00	
85	108780	AI076442	Hs.117938	collagen, type XVII, alpha 1	11.21		

	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
	108860	AA133334	Hs.129911	ESTs	6.09			
5	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bl	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines)	10.58			
	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
10	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AI866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-II		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
	109543	AA564994	Hs.222851	ESTs		12.67		
15	109648	H17800	Hs.7154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12876	ESTs		11.00		
	109792	R49625		gb:yg61f03.s1 Soares infant brain 1N1B H			12.60	
20	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
	110500	AA907723	Hs.36962	ESTs	4.50			
25	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
	110916	BE178102	Hs.24349	ESTs		6.80		
30	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837398	Hs.263925	US1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
35	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence	6.80			
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
	112054	R43590		gb:yc85g02.s1 Soares infant brain 1N1B H	10.80			
40	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1N1B H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	3.00			
45	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin			4.83	
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
	113984	R96696	Hs.35598	ESTs		7.80		
60	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
	114313	H18456	Hs.27946	ESTs			10.00	
65	114339	AA782845	Hs.22790	ESTs		7.80		
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f			4.14	
	114560	AI452469	Hs.165221	ESTs			9.80	
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
70	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31	
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3			4.03	
	115097	AA256213	Hs.72010	ESTs			35.40	
75	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m			4.19	
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
85	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			
	115793	AA424883	Hs.70333	hypothetical protein MGC10753			11.80	
5	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL			9.71	
	115892	AA291377	Hs.50831	ESTs		27.40		
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53			
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			34.29	
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g				8.23
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00			
	116090	AI591147	Hs.61232	ESTs	5.17			
	116096	AA682382	Hs.59982	ESTs		8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60		
15	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17			5.82	
	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypothet			4.08	
	116278	NM_003686	Hs.47504	exonuclease 1	9.50			
	116335	AK001100	Hs.41690	desmocollin 3	3.67			
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		
20	116503	AI925316	Hs.212617	ESTs			12.60	
	116674	AI768015	Hs.92127	ESTs		32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp	7.60			
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F	9.80			
	116993	AI417023	Hs.40478	ESTs			10.20	
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo			15.20	
	117317	AI263517	Hs.43322	ESTs			13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,			20.60	
	117396	W20128	Hs.296039	ESTs			10.60	
	117412	N32535	Hs.42645	ESTs			16.00	
30	117519	N32528	Hs.146286	kinesin family member 13A			9.11	
	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42				4.01
	117721	N46100	Hs.93939	EST			19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71			
	117903	AA768283	Hs.47111	ESTs			17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f				4.17
	118013	AI674126	Hs.94031	ESTs			10.60	
	118017	AI813444	Hs.42197	ESTs		8.82		
	118186	N22886	Hs.42380	ESTs		7.00		
40	118325	AI868065	Hs.166184	intersectin 2			13.80	
	118367	N64269	Hs.48946	EST		6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14			
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3		12.40		
	118709	AA232970	Hs.293774	ESTs			12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50			
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22			
	119052	R10889		gb:yl38d02.s1 Soares fetal liver spleen		9.60		
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome		6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593			10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa			9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot			11.80	
	119499	AI918906	Hs.55080	ESTs			14.80	
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00			
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50			
55	119941	AA699485	Hs.58896	ESTs		8.00		
	119994	AA642402	Hs.59142	ESTs	7.73			
	120102	W67353	Hs.170218	KIAA0251 protein			39.60	
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91			
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par		8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73			
	120599	AA804448	Hs.104463	ESTs		7.00		
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos			10.00	
	120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens		9.40		
65	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein			13.80	
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00		
	120880	AA360240	Hs.97019	EST		15.60		
	120983	AA398209	Hs.97587	EST			27.66	
	121034	AL389951	Hs.271623	nucleoporin 50kD			20.80	
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80		
70	121313	AA402713	Hs.97872	ESTs			10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71			
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte			5.42	
	121476	AA412311	Hs.97903	ESTs		8.30		
	121509	AA868939	Hs.97888	ESTs		8.59		
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50			
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00			
	121838	AA425680	Hs.98441	ESTs			10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			
	121991	AA430058	Hs.98649	EST			12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32		8.60		
	122105	AW241685	Hs.98699	ESTs		6.14		
	122163	AA435702	Hs.98829	EST			10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap			18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50			
	122338	AA443311	Hs.98998	ESTs	4.80			
85	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00		

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
	122852	AI580056	Hs.98992	ESTs		10.40	
5	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypothe		6.06	
10	123315	AA496369		gbzv37d10.s1 Soares ovary tumor NbHOT H		12.40	
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
	123614	AK000492	Hs.98806	hypothetical protein		7.80	
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L			10.60
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma		9.80	
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST			12.80
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha			35.80
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f			11.00
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo			16.00
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)			6.08
	124874	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog			21.00
30	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs			10.80
	125000	T58615	Hs.110640	ESTs			9.80
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
35	125299	T32982	Hs.102720	ESTs			9.57
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC			14.00
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs			13.20
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225			11.20
	125756	BE174587	Hs.289721	growth arrest specific transcript 5			4.31
	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass			15.60
45	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1N1B H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1			4.23
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein			3.98
	126034	H50340		gb:yr39b04.r1 Soares fetal liver spleen			10.60
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein			10.60
	126487	AA263809	Hs.184601	solute carrier family 7 (cationic amino			4.38
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi			14.80
	126543	AL035664	Hs.69517	cDNA for differentially expressed CO16 g			4.01
60	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_			11.60
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392			14.60
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs			22.83
	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937			11.80
70	126986	AI279892	Hs.46801	sorting nexin 14			11.60
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s			20.80
	127066	R25066		gb:yg42c07.r1 Soares Infant brain 1N1B H			27.60
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens			21.60
	127139	AA830233	Hs.293585	ESTs			11.20
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs			16.80
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,			13.60
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin		7.80	
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs			13.80
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			28.00
	127662	W80755	Hs.8294	KIAA0196 gene product			19.80
85	127668	AI343257	Hs.139993	ESTs			11.20

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836641	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
	128077	AI310330	Hs.128720	ESTs			9.60
10	128168	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9			10.00
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	16.80		
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
-25	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
30	129229	AF013758	Hs.109543	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
35	129466	L42583	Hs.334309	keratin 6A	12.94		
	129494	AI148976	Hs.112062	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
40	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12152	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56		
45	129945	BE514376	Hs.165998	PAI-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nuclear phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
	130149	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	2.74		
50	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (UBP1-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
55	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_00101072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (crotal			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
	131031	NM_001650	Hs.288650	aquaporin 4			9.80
70	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
75	131185	BE280074	Hs.23950	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00			
	131885	BE502341	Hs.3402	ESTs	6.48			
	131921	AA456093	Hs.34720	ESTs		8.40		
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00			
	131958	NM_014062	Hs.3556	ART-4 protein			3.82	
	131965	W79283	Hs.35962	ESTs	3.03			
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80		
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30			
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00			
	132114	NM_005152	Hs.40202	lymphoid-restricted membrane protein		8.40		
	132162	AA315805	Hs.94560	desmoglein 2			12.25	
	132164	A1752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70			
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71			
15	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83			
	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20	
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50			
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50			
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20	
20	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80	
	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60		
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40		
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38			
	132544	L19778	Hs.51011	H2A histone family, member P		7.00		
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64			
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60		
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95			
	132638	A1795870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20		
30	132653	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	4.38			
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36	
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60			
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48	
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83	
	132892	AW834050	Hs.9973	tensin			12.00	
	132906	BE613337	Hs.234896	geminin	3.09			
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87	
	132962	AA576635	Hs.6153	CGI-48 protein	3.50			
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18			
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19			
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.95			
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55			
	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00	
45	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96	
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28	
	133155	M58593	Hs.662	cerebellin 1 precursor			10.80	
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00			
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63	
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50		
	133421	AF134160	Hs.7327	claudin 1	2.85			
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p		6.80		
	133453	A1659306	Hs.73826	protein tyrosine phosphatase, non-recept			4.66	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14			
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55	
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80	
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85	
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34	
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00	
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11		
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07			
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60	
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00	
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85	
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56			
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20		
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08	
	134158	U15174	Hs.79428	BCI2/adenovirus E1B 19kD-interacting pro	31.00			
70	134160	T98152	Hs.79432	fibrillin 2 (congenital contractural ara		24.60		
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71	
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74	
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40		
	134272	X76040	Hs.278614	protease, serine, 15	4.50			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00		
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40	
	134387	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80			
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68			
	134423	H53497	Hs.83006	CGI-139 protein			3.84	
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81	
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21	
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30	
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60		
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70	
	134548	N95406	Hs.333495	Deleted in split-hands/split-foot 1 regio			4.63	
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00			

5	134724	AF045239	Hs.321576	ring finger protein 22		12.00
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00	
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20
	134806	AD001528	Hs.89718	spermine synthase		4.58
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle		4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20
	134891	R51083	Hs.90787	ESTs		7.40
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00	
	134993	BE409809	Hs.301005	purine-rich element binding protein B		4.48
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50	
	135080	AI761180	Hs.94211	rcd1 (required for cell differentiation,	5.00	
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin		4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00
	135242	AI583187	Hs.9700	cyclin E1	13.50	
	135286	AW023482	Hs.97849	ESTs	6.46	
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00	
	135371	NM_006025	Hs.997	protease, serine, 22	8.00	
20	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H66077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
50	114699	135322_1 AA127386 R15644 AA127404
	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA074946
	100867	ligr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AH167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI561350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193557 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
70		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516681 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI027663 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI886186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI685624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241680 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AJ004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 A1940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849
 A1288629 AA843996 W15260 A1188286 AW248079 R15836

119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA495369 AA496646

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59580 probesets on the Eos/Alfymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)		2.68
101972	S82472		gb:bela -pol-DNA polymerase beta (exon a		2.11
102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
102832	U92015		gb:Human clone 143789 defective mariner	13.50	
103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
103439	X98266		gb:H.sapiens mRNA for ligase like protal		2.50
103563	L02911	Hs.150402	activin A receptor, type I	9.00	
103857	A1076795	Hs.45033	lacrima proline rich protein		3.94
104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
106131	BE514788	Hs.296244	SNARE protein		2.17
106672	H47233	Hs.30643	ESTs	7.00	
106872	T56887	Hs.18282	KIAA1134 protein	11.50	
106960	AA156238	Hs.32501	ESTs		2.38
106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp43401572 (f	9.50	
107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protal		2.95
108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
108599	AB018549	Hs.69328	MD-2 protein	13.00	
108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
109247	AA314907	Hs.85950	ESTs	7.00	
109630	R44607	Hs.22672	ESTs		6.00
110193	A1004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
110234	H24458	Hs.32085	EST	16.50	
110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
111057	T79639	Hs.14629	ESTs	16.50	
111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
112291	R53972	Hs.26026	ESTs		3.00
112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
113009	T23699	Hs.7246	ESTs		4.50
113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
113121	T48011	Hs.8764	EST		2.21
113125	AA958672	Hs.8929	hypothetical protein FLJ11362	19.50	
113757	AA703095	Hs.18631	ESTs		2.65
113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
113884	A1333076	Hs.28529	chromosome 12 open reading frame 2		6.00
113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
114987	AA251016	Hs.87808	EST		6.00
115460	AW958439	Hs.38613	ESTs		2.27
115722	W91892	Hs.59609	ESTs		9.00
116261	AA481788	Hs.190150	ESTs	9.50	
116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
117178	H98675	Hs.269034	ESTs		2.68
117757	AF088019	Hs.46732	EST	7.50	
118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
118657	A1822106	Hs.49902	ESTs		2.39
120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
120524	AA261852	Hs.192905	ESTs	6.00	
120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 f1s, clone L	17.92	

	121558	AA412497	gb:z195g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146	ESTs	10.00
	121936	AI024600	Hs.98612	ESTs	15.00
5	121938	AA428659	Hs.98610	ESTs	14.00
	122177	AA435789	Hs.98833	EST	8.93
	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap		11.50
	123756	AA609971	Hs.112795	EST	11.00
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601	ESTs	6.50
	127477	BE328720	Hs.280651	ESTs	4.33
	127591	AI190540	Hs.131092	ESTs	3.02
	128252	AA455924	Hs.192228	ESTs	7.00
	128426	AI265784	Hs.145197	ESTs	2.08
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	2.11
	128945	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50
	129235	AW977238	Hs.126084	KIAA1055 protein	4.25
	129506	AB020684	Hs.11217	KIAA0877 protein	6.50
20	129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	10.00
	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00
	130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi	11.50
	131220	AB023194	Hs.300855	KIAA0977 protein	17.50
	131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10
25	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.15
	132458	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	5.58
	132647	NM_006927	Hs.54432	sialyltransferase 4B (beta-galactosidase	7.50
	132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.53
	132682	AI077500	Hs.54900	serologically defined colon cancer antig	2.50
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	2.83
	132812	R50333	Hs.92186	Leman coiled-coil protein	3.82
	133337	AF085983	Hs.293676	ESTs	5.00
	133876	AL134908	Hs.771	phosphorylase, glycogen; liver (Hers dis	3.00
	134119	AW157837	Hs.79226	fasciculation and elongation protein zet	2.06
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit	2.27
	134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	11.50
	135002	AA448542	Hs.251677	G antigen 7B	87.00
	135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL	6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigenelD:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.				
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.				
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
	101046	K01160		(NONE)	672.00	
20	101066	AW970254	Hs.889	Charot-Leyden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	185.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialyltransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (lazar	67.00	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	sympleklin; Huntinglin interacting protei		58.80
	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	casein, alpha		130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
45	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5648076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
	109691	T65568	Hs.12860	ESTs		58.70
55	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80	
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
70	118466	N66741		gb:yz33g08.s1 Morton Fetal Cochlea Homo		63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983	AA398209	Hs.97587	EST		81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
	121423	AW973352	Hs.290585	ESTs	64.40	
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
	124472	N52517	Hs.102670	EST	71.00	
	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci		104.80
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
	126020	H79863	Hs.114243	ESTs		62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
	127987	AI022103	Hs.124511	ESTs	96.60	
5	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
15	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
20	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 protein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
25	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI584123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
40	103207	30635_4	X72790
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
45	116571	genbank_D45652	D45652
	118466	genbank_N66741	N66741
	101046	entrez_K01160 K01160	
	101941	entrez_S77583 S77583	
	103351	entrez_X89211 X89211	
50	123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Arraymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
15	300097	AI916973	Hs.213603	ESTs	5.46	4.69
	300117	AW189787	Hs.147474	ESTs	0.58	0.56
	300197	AI686661	Hs.218286	ESTs	4.26	5.44
	300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
	300225	AI989963	Hs.197505	ESTs	1.68	1.75
20	300247	AW274682	Hs.161394	ESTs	1.08	2.28
	300258	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
	300337	AI707881	Hs.202090	ESTs	5.80	9.09
	300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
	300374	AI859947	Hs.314158	ESTs	2.99	4.38
25	300387	AW270150	Hs.254516	ESTs	1.50	2.53
	300440	AI421541	Hs.146164	ESTs	3.98	5.25
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
	300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
	300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
	300630	AW118822	Hs.128757	ESTs	2.91	5.86
	300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
	300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
	300790	AI492471	Hs.188270	ESTs	1.29	1.18
	300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
40	300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
	300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
	300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
	300960	AI041019	Hs.152454	ESTs	2.74	4.46
	300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
45	300962	AA593373	Hs.293744	ESTs	1.46	1.51
	300967	AA565209	Hs.269439	ESTs	0.39	1.30
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
	300988	AI927208	Hs.208952	ESTs	0.16	0.37
	301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen I	3.23	1.94
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28
	301157	AA729905	Hs.231916	ESTs	3.16	8.85
	301162	AI142118	Hs.129004	ESTs	1.68	7.18
	301170	AA737594	Hs.247606	ESTs	4.40	6.42
	301192	AI808751	Hs.121188	ESTs	6.38	11.59
55	301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
	301267	AW297762	Hs.255690	ESTs	1.56	1.61
	301281	AA843986	Hs.190586	ESTs	2.19	1.78
	301341	AI819198	Hs.208229	ESTs	0.76	0.76
	301382	AA912839	Hs.163369	ESTs	1.00	1.81
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51
	301452	AA975688	Hs.159955	ESTs	0.51	1.46
	301483	AW272467	Hs.254655	Untitled	2.40	5.02
	301494	AI678034	Hs.131099	ESTs	2.79	3.41
	301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
65	301531	AI077462	Hs.134084	ESTs	2.52	3.76
	301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
	301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
	301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
75	301882	T78054		gb:yc97g09.r1 Soares infant brain 1N18 H	2.28	3.80
	301905	AI991127	Hs.117202	ESTs	1.00	1.00
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
	302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
	302094	AI286176	Hs.6786	ESTs	0.52	1.20
	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
85	302148	AW269618	Hs.23244	ESTs	3.04	3.87

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal-betaGlcNAc beta 1,4-galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucln 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U06751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
15	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine-a-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
20	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
	302476	AF182234	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
30	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
50	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFV antibody	1.41	1.86
	303013	F07898	Hs.288958	RAB22A, member RAS oncogene family	1.51	1.19
55	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	0.72	0.76
	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	OC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis 1 Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.08	11.86
	303978	AW513315		gb:xa43c12.x1 NCL_CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xa71a11.x1 NCL_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCL_CGAP_U12 Homo sapiens	2.20	9.35
85	303999	AW516611		gb:xp70b11.x1 NCL_CGAP_Ov39 Homo sapiens	4.85	6.28
	304006	AW517947		gb:xt66h02.x1 NCL_CGAP_U12 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yl87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1N1B H	1.00	2.76
	304155	H68696		gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	fertilin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nm13g09.s1 NCI_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588167	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304966	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nl01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GC80 Homo sapiens4.9	8.71	8.71
	305680	AA813477		gb:ai67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA854374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1.56	5.21	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	1.96	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306065	AA906725		gb:ok78g02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:og35e09.s1 NCI_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:og72e12.s1 NCI_CGAP_Kid6 Homo sapiens	3.92	6.27

5	306458	AA978186		gbxp33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA98546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA995248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h08.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:xp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290295		gb:xqm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:lb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:ql43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:ql27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:qt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:qt09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:qt19a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:xq20g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:jt77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38	1.30	8.72
65	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_U12 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (K1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosin	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:lr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:al48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AJ832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AJ833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.05	2.65
	308898	AJ858845		gb:w32d10.x1 NCI_CGAP_U11 Homo sapiens	2.45	3.44
5	308934	AJ855023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
	308966	AJ870704		gb:w47h01.x1 NCI_CGAP_U11 Homo sapiens	1.00	1.00
	308979	AJ873111		gb:w52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AJ910902		gb:tq39f01.x1 NCI_CGAP_U11 Homo sapiens	0.61	0.59
	309051	AJ911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AJ917366	Hs.78202	SW/SNF related, matrix associated, act	3.27	5.88
	309083	AJ922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AJ925503	Hs.265884	ESTs	5.54	17.78
	309122	AJ928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
	309128	AJ928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AJ937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
	309177	AJ951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AJ991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_U14 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
25	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
	309532	AW151119		gb:xg33e10.x1 NCI_CGAP_U11 Homo sapiens	1.18	4.40
	309526	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309856	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
40	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_U12 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AJ439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AJ685841	Hs.161354	ESTs	0.31	0.76
	310109	AJ203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AJ611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	AJ206614	Hs.197422	ESTs	9.50	15.31
	310193	AJ627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AJ240483	Hs.201217	ESTs	3.28	4.40
	310264	AJ915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AJ242102	Hs.213636	ESTs	5.43	8.19
	310282	AJ243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
60	310333	AJ253200	Hs.145402	ESTs	1.17	1.91
	310346	AJ261340	Hs.145517	ESTs	4.81	9.95
	310385	AJ263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AJ275715	Hs.145926	ESTs	2.18	3.85
	310468	AJ984074	Hs.196398	ESTs	3.39	5.19
	310477	AJ948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AJ681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AJ302654	Hs.208024	ESTs	3.26	3.46
	310584	AJ653007	Hs.156304	ESTs	2.39	4.08
	310608	AJ962234	Hs.196102	ESTs	5.60	6.49
	310624	AJ341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AJ814373	Hs.164175	ESTs	1.85	1.71
	310648	AJ347863	Hs.156672	ESTs	0.17	0.69
	310694	AJ654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AJ472124	Hs.157757	ESTs	4.82	6.27
	310714	AJ418446	Hs.157882	ESTs	1.76	3.51
80	310722	AJ989803	Hs.157289	ESTs	1.14	6.85
	310756	AJ916560	Hs.158707	ESTs	8.46	13.01
	310764	AJ376769	Hs.167172	ESTs	4.76	7.37
	310848	AJ459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AJ421677	Hs.161332	ESTs	6.37	7.94
	310858	AJ871000	Hs.161330	ESTs	6.07	9.84

	310864	AI924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AI560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AI990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	peritaxdn	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
15	311220	AI656040	Hs.196532	ESTs	1.10	2.52
	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	AI653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AI671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
	311420	AI936291	Hs.209867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
30	311479	AI933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfatpin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AI805121	Hs.211828	ESTs	3.69	5.85
	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450575	Hs.212709	ESTs	1.00	1.00
	311621	AI924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
50	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447		gb:U1-H-B11-afg-g-02-0-U1.s1 NCL_CGAP_Su	1.66	1.13
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AI597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AI382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AI580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
	312097	AI352096	Hs.112180	zinc finger protein 148 (pH2-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89655	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AI052572	Hs.269864	ESTs	2.41	3.32
	312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
85	312252	AI128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.146924	ESTs	1.11	1.00
	312507	AI168177	Hs.143653	ESTs	5.89	8.24
15	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
	312599	AI865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.60	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	AI651930	Hs.135684	ESTs	1.51	2.04
	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekt	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCI_CGAP_AM1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCL_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	ESTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116998	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42		1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgeline-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.66	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
15	315730	H25899	Hs.201591	ESTs	0.11	0.60
	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gbz115a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gbod10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
50	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	AI380429	Hs.172445	ESTs	0.72	1.56
60	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126860	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.46	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH188 HTCCL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T68115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1NIB H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
75	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308288	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
80	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13578	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12577	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.18	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	AI382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
	319523	T69499	Hs.191184	ESTs	1.55	3.25
25	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HT0	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
40	319708	R15372	Hs.22664	ESTs	1.00	1.22
	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
45	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
50	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
55	320007	AA336314		gb:EST40943 Endometrial tumor Homo saple	3.42	6.29
	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	AI699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320066	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	tektin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	AI167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320368	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.38
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436	AA253352	Hs.293563	ESTs	2.22	3.49
	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AJ240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA; cDNA DKFZp554M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folliculin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
20	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb: yq04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
25	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uropod 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
35	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb: yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb: za40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
45	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb: yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
50	321199	AW385512		gb: yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp554B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF058654		gb: Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
55	321270	R83560		gb: yv76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937050	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
60	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb: H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
65	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
	321467	X13075		gb: Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
70	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.08	7.19
	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb: ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
75	321581	AA019964	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb: ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
80	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb: af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI594875	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.00	1.00
5	321777	AI537993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
15	321956	AL110177	Hs.132882	ESTs	0.32	1.25
	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp554O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapia	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341837		gb:qt10a03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gb:y185d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:y188g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:y194c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	AI890619	Hs.179662	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
40	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zl03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
80	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322958	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
85	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	A1733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	A1697556	Hs.292559	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	A1336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18
	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	A1672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	A1652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	A1185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	A1814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
40	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	A1869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	A1472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	A1381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTs	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324312	A1188841	Hs.128173	ESTs	4.06	5.91
70	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	A1924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AL148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.95	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
5	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 lis, clone K	1.68	1.21
10	324886	AA806794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
15	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
	325114	D83901	Hs.315562	ESTs	2.73	3.17
20	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
	325235				2.64	4.12
25	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
	325389				0.88	1.05
30	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
	325559				7.48	21.40
35	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
	325597				2.98	13.40
40	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
	325739				0.59	0.88
45	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
	325895				7.78	15.98
50	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
	325971				4.88	7.42
55	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
	326163				3.27	5.70
60	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
	326274				1.00	8.09
65	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
	326589				9.20	13.49
70	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
	326720				0.19	0.65
75	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
	326964				0.41	1.70
80	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
	327053				3.55	6.31
85	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327606	2.06	3.61
	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
25	327775	1.46	11.79
	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
65	328934	1.73	4.45
	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329057	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	8.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50
	329816			2.09	5.44
	329860			3.13	10.77
5	329993			7.83	14.21
	330020			5.58	13.12
	330036			3.32	5.57
	330052			4.31	7.97
	330085			1.34	1.76
	330088			4.70	12.46
10	330093			0.44	1.06
	330100			3.47	4.83
	330106			2.14	3.61
	330107			3.17	6.87
15	330120			5.61	11.89
	330123			4.50	12.74
	330208			1.55	7.62
	330263			13.10	23.38
	330300			2.81	4.98
	330313			3.00	4.41
20	330366			0.67	0.76
	330372			4.76	11.82
	330385	AA449749	Hs.182971	2.14	2.15
	330397	D14659	Hs.154387	0.40	1.15
25	330468	L10343	Hs.112341	1.11	0.94
	330472	L24203	Hs.82237	1.67	1.17
	330478	L38486	Hs.296049	0.46	1.07
	330493	M27826	Hs.267319	1.07	0.95
	330495	M31328	Hs.71642	0.97	0.96
30	330506	M61906	Hs.6241	0.17	3.66
	330512	M80563	Hs.81256	0.60	1.06
	330537	U19765	Hs.2110	2.81	2.07
	330547	U32989	Hs.183671	3.91	1.49
	330551	U39840	Hs.299867	1.15	1.03
35	330568	U56244		2.83	4.79
	330599	U90437		2.08	1.54
	330601	U90916	Hs.82845	0.89	1.35
	330605	X02419	Hs.77274	1.87	1.55
	330609	X04741	Hs.76118	1.83	1.30
40	330617	X53587	Hs.85266	1.54	1.15
	330630	X78669	Hs.79088	1.39	1.19
	330644	Y07755	Hs.38991	3.83	1.13
	330650	Z68228	Hs.2340	1.25	0.95
	330660	AA347858	Hs.139293	15.50	29.07
45	330692	AA017045	Hs.6702	1.00	1.00
	330707	AA133891	Hs.293690	0.20	1.35
	330715	AA233707	Hs.11571	0.12	1.40
	330717	AA233926	Hs.52620	6.62	5.42
50	330722	AA243560	Hs.34382	1.40	1.65
	330740	AA297746	Hs.22654	0.27	2.04
	330742	AA400979	Hs.25691	0.44	0.90
	330744	AA406142	Hs.12393	0.71	3.23
	330751	AA428286	Hs.29643	1.66	1.52
	330760	AA448663	Hs.30469	0.52	0.90
55	330763	AA450200	Hs.274337	0.37	0.97
	330786	D60374	Hs.49136	0.78	0.84
	330790	T48536	Hs.105807	0.23	3.17
	330814	AA015730	Hs.265398	0.37	2.07
	330827	AA040332	Hs.12744	1.60	1.00
60	330844	AA063037	Hs.66803	0.93	1.16
	330901	AA157818	Hs.267319	1.02	1.03
	330931	F01443	Hs.284256	0.24	0.88
	330952	H02855	Hs.29567	0.08	1.31
	330961	H10998	Hs.7164	1.29	1.26
65	330968	H16568	Hs.23748	0.48	0.96
	331014	H98597	Hs.30340	0.29	0.74
	331046	N66563	Hs.191358	0.99	8.56
	331060	N75081	Hs.157148	1.24	1.00
	331099	R36671	Hs.83937	0.75	1.03
70	331108	R41408	Hs.21983	1.00	2.75
	331131	R54797		6.04	10.68
	331135	R61398	Hs.4197	0.80	0.96
	331170	T23461	Hs.159293	2.63	4.29
	331180	T32446	Hs.6640	1.78	2.71
75	331183	T40769	Hs.8469	1.00	3.01
	331203	T82310		1.70	3.80
	331271	AA059347	Hs.82226	1.20	3.19
	331306	AA252079	Hs.63931	0.31	1.30
	331327	AA281076	Hs.109221	2.09	2.41
	331341	AA303125	Hs.23240	0.72	2.43
80	331359	AA416979	Hs.46901	0.09	0.91
	331363	AA421562	Hs.91011	1.02	0.87
	331378	AA448881	Hs.49282	1.03	1.23
	331384	AA456001	Hs.93847	1.40	1.00
	331402	AA505135	Hs.44037	1.80	3.93
85	331422	F10802	Hs.163628	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:od74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rho-kinase (M.musc)	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl)	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
15	331718	AA191404	Hs.104072	ESTs	6.80	11.77
	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:aa41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
30	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	nectin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	tryptase beta 1	0.51	1.00
50	332504	AA053917	Hs.15108	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
	333260	0.75	1.01
5	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
15	333628	1.90	1.90
	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
35	333966	8.10	14.30
	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
65	335015	5.88	18.65
	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
15	335995	0.37	1.17
	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
	338937	6.55	12.26
25	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 'Accession' column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
322044	187363_1	AW340926 AA249063 N86075
322060	44320_1	AI341937 AW003063 U34725 AA904742
321430	42705_1	X57414 X57415
321467	43034_1	X13075 X13076
322125	46779_1	R93901 AF075073 R93902
322166	46861_1	H69434 AF085958 H69846
322173	46873_1	H52567 H52557 AF085970 H52164
322178	46882_1	H56535 AF085980 H56712
322179	46885_1	H92891 AF085982 H92777
321577	1615102_1	H84849 H84252 H84260 H86664 H85320
321587	1615333_1	H95531 H95521 H84529
313723	111953_1	AA070412 AA102346 AA081885
320997	627492_1	H22544 H46842 AI204929
322278	47271_1	W69304 AF086283 W69200
321687	218439_1	AA625149 AA313030 AA313052 H97463
313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
322320	47422_1	W79150 AF086419
322339	814584_1	AI668646 AI734214 W17348
314648	293660_1	AW979268 AA878419 AA431342 AA431628
300201	682222_1	AI308300 AI308296
306897	25196_-2	AI093967
323155	979809_1	AL120701 AL135041 AL121524
322527	38927_1	AF147359 T58511 T58560
322585	473768_2	W88919 W89125
300362	1574395_1	Z42308 H23514
322635	82296_1	AA005129 AA679084 AA694399
322664	85042_1	AA011522 AA702841 AA011691 AA330797
315454	380580_1	AI239464 AI239473 AA625812 AI208703
322687	37372_1	AF074666 AI110759 AF090902
314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
307783	697809_1	AI347274 AW844024
324072	269032_1	AA381722 AA381829 AW963906 AW963902 AA381242
300527	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
315791	403558_1	AA678177 AA677034
324303	233842_1	AL118754 AA333202 H38001
316519	442885_1	AA847835 AA768376
300926	333127_1	AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909250 AI909259
15	312094	797889_1	Z78390 T97427
	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	AI863140 W80703 R43474
	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
65	308808	AI818289	
	308875	AI832332	
	308886	AI833240	
	308898	AI858846	
	308966	AI870704	
	308979	AI873111	
70	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
	303998	AW516449	
80	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
85	305447	AA737856	
	321244	29327_1	AF068654 AF068656 AF068655

	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
	302679	311853_1	H65022 AA186889
45	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
	302705	31765_1	U09060 U09061
50	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81608	
	304348	AA179868	
	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
	330568	NOT_FOUND_entrez	U56244
80	330599	15323_-12 U90437	
	331131	genbank_RS4797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1 AA828597	N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et al.	Plus	73381-73768
	332816	Dunham, I. et al.	Plus	359844-360030
15	332906	Dunham, I. et al.	Plus	1923101-1923205
	332911	Dunham, I. et al.	Plus	1961767-1961858
	332912	Dunham, I. et al.	Plus	1962120-1962246
	332922	Dunham, I. et al.	Plus	2009620-2009738
	332956	Dunham, I. et al.	Plus	2510528-2510658
20	332959	Dunham, I. et al.	Plus	2518145-2518213
	333138	Dunham, I. et al.	Plus	3369205-3369323
	333139	Dunham, I. et al.	Plus	3369495-3369571
	333221	Dunham, I. et al.	Plus	3978070-3978187
	333380	Dunham, I. et al.	Plus	4904775-4904846
25	333387	Dunham, I. et al.	Plus	4910935-4910997
	333512	Dunham, I. et al.	Plus	5560510-5560564
	333524	Dunham, I. et al.	Plus	5612620-5612780
	333585	Dunham, I. et al.	Plus	6234778-6234894
30	333618	Dunham, I. et al.	Plus	6562391-6562566
	333627	Dunham, I. et al.	Plus	6620584-6620903
	333628	Dunham, I. et al.	Plus	6629004-6629233
	333650	Dunham, I. et al.	Plus	6796852-6797128
	333678	Dunham, I. et al.	Plus	7068223-7068288
	333750	Dunham, I. et al.	Plus	7608165-7608234
35	333763	Dunham, I. et al.	Plus	7692491-7692630
	333767	Dunham, I. et al.	Plus	7694407-7694623
	333768	Dunham, I. et al.	Plus	7695440-7695597
	333769	Dunham, I. et al.	Plus	7696625-7696707
40	333772	Dunham, I. et al.	Plus	7706773-7706902
	333777	Dunham, I. et al.	Plus	7746805-7746916
	333846	Dunham, I. et al.	Plus	8008623-8008757
	333884	Dunham, I. et al.	Plus	8153960-8154161
	333887	Dunham, I. et al.	Plus	8154882-8155025
	333891	Dunham, I. et al.	Plus	8156437-8156709
45	333892	Dunham, I. et al.	Plus	8156825-8157001
	333948	Dunham, I. et al.	Plus	8583497-8583627
	333954	Dunham, I. et al.	Plus	8563186-8563335
	333966	Dunham, I. et al.	Plus	8655643-8655826
50	333968	Dunham, I. et al.	Plus	8681004-8681241
	334061	Dunham, I. et al.	Plus	9586941-9587077
	334094	Dunham, I. et al.	Plus	9889953-9890105
	334113	Dunham, I. et al.	Plus	10282459-10282597
	334161	Dunham, I. et al.	Plus	10599033-10599180
55	334219	Dunham, I. et al.	Plus	12716160-12716384
	334239	Dunham, I. et al.	Plus	13056569-13056693
	334333	Dunham, I. et al.	Plus	13603544-13603657
	334378	Dunham, I. et al.	Plus	13907239-13907370
	334382	Dunham, I. et al.	Plus	13915866-13916036
60	334562	Dunham, I. et al.	Plus	14987847-14987940
	334588	Dunham, I. et al.	Plus	15032740-15032817
	334616	Dunham, I. et al.	Plus	15176123-15176470
	334633	Dunham, I. et al.	Plus	15333206-15333305
	334866	Dunham, I. et al.	Plus	18872214-18872317
65	334891	Dunham, I. et al.	Plus	19299770-19299944
	334934	Dunham, I. et al.	Plus	20103970-20104058
	335015	Dunham, I. et al.	Plus	20682792-20682945
	335120	Dunham, I. et al.	Plus	21436286-21436384
	335125	Dunham, I. et al.	Plus	21441390-21441471
	335179	Dunham, I. et al.	Plus	21634405-21634526
70	335188	Dunham, I. et al.	Plus	21669118-21669328
	335211	Dunham, I. et al.	Plus	21774611-21774680
	335361	Dunham, I. et al.	Plus	22807292-22807445
	335379	Dunham, I. et al.	Plus	22899306-22899420
	335414	Dunham, I. et al.	Plus	23235546-23235684
75	335416	Dunham, I. et al.	Plus	23237354-23237465
	335496	Dunham, I. et al.	Plus	24164386-24164545
	335497	Dunham, I. et al.	Plus	24167666-24167869
	335558	Dunham, I. et al.	Plus	24740167-24740347
	335586	Dunham, I. et al.	Plus	24990333-24990497
80	335686	Dunham, I. et al.	Plus	25439839-25439920
	335784	Dunham, I. et al.	Plus	25942710-25942792
	335823	Dunham, I. et al.	Plus	26365925-26366004
	335983	Dunham, I. et al.	Plus	27938968-27939070
85	335995	Dunham, I. et al.	Plus	28009044-28009184
	336021	Dunham, I. et al.	Plus	28686482-28686559

	336034	Dunham, I. et al.	Plus	29014404-29014590
	336038	Dunham, I. et al.	Plus	29022963-29023165
	336107	Dunham, I. et al.	Plus	29987731-29987869
5	336632	Dunham, I. et al.	Plus	983890-985529
	336633	Dunham, I. et al.	Plus	985591-986221
	336634	Dunham, I. et al.	Plus	986296-986570
	336635	Dunham, I. et al.	Plus	987908-988364
	336636	Dunham, I. et al.	Plus	988418-989185
10	336637	Dunham, I. et al.	Plus	989276-990813
	336638	Dunham, I. et al.	Plus	991906-993240
	336659	Dunham, I. et al.	Plus	1896402-1895478
	336694	Dunham, I. et al.	Plus	2420546-2420616
	336721	Dunham, I. et al.	Plus	3371522-3371586
15	336900	Dunham, I. et al.	Plus	10236423-10236523
	336948	Dunham, I. et al.	Plus	12692290-12692381
	337028	Dunham, I. et al.	Plus	16644817-16644942
	337054	Dunham, I. et al.	Plus	17821742-17821922
	337162	Dunham, I. et al.	Plus	23478943-23479145
20	337183	Dunham, I. et al.	Plus	23943605-23943696
	337184	Dunham, I. et al.	Plus	23973949-23974016
	337268	Dunham, I. et al.	Plus	28011979-28012034
	337299	Dunham, I. et al.	Plus	29022656-29022775
	337389	Dunham, I. et al.	Plus	31401509-31401579
25	337493	Dunham, I. et al.	Plus	33330760-33330981
	337549	Dunham, I. et al.	Plus	34474472-34474531
	337755	Dunham, I. et al.	Plus	3971764-3971900
	337809	Dunham, I. et al.	Plus	4449069-4449193
	337871	Dunham, I. et al.	Plus	5443027-5443101
30	337958	Dunham, I. et al.	Plus	6969162-6969270
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338110	Dunham, I. et al.	Plus	10384481-10384621
	338112	Dunham, I. et al.	Plus	10391398-10391600
35	338145	Dunham, I. et al.	Plus	11386629-11386692
	338148	Dunham, I. et al.	Plus	11448985-11449085
	338179	Dunham, I. et al.	Plus	12808775-12808833
	338197	Dunham, I. et al.	Plus	13638107-13638181
	338279	Dunham, I. et al.	Plus	16168944-16169091
40	338316	Dunham, I. et al.	Plus	17089711-17089988
	338322	Dunham, I. et al.	Plus	17132477-17132547
	338357	Dunham, I. et al.	Plus	18062184-18062402
	338359	Dunham, I. et al.	Plus	18074402-18074501
	338366	Dunham, I. et al.	Plus	18252026-18252189
45	338374	Dunham, I. et al.	Plus	18371200-18371282
	338414	Dunham, I. et al.	Plus	19345573-19345660
	338418	Dunham, I. et al.	Plus	19435506-19435596
	338501	Dunham, I. et al.	Plus	21244713-21244828
	338506	Dunham, I. et al.	Plus	21221871-21221953
50	338523	Dunham, I. et al.	Plus	21509763-21509864
	338662	Dunham, I. et al.	Plus	24404720-24404899
	338804	Dunham, I. et al.	Plus	27236005-27236108
	338836	Dunham, I. et al.	Plus	27792166-27792272
	338879	Dunham, I. et al.	Plus	28410653-28410734
55	338937	Dunham, I. et al.	Plus	29160655-29160725
	338993	Dunham, I. et al.	Plus	30077787-30078184
	339047	Dunham, I. et al.	Plus	30760793-30760968
	339100	Dunham, I. et al.	Plus	31141580-31141765
	339114	Dunham, I. et al.	Plus	31456454-31456519
60	339121	Dunham, I. et al.	Plus	31583467-31583536
	339170	Dunham, I. et al.	Plus	32216399-32216527
	339293	Dunham, I. et al.	Plus	33223671-33223819
	332858	Dunham, I. et al.	Minus	1339607-1339397
	332982	Dunham, I. et al.	Minus	2628296-2628109
65	332984	Dunham, I. et al.	Minus	2632606-2632457
	332998	Dunham, I. et al.	Minus	2711704-2711565
	333058	Dunham, I. et al.	Minus	3028925-3028811
	333097	Dunham, I. et al.	Minus	3204124-3204036
	333121	Dunham, I. et al.	Minus	3308446-3308358
70	333122	Dunham, I. et al.	Minus	3309596-3309531
	333123	Dunham, I. et al.	Minus	3310817-3310749
	333140	Dunham, I. et al.	Minus	3377220-3376309
	333260	Dunham, I. et al.	Minus	4308400-4308304
	333603	Dunham, I. et al.	Minus	6466335-6465727
75	333604	Dunham, I. et al.	Minus	6467090-6466768
	333904	Dunham, I. et al.	Minus	8217374-8217261
	333906	Dunham, I. et al.	Minus	8218238-8218063
	334183	Dunham, I. et al.	Minus	11832582-11832508
	334187	Dunham, I. et al.	Minus	11921456-11921205
80	334222	Dunham, I. et al.	Minus	12732417-12732289
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334255	Dunham, I. et al.	Minus	13200776-13200692
	334492	Dunham, I. et al.	Minus	14478333-14478172
	334648	Dunham, I. et al.	Minus	15363301-15363222
85	334787	Dunham, I. et al.	Minus	16299093-16298937
	334933	Dunham, I. et al.	Minus	20078117-20077991

	334945	Dunham, I. et.al.	Minus	2013885-20138637
	334967	Dunham, I. et.al.	Minus	20173311-20173218
	334990	Dunham, I. et.al.	Minus	20341159-20341087
5	335093	Dunham, I. et.al.	Minus	21297367-21297214
	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335289	Dunham, I. et.al.	Minus	22305950-22305708
	335548	Dunham, I. et.al.	Minus	24662773-24662673
	335551	Dunham, I. et.al.	Minus	24679828-24678961
10	335619	Dunham, I. et.al.	Minus	25082677-25082498
	335620	Dunham, I. et.al.	Minus	25092561-25092434
	335621	Dunham, I. et.al.	Minus	25098878-25098767
	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
15	335814	Dunham, I. et.al.	Minus	26320043-26319845
	335815	Dunham, I. et.al.	Minus	26320518-26320421
	335835	Dunham, I. et.al.	Minus	26393311-26393245
	335851	Dunham, I. et.al.	Minus	26604863-26604742
	335868	Dunham, I. et.al.	Minus	26711437-26711300
20	335896	Dunham, I. et.al.	Minus	26977639-26977558
	335936	Dunham, I. et.al.	Minus	27360474-27360400
	335948	Dunham, I. et.al.	Minus	27555924-27555788
	336066	Dunham, I. et.al.	Minus	29241080-29240842
	336205	Dunham, I. et.al.	Minus	30477456-30477311
25	336275	Dunham, I. et.al.	Minus	32086675-32086536
	336292	Dunham, I. et.al.	Minus	32818035-32817927
	336331	Dunham, I. et.al.	Minus	33594527-33594371
	336419	Dunham, I. et.al.	Minus	34052568-34052445
	336675	Dunham, I. et.al.	Minus	2020758-2020664
30	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336716	Dunham, I. et.al.	Minus	3259952-3259862
	336798	Dunham, I. et.al.	Minus	5888954-5888757
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337046	Dunham, I. et.al.	Minus	17610892-17610821
35	337128	Dunham, I. et.al.	Minus	22215251-22215034
	337192	Dunham, I. et.al.	Minus	24591853-24591771
	337194	Dunham, I. et.al.	Minus	24610510-24610359
	337229	Dunham, I. et.al.	Minus	26716579-26716481
	337325	Dunham, I. et.al.	Minus	30015948-30015800
40	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337500	Dunham, I. et.al.	Minus	33376212-33376158
	337603	Dunham, I. et.al.	Minus	1299296-1299194
	337605	Dunham, I. et.al.	Minus	1346555-1346397
	337671	Dunham, I. et.al.	Minus	3260634-3260547
45	337786	Dunham, I. et.al.	Minus	4133203-4133081
	337862	Dunham, I. et.al.	Minus	5347658-5347550
	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338158	Dunham, I. et.al.	Minus	11794465-11794343
	338161	Dunham, I. et.al.	Minus	12124716-12124658
50	338182	Dunham, I. et.al.	Minus	12824919-12824827
	338189	Dunham, I. et.al.	Minus	12878594-12878478
	338199	Dunham, I. et.al.	Minus	13760865-13760780
	338215	Dunham, I. et.al.	Minus	14055447-14055355
55	338469	Dunham, I. et.al.	Minus	20520387-20520242
	338549	Dunham, I. et.al.	Minus	22049171-22049081
	338561	Dunham, I. et.al.	Minus	22311966-22311856
	338671	Dunham, I. et.al.	Minus	24508421-24508346
	338676	Dunham, I. et.al.	Minus	24637427-24637369
	338726	Dunham, I. et.al.	Minus	25926206-25925618
60	338779	Dunham, I. et.al.	Minus	27030151-27029795
	338871	Dunham, I. et.al.	Minus	28301708-28301611
	338872	Dunham, I. et.al.	Minus	28300921-28300790
	338966	Dunham, I. et.al.	Minus	29614876-29614749
	339229	Dunham, I. et.al.	Minus	32722330-32722199
65	339264	Dunham, I. et.al.	Minus	32975145-32975053
	325228	6381940 Plus		2630-2694
	325235	6381943 Minus		162154-162264
	329588	3962484 Plus		1169-1619
	329560	3962491 Plus		2095-2990
70	329541	3983503 Minus		2765-3059
	325328	5866875 Plus		86780-86854
	325340	6017033 Minus		166656-166819
	325373	5866920 Minus		1136686-1136777
	325367	5866920 Minus		922881-922958
	325389	5866921 Plus		239672-239759
75	325436	5866939 Minus		29778-29907
	325498	5866967 Plus		173372-173930
	325471	6017034 Minus		289268-289342
	325557	6056302 Plus		50921-51050
80	325559	6249595 Minus		118590-119172
	325560	6249595 Minus		133794-133981
	325569	6249599 Plus		79927-80217
	325587	6682462 Plus		126724-126967
	325585	6682462 Plus		73476-73574
85	325597	5866992 Plus		1065020-1065089
	325639	5867002 Plus		253525-253608

	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	329643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867087	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
	326742	5867611	Minus	95187-95248
50	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327608	6004463	Plus	200262-200495
	327611	5867868	Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583

	327775	5867964	Minus	130791-130871
	327795	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
25	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
	328934	5868500	Plus	846342-846448
45	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigeneID's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
400195			NM_007057:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586:g 6330167 dbj BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457:g 7512178 pir T30337 polypr	1.00	400.00
401411			ENSP000000247172:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397:g 7499898 pir T33295 hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP000000241802:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP000000251056:Plasma membrane calcium	1.00	1.00
402260			NM_001436:Homo sapiens fibrillarin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823:g 10432400 emb CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP000000231844:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813:g 12737279 ref XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP000000237855:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950:g 423560 pir A47318 RNA-bind	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP000000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058:Homo sapiens H2B histone fami	1.00	1.00

404287			C6001909:gi 704441 dbj BAA18909.1 (D298	29.71	42.00
404298			C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
404347			Target Exon	1.00	1.00
404440			NM_021046:Homo sapiens melanoma antigen,	1.00	15.00
404721			NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
404854			Target Exon	1.61	2.01
404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
404927			Target Exon	1.00	1.00
404998			Target Exon	1.00	1.00
405449			CY000047*:gi 11427234 ref XP_009399.1 z	1.00	1.00
405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
405572			Target Exon	0.76	1.14
405646			C12000200:gi 4557225 ref NP_000005.1 al	1.01	1.28
405676	BE336714		cytochrome c-1	1.13	2.89
405770			NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
405932			C15000305:gi 3806122 gb AAC69198.1 (AFO	1.99	1.99
406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
406360			Target Exon	1.00	35.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406467			Target Exon	1.00	1.00
406621	X57809	Hs.181125	immunoglobulin lambda locus	1.41	1.74
406642	AJ245210		gb:Homo sapiens mRNA for Immunoglobulin	2.16	3.91
406663	U24683	Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
406678	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
406685	M18728		gb:Human nonspecific crossreacting antig	1.46	2.85
406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
406851	AA609784		major histocompatibility complex, class	0.75	1.91
406964	M21305		gb:Human alpha satellite and satellite 3	38.15	1114.00
406967	M24349		gb:Human parathyroid hormone-like protei	1.00	1.00
406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
407128	R83312	Hs.237260	EST	1.00	1.00
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
407168	R45175	Hs.117183	ESTs	2.16	18.00
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
407242	M18728		gb:Human nonspecific crossreacting antig	1.12	2.85
407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
407430	AF169351		gb:Homo sapiens protein tyrosine phospho	1.00	25.00
407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
407710	AW022727	Hs.23616	ESTs	1.00	28.00
407720	AB037776	Hs.38002	KIAA1355 protein	1.89	1.31
407746	AK001962		hypothetical protein FLJ11100	1.00	1.00
407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	5.00
407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	7.88	3.83
407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag	89.96	109.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
408063	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	195.78	231.00
408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
408122	AI432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
408212	AA297567	Hs.43728	hypothetical protein	5.88	7.91
408243	Y00787	Hs.624	interleukin 8	4.27	9.98
408349	BE546947	Hs.44276	hemo box C10	3.79	3.46
408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
408354	AI382803	Hs.159235	ESTs	1.00	73.00
408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	1.41	16.50
408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
408536	AW381532	Hs.135188	ESTs	1.55	1.50
408545	AW235405	Hs.253690	ESTs	1.00	1.00
408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, deli	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AJ979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:U1-HF-BR0p-ajr-f-11-0-U1.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
45	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
70	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 18	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
85	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protel	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
	412811	H06382		ESTs	1.00	11.00
5	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
	413011	AW068115	Hs.821	biglycan	1.22	1.88
10	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
	413223	AI732182	Hs.191866	ESTs	5.73	27.00
15	413248	T64858	Hs.21433	hypothetical protein DKFZp547J038	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
20	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
30	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
80	415709	AA649850	Hs.78558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypothei	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
	416177	AA174069	Hs.187607	ESTs	1.00	9.00
5	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
10	416322	BE019494	Hs.79217	pyruvate-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42887	ESTs, Weakly similar to S21348 probable	1.00	1.00
	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
20	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurotrophic growth-promoting factor	2.59	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
40	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
45	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.11154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	cathepsin K (pseudosialosylase)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgedin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.11174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1169	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
85	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor I	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:na53a03.s1 NCL CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AI792788		gb:ol91d05.y5 NCL CGAP_Kid5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RPS-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
45	420281	AI623693	Hs.323494	ESTs	45.04	54.00
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibitor	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
50	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.78
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
15	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	95.00
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422656	AI870435	Hs.1569	LM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.83	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
85	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424354	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285429	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146588	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
10	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVI, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV Integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
25	425081	X74794	Hs.154443	minichromosome maintenance deficient (S,	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypothe	1.00	53.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	100.77	44.00
30	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AJ751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
35	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AJ923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AJ077288	Hs.286323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
60	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AJ949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (protat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AJ493134		sclerostin	1.00	1.00
85	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:aa70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427355	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078	glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50	3.24
	427562	R56424	Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	A1741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	A1791495	Hs.180142	calmodulin-like skin protein	1.37	1.88
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	29.55	67.00
	427677	NM_007045	Hs.180296	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	A1393122	Hs.134726	ESTs	7.03	4.52
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.92	1.74
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	23.82	1.00
	428023	AK038843		Homo sapiens cDNA: FLJ23602 fis, clone L	1.40	1.33
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60
35	428129	A1244311	Hs.26912	ESTs	1.00	42.00
	428169	A1928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57	21.64
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.77	15.90
	428434	A1909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184539	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratlin	6.00	4.60
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	56.54	16.00
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37	255.00
	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98	92.00
55	428801	AW277121	Hs.254881	ESTs	1.67	6.15
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	15.16	27.00
60	428969	AF120274	Hs.194689	artemin	1.36	1.24
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	A1753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	6.82	16.47
	429164	A1688663	Hs.116586	ESTs	19.08	67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.33	1.09
	429220	AW207206		ESTs	1.00	7.00
	429228	A1553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.70	142.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.19	1.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551	AW450624	Hs.220931	ESTs	2.89	65.00
	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	1.49	1.37
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
85	429616	A1982722	Hs.120845	ESTs	1.00	1.00
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

5	429663	M58874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfamily	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory subunit	11.80	1.00
	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	gene oculis homeobox (Drosophila) homolog	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical	1.00	51.00
	430147	R60704	Hs.234434	hair/anchorage-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
15	430300	U60805	Hs.238648	oncocalin M receptor	1.00	35.00
	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.25556	tumor necrosis factor receptor superfamily	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
20	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
25	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, family	12.28	41.00
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypothetical	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
30	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
35	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 f1s, clone L	0.44	2.20
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
50	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphat	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
55	431770	BE221880	Hs.268555	5'-3' exonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uropod 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
60	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	1.00	1.00
65	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 f1s, clone PL	157.34	37.00
70	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 f1s, clone C	137.72	98.00
75	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid	1.92	5.29
80	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 f1s, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
85	432867	AW016936	Hs.233364	ESTs	1.00	1.00
	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201987	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
15	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
20	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1965	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
25	434217	AW014795	Hs.23349	ESTs	14.11	57.00
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	1.48	1.56
30	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW976241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AA58679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV Integration site faml	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
85	437016	AJ076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

	437181	AJ305615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	AJ377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AJ125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AJ306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AJ954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
15	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
	437814	AJ088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [Hsa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AJ637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AJ917222	Hs.121655	ESTs	1.00	1.00
	437942	AJ888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group I, m	1.53	10.85
25	438113	AJ467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AJ918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
30	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AJ879064	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
35	438746	AJ885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AJ886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438916	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438958	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R96696	Hs.35598	ESTs	1.00	28.00
45	439128	AJ949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.78	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (ig),	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AJ805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146181	hypothetical protein MGC2408	2.02	1.41
	440994	AJ160011	Hs.272068	ESTs	1.29	1.14
	441020	AA401369	Hs.190721	ESTs	142.99	17.00
85	441031	AJ110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256	ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	RAD51 (S. cerevisiae) homolog (E coli Ra	130.23	43.00
5	441377	BE218239	ESTs	22.03	1.00
	441390	AI692560	ESTs	3.65	7.70
	441497	R51064	ESTs	1.00	1.00
	441525	AW241867	ESTs	1.53	1.42
	441553	AA281219	ESTs	1.89	1.57
10	441607	NM_005010	neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	ESTs	44.15	17.00
15	441801	AW242799	ESTs	1.00	1.00
	441919	AI553802	ESTs	1.00	122.00
	441937	R41782	ESTs	0.86	1.37
	441954	AI744935	Fanconi anemia, complementation group G	1.48	1.39
20	442025	AW887434	CDA11 protein	1.00	46.00
	442029	AW956698	neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	ESTs	3.61	3.14
	442117	AW664964	ESTs	3.00	5.49
	442137	AA977235	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
25	442159	AW163390	heterochromatin-like protein 1	1.92	1.66
	442179	AA983842	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
30	442547	AA306997	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
	442556	AL137761	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	ESTs	1.00	19.00
	442717	R88362	ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
35	442875	BE623003	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	ESTs	8.45	64.00
	443068	AI188710	ESTs	1.00	27.00
40	443204	AW205878	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	ESTs	12.42	2.00
	443247	BE614387	c-Myc target JPO1	128.84	96.00
	443324	R44013	ESTs	0.02	4.59
	443383	AI792453	ESTs	1.00	47.00
45	443400	R28424	ESTs	18.52	61.00
	443426	AF098158	chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	fibrinogen, B beta polypeptide	1.00	16.00
50	443633	AL031290	similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	ESTs	39.81	70.00
	443715	AI583187	cyclin E1	48.74	7.00
	443723	AI144442	syntaxin 6	1.29	1.30
	443802	AW504924	KIAA1291 protein	1.75	1.61
55	443859	NM_013409	folliculin	1.35	1.13
	443892	AA401369	ESTs	1.00	17.00
	443947	W24187	gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	potassium intermediate/small conductance	5.71	6.87
	444006	BE395085	type I transmembrane protein Fn14	1.47	1.92
60	444009	AI380792	ESTs	1.00	77.00
	444017	U04840	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	ESTs	1.00	29.00
	444129	AW294292	ESTs	1.00	1.00
	444279	U62432	cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	forkhead box M1	2.91	1.14
	444378	R41339	ESTs	1.00	1.00
	444381	BE387335	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	KIAA0877 protein	24.91	90.00
70	444489	AI151010	ESTs	1.00	111.00
	444619	BE538082	ESTs, Moderately similar to A46010 X-in	1.00	70.00
	444665	BE613126	B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	desmocollin 3	1.00	1.00
	444735	BE019923	hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	ESTs	1.00	73.00
	445413	AA151342	CGI-147 protein	28.14	50.00
80	445417	AK001058	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	ESTs	1.00	1.00
	445462	AA378776	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	hypothetical protein	1.87	70.00
	445537	AJ245671	EGF-like domain, multiple 6	1.71	2.72
85	445580	AF167572	skb1 (S. pombe) homolog	1.52	1.34
	445654	X91247	thioredoxin reductase 1	1.51	1.52

	445669	AJ570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	49.42	54.00
5	445885	AJ734009	Hs.127699	KIAA1603 protein	1.00	132.00
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AJ347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
10	446078	AJ339982	Hs.156051	ESTs	1.00	42.00
	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
15	446293	AJ420213	Hs.149722	ESTs	1.00	2.00
	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AJ377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
20	446574	AJ310135	Hs.335933	ESTs	3.89	72.00
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
25	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
	446856	AJ814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AJ811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
30	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AJ357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarol	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AJ878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AJ199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AJ375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AJ963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	118.00
	447924	AJ817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AJ538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AJ955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AJ366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked mol	2.34	1.97
75	448826	AJ580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AJ581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AJ471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AJ825777	Hs.344766	ESTs	8.33	44.00
85	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCL CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	56.80	216.86
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complemental	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protein	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCL CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018699	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451808	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
50	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19.00
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28681	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodomain	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	lg superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252766	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
85	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU 5	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10887	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566i133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240655	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.comp		Hs.181163	hypothetical protein MGC5629	4.58	90.00	
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI961486	Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
25	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	statherin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.61		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	titin	1.00	1.00		
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
70	Pkey	CAT Number	Accession
	407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
			AW271982 AA730033 AA576507 AA991217 AA782067 AI985951 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
			D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1	AW148852 BE350895
	408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
75	409522	113735_1	AA075382 AA075431
	409866	1156522_1	AW502152 H41202 H29772
	410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386
			AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
80	411152	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202
			AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
	412537	1304_1	AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
			T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167568 AI862075 AI375230 AI208445 AW235763 AI044113 AA382556
			AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 ALD44114 AI684577 AI809865

412811 132943_1
5
413690 1383256_1
414883 15024_1
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

415989 156454_1
417324 166714_1
418574 17690_1
418712 1784125_1
419443 184788_1
419502 18535_1
419936 189181_1
421582 2041_1
422128 211994_1
423034 224122_1
423816 23234_1
424200 236595_1
424999 245835_1
426966 273896_1
426991 27415_1
427260 276598_1
428023 28589_2
429220 301384_1
429978 31150_1
430439 31808_1
430935 325772_1
431089 327825_1
431322 331543_1
432407 34624_1
434414 38585_1
436608 42361_3

AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982
AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026
H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148
AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240
AA121202 R17734
BE157489 BE157560
AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
AA292753 AA177048 NM_001826 X54941 BE314356 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
AA872039 W72395 T99530 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910844 AA459522 AA293140 AW514667
R75953 AW662396 AA662522 AI865147 AI423153 AW26230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AI129784 AI071623 AI075239
AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
AI494211 AW059601 AW866710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99531 AW300758 H03431 R76789
AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H95952 AA701624 N74173 R54704 H79520 H79223
H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129
W00051 AI038748 AA831327 AI925845 AW945895
Z42183 T31621 T97478
D62703 AA242966 D79798
AU067604 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T76864 T60630
T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242
T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277
T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719
T74766 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107
T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R05796
H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897
N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395
AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596
AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810
AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293
T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778
AI344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293
T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T76633 T29500
T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057
T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964
T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375
AA345234 T67698 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978
AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862
AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835
T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
AI792788 BE142230 AA252019
AI910275 X00474 X52003 X05030 NM_003225 AA134326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818
AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126
BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA588276 R55389 AI001051 AW050700 AW750216 AA614539
BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292
AWB81145 AA490718 M85637 AA304575 T08067 AA331991
AL119930 AA320696 AW752565
AL031985 AI137241 AI792386 AI733664 AI857654 AI049911
AA337221 AA336756 AW966196
AW953120 R56325 AA349562
AI493134 AI498691 AW771508 AI498457 AI768408 AI763524 AI383985 AI580267 D79813 AA393768
AK001535 AA191092 AW510354 AI554256 AL353968 AA134266
AA663848 AA400100 AA401424
AL038843 AI161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 H47392 AI928802 AW182584 AW027872 AI819831
AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064
AI034339 AW674593 N72156 AI079733 AI038683 AI291616 AA491599 AA93675 AA837360 BE006554 BE006473 AI087090 T33044
AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444
AI932767 W02632 BE396786 R37261
AW207206 AW341473 AA448195 AI951341
AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762
AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441
AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI080882 AI919424
AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863585 D79662 BE221049
AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115
AL133561 AL041090 AL117481 AL122069 AW439292 AI968826
AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
BE041395 AA491826 AA621946 AA715980 AA665102
AI970622 AA503009 AA502998 AA502989 AA502805 T92188
AA221036 R87170 BE537068 BE544757 C16935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639
BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720
AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
AW817705 AW817703 AW817659 BE081531 H59570
AA628880 AI126603 BE504035

438091 44964_1 AW373052 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
 AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400
 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AAB45571
 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994
 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
 AW979121 AA847956 AA829098
 439000 467716_1 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI366341 AI867454 N54784 AI655270 AI421279 AW014882
 439285 47065_1 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
 439780 47673_1 AL109688 R23665 R26578
 441128 51021_2 AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171
 AI359627 AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
 AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
 443068 558874_1 W24187 W24194 R17789
 443947 586160_1 Y10043 NM_005342 L05085 AL034450 BE514226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649
 447636 7301_1 AA369318 AW957081 R05760 AA039903 AI885597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883
 AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659
 AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
 AA096002 N83992
 448993 79225_1 AI471630 BE540637 BE265481 AW07710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA283504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245
 AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417
 AA911497 BE537702
 449305 804424_1 AI638293 AW813561
 451105 859083_1 AI761324 AW880941 AW880937
 451320 86576_1 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
 451807 8865_1 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291
 452410 9163_1 AW450852 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
 AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
 R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813
 AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316
 AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
 454241 1067807_1 BE144666 BE184942 AW238414 BE184946
 455175 1257335_1 AW993247 AW861464
 456237 168730_1 AA203682 R11958
 458098 47395_1 BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393
 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395
 AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407
 BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491

	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39280-39502
	402802	3287158	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404936	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405876	4557087	Plus	73195-73917
	405770	2735037	Plus	61067-62075
	405932	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease

Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking Unigenes/D's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
404394			ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
404916			Target Exon	1.00	159.00
405257			Target Exon	1.00	422.00
407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
407568	AA740964	Hs.62699	ESTs	1.00	123.00
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
410434	AF051152	Hs.63668	tol-like receptor 2	39.65	149.00
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
410808	T40326	Hs.167793	ESTs	1.14	13.14
412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
413795	AL040178	Hs.142003	ESTs	0.10	11.90
414154	AW205314	Hs.323060	ESTs	0.62	2.09
414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
415122	D60708	Hs.22245	ESTs	0.07	8.97
415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.29	2.64
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00

	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
10	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrophin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	338.00
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
15	420556	AA279098	Hs.187636	ESTs	1.65	8.07
	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AJ076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
30	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	angiotensin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
40	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	AJ221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
45	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gbmv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
55	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
	447357	AI375922	Hs.159367	ESTs	0.46	2.64
65	448106	AI800470	Hs.171941	ESTs	18.05	296.00
	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periaxin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
80	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421799	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2082 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
15	443709	AI082692	Hs.134662	ESTs	0.00	3.02
	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
	400754			Target Exon	1.00	297.00
	401045			C11001883*:g 6753278 ref NP_033938.1 c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:g 9955960 ref NP_063957.1 AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
30	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:g 5032241 ref NP_005732.1 z	1.00	235.00
	405381			Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
45	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
50	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
60	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
65	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein (1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
75	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
80	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.15	15.54

	418067	AJ127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/aplthe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
10	420256	U84722	Hs.76205	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
15	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALLJ4_HUMAN A	1.00	129.00
20	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
25	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
30	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	tol-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
40	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AI478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
45	430212	AA469153		gb:nc67f04.s1 NCL CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292023	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AJ734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
55	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
	432596	AJ224741	Hs.278461	maltrin 3	0.04	5.79
60	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AJ732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
	434445	AI349306	Hs.11782	ESTs	0.60	1.84
65	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AJ248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene fami	1.00	77.00
75	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
	442200	AW590572	Hs.235768	ESTs	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
	443951	F13272	Hs.111334	femlin, light polypeptide	0.55	2.09
85	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nucleoside diphosphate linked mol	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothet	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
25	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA852496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
	408074	103584_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW851034
45	413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
	423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AJ797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564365 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896
50	423698	23112_1	Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW183262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	430212	314437_1	AA469153 AI718503 AA469225
55	436532	421802_1	AA721522 AW975443 T93070
	453531	97026_1	AA417940 AA036735 T07025
	454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	400754	7331445	Plus	144559-144684
70	401045	8117619	Plus	90044-90184,91111-91345
	401083	3242744	Plus	33192-33360
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
	403021	7547270	Plus	120799-120956
75	403421	9665041	Minus	126609-126773,139986-140205
	403438	9719679	Plus	90792-90938
	403687	7387384	Plus	9009-9534
	403764	7717105	Minus	118692-118853
	404277	1834458	Minus	91665-91946
	404288	2769644	Plus	3512-3691
80	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404518	8151988	Plus	84494-84603
	404916	7341826	Plus	91057-91188
	405106	8079395	Minus	80877-81418
85	405257	7329310	Plus	73121-73273
	405381	6006920	Minus	7636-8054

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymatrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigenelD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: UnigenelD number
 Unigenel Title: UnigenelD gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigenel Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122: Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	A1827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW246508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI688872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431586	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285581	Williams-Beuren syndrome chromosome regl	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

5	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
	443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
	444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
	444931	AV652056	Hs.75113	general transcription factor IIIA	1.00	54.00
10	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogentil	1.00	11.00
	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
15	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	452689	F33868	Hs.284176	transferrin	1.54	1.44
20	453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
	453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

25	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
30	Pkey	CAT Number	Accession
	410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872835 BE298825 BE299889 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI468480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA505787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA588276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
35			
40			
45			
50			
55	421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA505787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA588276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756
	437866	44433_2	
60	451807	8865_1	

TABLE 11C

70

Pkey:

Ref:

Strand:

NI_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

Pkey

Ref

Strand

NI_position

403329

8516120

Plus

96450-96598

406399

9256288

Minus

63448-63554

75

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymatrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 'Accession' column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccon	UnigenelD	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AJ541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornelin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uropod 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806507	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439605	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41696	keratin, hair, acidic,1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165998,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: UnigenelD number
 Unigenel Title: Unigenel gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccon	UnigenelD	Unigenel Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429498	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178535	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.258107	multimerin	1.00	157.00
436532	AA721522		gb:mv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_Uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125572-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: UnigenelD number

Unigene Title: Unigene gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kallini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibritin 2 (congenital contractural ara	diag	extracellular
417034	NM_008183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurtle growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrimin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103932	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296538	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW359908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perforin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (periphagus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNC protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	433505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
40	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folliculin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
60	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.25620	Integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450376	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
70	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	extracellular
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	plasma membrane
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	nuclear
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE556245
 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
 450375 83327_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probaset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number
 Pkey: Unique Eos probaset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
Seq ID No: 37 & 38	429510	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uropod 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifer
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
5	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	438606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
20	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
	Seq ID No: 165 & 166	413281	AA851271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
25	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin 1 precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
40	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
45	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
55	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
65	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
70	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor
	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gbys53h05.s1 Soares fetal liver spleen
	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
85	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

Seq ID No: 293 & 294	424629	M30656	Hs.151393	glutamate-cysteine ligase, catalytic sub
Seq ID No: 295 & 296	437789	A1581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 297 & 298	437789	A1581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 299 & 300	437789	A1581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 301 & 302	437789	A1581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 303 & 304	437789	A1581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
Seq ID No: 307 & 308	403478			NM_022342 Homo sapiens kinesin protein 9
Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGCS350
Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
Seq ID No: 326 & 327	403329			unnamed protein product [Homo sapiens]
Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
Seq ID No: 362 & 363	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4
Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
Seq ID No: 400 & 401	423961	D13666	Hs.136348	perforin (OSF-2os)
Seq ID No: 402 & 403	414812	X72755	Hs.77357	monokine induced by gamma interferon
Seq ID No: 404 & 405	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein
Seq ID No: 406 & 407	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein
Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlcan
Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stannocalcin 2
Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
Seq ID No: 432 & 433	432201	A1538613	Hs.298241	Transmembrane protease, serine 3
Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid melaph
Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
Seq ID No: 440 & 441	447033	A1357412	Hs.157601	ESTs
Seq ID No: 442 & 443	447033	A1357412	Hs.157601	ESTs
Seq ID No: 444 & 445	447033	A1357412	Hs.157601	ESTs
Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara
Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag

	Seq ID No: 462 & 463	437852	BE001838	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s.a
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0
	Seq ID No: 486 & 487	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (C)
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
40	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
45	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2 -
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting anti
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting anti
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gaslin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrophin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cytokine)
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precursor
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin)
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophosphatidic acid
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acid
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AJ186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin)
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
		AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265
		AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
		AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

	1	11	21	31	41	51	
10	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCTCGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGCCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTCAACCCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
15	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCCTCA	AGAACCCAG	420
	AATAATGCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CCGCCCTGGC	CCCGGGTGTC	CCCAGCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCCAGC	TGCGCCGCTT	CTGCCCGGCC	CTGCGCCCCC	TGGAACCTCT	GGGCTTCCAG	600
20	CTCCCGCGCG	TCCAGAACT	GCGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTTG	660
	CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGCTGCAGG	TGCTCGGGC	TCGAGACACA	CTGTGAAGG	CCACGTTTC	780
	CCTGCGGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	GGGCGCCCGG	GAGGCTGGC	CGTGTGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAAGAAAC	900
25	AGTGCTATG	AGCAGTTGCT	GTCCTGCTTG	GAAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGGTCCCAG	GACTGGACAT	ATCTGCATCT	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCAGGGTG	TCATCTGGAC	TGTGTTTAAAC	1080
	CAGACAGTGA	TGCTGAGTGC	TAAGCAGCTC	CACACCTCT	CTGACACCCT	GTGGGACCT	1140
	GGTGACTCTC	GGCTACAGCT	GAACTTCCGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
30	GAGGCTCCT	TCCCTGCTGG	AGTGGACAGC	AGTCTCGGG	CTGCTGAGCC	AGTCCAGCTG	1260
	AATTCTGCGC	TGGCTGCTGG	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT	TTTTGCTGTC	1320
	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GAAAGGGAAC	CAAAGGGGGT	1380
	GTGAGCTACC	GCCCAGCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGGAGAA	1440
	TGTGAGAAAG	CAGCCAGAGG	CATCTGAGGG	GGAGCCCGTA	ACTGTCTCTG	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTTAAGT	CCAAGAAATT	TTTTAAATA	AATATTATA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

	1	11	21	31	41	51	
40	MAPLCPSWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQL	PRMQEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREDPPGE	EDLPGEEDLP	GEEDLPVKP	KSEEGSLKL	EDLPTVEAPG	120
	DQEPQNNAH	RDKEGDDQSH	WRYGGDPWP	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
45	ELLGQLPPL	PELRLRNNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFPAEI	HVVHLSTAF	RVDEALGRPG	GLAVLAAPLE	EGPEENSAYE	QLLSRLLEIA	300
	EEGSETQVPG	LDSALLPSD	FSRYFYQYEGS	LTPPCAGQV	IWTFVNQTM	LSAQLHLTSL	360
	DTLWGPQDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSFRA	AEFVQLNSCL	AAGDILALVF	420
	GLLFAVTSVA	FLVQMRQRH	RGTGKGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

	1	11	21	31	41	51	
55	AGCGGGGTTG	TCTATTAAC	TGTTCAAAAA	GTATCAGGAG	TTGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGC	AAGGGGGA	GTAGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAGAA	120
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TTCAAAAAA	180
60	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TGCGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTCTT	CGCTGATTT	300
	TCTCGCGGA	GCCCTGCGCT	CCGACACCC	CCGCGCGCCT	CCCCTCTCC	TCTCCCCCG	360
	CCCGCGGGCC	CCCCAAAGTC	CCGCGCGGGC	CGAGGGTCGG	CGGCGCGCGG	CGGCGCGGGC	420
	CCGCGCAGAG	CGCCCCCATG	TACAACATGA	TGAGAGCGGA	GCTGAAGCCG	CCGCGCGCGC	480
65	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGCGCGGC	GGCAACCAGA	540
	AAAACAGCCC	GGACCGCGTC	AAGCGGCCCA	TGAATGCCTT	CATGGTGTGG	TCCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAACCCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCGGA	GTGGAACCTT	TTGTCGGAGA	CGGAGAAGCG	GCCGTTTCATC	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCGGATTA	TAAATACCGG	CCCGGCGGGA	780
70	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGGCGGGCTG	CTGGCCCCCG	840
	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCCGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACCAGCT	GGGCTACCCG	CAGCACCCCG	GCCTCAATGC	GCACGGCGCA	GCGCAGATGC	1020
	AGCCCATGCA	CCGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
75	CCTACATGAA	CGGCTGCCCC	ACCTACAGCA	TGTCCTACTC	GCAGCAGGGC	ACCCCTGGCA	1140
	TGGCTCTTGG	CTCCATGGGT	TCGGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCTGTGG	1200
	TTACCTCTTC	CTCCACTCTC	AGGGCGCCCT	GCCAGGCCGG	GGACCTCCGG	GACATGATCA	1260
	GCAATGATCT	CCCCGGCGCG	GAGGTGCCGG	AACCGCGCGC	CCCCAGCAGA	CTTCAATGT	1320
	CCAGCAGCTA	CCAGAGCGGC	CCGTGCCCG	GCAAGGCCAT	TAAAGGCACA	CTGCCCTCT	1380
80	CACACATGTG	AGGGCCGGAC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAA	GAAAAACGAG	1440
	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
	TCAAAAA	AAAAA	AAAAATCCAT	CACCCACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GGACTCTCTT	TKGGGGGACT	ATTTTGTAC	AGAGAAAAAC	TGGGGAGGGT	1680
85	GGGGAGGGCG	GGGGAATGGA	CCTGTATAG	ATCTGGAGGA	AAGAAAGCTA	CGAAAACTT	1740
	TTTAAAGTT	CTAGTGTATC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
	TAATATTAG	AGCTAGTCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTGT	CAAGCAACTT	1860
	TTGTACAGTA	TTTATCGAGA	TAAACATGCG	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGGCCAA TATTTTCAA GGAGAGGCTT CTTGCTGAAT TTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAAAACGT AAAAGAAGAA AATATTCAA ATTTGGACAT TTTAATTGTT 2040
 TAAAAATTGT ACAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAGG GGCAAAAGT TTAGACTGTA CTAATTTTA TAACCTACTG TTAAGAGCAA 2160
 AAATGGCCAT GCAGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTT GATCCCAACT 2220
 TTCCATTTTG TTCAAGTAA AAAAACCATG AAATTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAATA TTCTGTAAA TTTATTGTA TATTTTAAGG TTTTCCCCC TTTATTTTCC 2340
 GTAGTTGTAT TTTAAAGAT TCGGCTCTGT ATTATTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAACTAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTCTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAAT TTTGAAATAT GGACACTGAA AAAAAAAGAA 2520
 AAAAAACAA AAAAAAAGAA CAAAAACAA AACACAGAAA AACAAAAAA AAAAAACAA 2580
 CACAACAAA AACAAAAAA AAAAAAAGAA AACAAACACA CAACACAACA CAACACAACA 2640
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:
 Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLESETEKRPF IDEAKRLRAL HMKEHPDYKY RPRRKTTLML 120
 KDKYTLPGG LLAPGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMNQDQLGY 180
 PQHPGLNAHG AAQMQPMHRY DVSALQYNM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPVVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS 300
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTG GCAAGAAGGA AACTTCTTAC 300
 TGCTTTAGAT GGCCTTAGCT TGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GGAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACGGCAA 480
 GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTTTATT ACATGTGATT GTGATTTCAT ATCCCTTAAT TAAATATCAA 600
 ATTATATTGG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAAGAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
 Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNWNLS PAETEGVHE EELVARRKLP TALDGFSLER MLTIYQLHKI CHSRAFOHWE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSEYY

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCTTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300
 ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAATAGT CATAGTGAAT GACTGGTATG GGGCAGATGG AGATGATCCA 480
 TACACCCTAC AATACAGAGG GTGTGAAAA GAGGGAAAAT ACATTCATTT CACACCTAAT 540
 TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCGGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTCTTAC 660
 ATAAATGGGC AAAATCAAT TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGTCTCTG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGTTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCACAA 900
 CTACAGAACC AGATGTGCAG CTTGAGAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTCAACCA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCTCCAC ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGATTTT ATTTGATGCA GATTGTTGAA 1140
 ATTCAATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCCAGCTA 1200
 CACCAAAATTA ACAGCAATGA TTGCTGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGACATCAG CATTGTGTTA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA 1320
 AAATGGAATG GAAAGCTTA TGGCTCTGTG ATGATATTAG TGACAGCGG AGATGATAAG 1380
 CTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440

CTGGGTTCAT CTGCAGCCCC AAATCTGGAG GAATATACAC GTCTTACAGG AGGTTTAAAG 1500
 TTCTTTGTTC CAGATATATC AAATCTCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
 TCTGGAACCTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC 1620
 AAACCTCACC ATCAATTGAA AACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
 5 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTAT TGTCTCTGAT 1740
 GGACGAAAAA ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
 TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT 1860
 TCTCTGCAAG CCCTGAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920
 10 GCCACTGTGG AAGCCTTTGT GGAAGAGAC AGCCTCCATT TTCTCATCC TGTGATGATT 1980
 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCC TGCCACAGTT 2040
 GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTAATCGAGG TATTTTCTT CCTTTGCTGC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCAATG CAATCACTCT CCCAGCATAA GCACCCCAAC CCACCTCTATT 2220
 CCAGGGAGTC ATGCTATGTA TGTACCAAGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
 15 GCCTCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCCC TGATGTGTTT 2400
 CCACCATGCA AAATTATTGA CTTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCTATCT 2460
 TGGACAGCAC CTGGAGAAGA CTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAAATG 2520
 20 AGTAAAAGTC TACAGAAATAT CCAAGATGAC TTTAAACAATG CTATTTTAGT AAATACATCA 2580
 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTC 2640
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCAGGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 25 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTGG ACTACAAAAA 3000
 CACTACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
 ATACAGATAA GATTTTACA TGGTAGATCA ACAATCTTT TTGGGGGTAG ATTAGAAAAA 3120
 30 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAGTAAT GTCCTTAAAG 3180
 GCAAAGGGA GGGTAAAGT GCACAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240
 AATAGCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAAGTCTCTG TGTGAAGCAA 3300
 TCATTTAGTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCACTAC AGTTGCTTG 3360
 35 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAGG CTCTTTACCT 3420
 CTGTCTATTT TGTATATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTGTCTCT TCATACGGGT 3540
 TTTATGACAA AGGTCTATTG AATTATTATT TNTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATTGCTTGG GTTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
 TACCTAGGAA A

Seq ID NO: 8 Protein sequence:
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
 45 MTQRSIAGPI CNLKFVTLV ALSSLEPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISS 60
 IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAAH 120
 GDDPYTLQYR GCKEKGKVIH FTFNLLNDN LTAGYGSRRG VFWHEMAHLR WGVFDEYNMD 180
 KEFFYINGQNK IKVTRCSSDI TGFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
 50 MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSANDVIT DSADFHHSFP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAEEFYLM QIVEIHTFVG IASFDKSGEI 360
 RAQLHQINSN DDKRLVSVL PTTVSAKTDI SICSGLLKGF EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSLRT GGLKFFVDPD SNSNSMIDAF 480
 SRISSTGTDI FVLLHQLEST GENVKPHQL KNTVTVDNTV GNDTFLVTV QASGPPPIIL 540
 55 FDFPDRKYIT NNFITNLTFR TASLWIPGTA KPGHWYTLN NTHSLQALK VTVTSRASNS 600
 AVPPATVEAF VERDSLHFPF PMIYANVKQ GFYPIILNATV TATVEPETGD PVTLRLLDDG 660
 AGADVINKDG IYSRYFFSFA ANGRYSLKVH VNRSPSISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAPRKSV GRNEEERKMG FSRVSSGGSF SVLGVPAGPH PDVPPCKII DLEAVKVEEE 780
 LTLSWATPGE DFDQGGATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQQ AGIREIFTFS 840
 60 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
 LILKGVLTAM GLIGITCLII VVTHHTLSRK KRADKENGTT KLL

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-632

1 11 21 31 41 51
 70 CTCCCCCTCAC CCGGTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
 GAGCTGGCAC TCTCTGGAG GGAGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAATGCC AAGTTGGGG 240
 CCAGTGGGCG CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTCCT 300
 75 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACCTC TGCACAAGGA GCTGCCAGC TTTGTGGGG 480
 AGAAAGTGA TGAGGAGGGG CTGAAGAAGC TGATGGGCAG CCTGGATGAG AACAGTGACC 540
 AGCAGGTGGA CTTCAGGAG TGTCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG 600
 80 ACTTCTTCCA GGGCTGCCA GACCGACCTT GAAGCAGAAC TCTTGACTTC CTGCCATGGA 660
 TCTCTTGGGC CCAGGACTGT TGATGCCTTT GAGTTTGTGA TTCAATAAAC TTTTGTGTC 720
 TGTGTATAAT ATTTTAATG CTCAGTGATG TTCCATAACC CGGTGGCTC AGCTGGAGTG 780
 CTGGGAGATG AGGGCCTCCT GGATCCTGCT CCCCTCTGGG CTCTGACTCT CCTGGAATC 840
 TCTCCAAGGC CAGAGCTATG CTTTAGGTCT CAATTTTGGG ATTTCAAAAC CCAGCAAAAA 900
 85 ATTGGAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAAGGC 960
 AAATACCA

Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

5
 1 11 21 31 41 51
 | | | | |
 MNCSSLEQAL AVLVTTFHKY SQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKILM 60
 GSLDENSDDQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 336-626

15
 1 11 21 31 41 51
 | | | | |
 CTCCCTCAC CCCGGTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG 60
 CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCTCCCCCA GCTGGTGGTG 120
 GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
 CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTGGTTTCC TTAAATGCC AAGTTGGGGG 240
 CCAGTGGGGC CCACATATAA ATCTCACCC TGGGAGCCTG GCTGCCTTGC TCTCCTTCT 300
 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
 CGCTGGCTGT GCTGGTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
 AGCTGAGTAA GGGGGAATG AAGGAACTTC TGCACAAGGA GCTGCCCAGC TTTGTGGGGC 480
 ATTCAGAGA ACCATGTGCT GTGAGGGCCT TCCGAGTCCA TCTGTTTAAAT CCTGTTCATTG 540
 GAGACTTGAG AAACCCAGAGC CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
 25 GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
 CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA CTCATCACTG TCATGTGCAA 720
 TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
 GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTG TATTCAATAA ACTTTTTTTG 840
 TCTGTTGATA ATATTTTAAAT TGCTCAGTGA TGTTCATAA CCGGGCTGGC TCAGCTGGAG 900
 30 TGCTGGGAGA TGAGGCGCTC CTGGATCCTG CTCCTTCTG GGCTCTGACT CTCCTGGAAA 960
 TCTCTCCAG GCCAGAGCTA TGCTTAGGT CTCATTTTG GAATTTCAA CACCAGCAA 1020
 AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAAGAT ATTAATAAAG 1080
 GCAATACCA

Seq ID NO: 12 Protein sequence:
 Protein Accession #: Eos sequence

40
 1 11 21 31 41 51
 | | | | |
 MNCSSLEQAL AVLVTTFHKY SQEGDKFKL SKGEMKELLH KELPSFVGH S REPCA VRAFR 60
 VHLFPNVIDG LRNQSPGK S DCPKITQHWR KWMRRG

Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 58-354

50
 1 11 21 31 41 51
 | | | | |
 GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAAACAAG TACACAGCCA CAGATCCATG 60
 ATGTGCACTT CTCTGGAGCA GCGCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
 TGCCAAGAGG GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAAT TCTGCACAAG 180
 GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTTGCCA 300
 55 CTCATCACTG TCATGTGCAA TGACTTCTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
 ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTG 420
 TATTCAATAA ACTTTTTTTG TCTGTTGATA ATATTTTAAAT TGCTCAGTGA TGTTCATAA 480
 CCGGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540
 60 GGCTCTGACT CTCCTGAAA TCTCTCAAAG GCCAGAGCTA TGCTTAGGT CTCATTTTG 600
 GAATTTCAA CACCAGCAA AAATTGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC 660
 AAATAAAGAT ATTAATAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_005969.1

65
 1 11 21 31 41 51
 | | | | |
 MNCSSLEQAL AVLVTTFHKY SQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKILM 60
 GSLDENSDDQ VDFQEYAVFL ALITVMCNDP FQGCPRDP

Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 62-358

75
 1 11 21 31 41 51
 | | | | |
 GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
 CATGATGTGC AGTTCTCTGG AGCAGCGCT GGCTGTGCTG GTCACTACCT TCCACAAGTA 120
 CTCTGCCAA GAGGGGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAG AACTTCTGCA 180
 CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240
 80 GGGCAGCCTG GATGAGAACCA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTCTCT 300
 GGCACCTATC ACTGTCTATG GCAATGACTT CTTCCAGGGC TGCCAGACC GACCCTGAAG 360
 CAGAATCTT GACTTCTGTC CATGGATCTC TTGGGCCAG GACTGTTGAT GCCTTTGAGT 420
 TTTGATTCA ATAACTTTT TTGTCTGTT GATAATATT TAATTGCTCA GTGATGTTCC 480
 85 ATAAACCCGC TGGCTCAGCT GAGTGCTGG GAGATGAGGG CCTCTGGAT CTGCTCCCT 540
 TCTGGGCTCT GACTCTCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
 TTTGGAATTT CAAACACCAG CAAAAAATTG GAAATCGAGA TAGGTTGCTG ACTTTTATT 660

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51
| | | | |
MMCSSELEQAL AVLVTFPHKY SQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSQQ VDFQEYAVFL ALITVNCNDF FQGCPRDP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1 11 21 31 41 51
| | | | |
AAGACGGATT CTCAGACAAG GCTTGCAAAT GCCCGCAGC CATCATTTAA CTGCACCCGC 60
AGAAATAGTTA CGGTTTGTCA CCCGACCCCTC CCGGATCGCC TAATTTGTCC CTAGTGAGAC 120
CCGAGGGCTC TGCCCGCGCC TGGCTTCTTC GTAGCTGGAT GCATATCGTG CTCGGGCGAG 180
CGCGGGCGCA GGGCAGCGGT TCGCGCACAC CCTAGCACAC ATGAACACGC GCAAGAGCTG 240
AACCAAGCAC GGTTTCCATT TCAAAAAGGG AGACAGCCTC TACCGCGATT GTAGAAGAGA 300
CTGTGGTGTG AATTAGGGAC CGGGAGGCGT CGAACGGAGG AACGGTTCAT CTTAGAGACT 360
AATTTTCTGG AGTTTCTGCC CTGCTCTGTC GTACGCCCTC ACGTCACTTC GCCAGCAGTA 420
GCAGAGGCGG CGGCGGCGGC TCOCGGAATT GGGTTGGAGC AGGAGCCTCG CTGGCTGCTT 480
CGCTCGCGCT CTACGCGCTC AGTCCCCGGC GGTAGCAGGA GCCTGGACCC AGGCGCGGCC 540
GGCGGGCGTG AGGCGCGCGA GCCCGGCCCTC GAGGTGCATA CCGGACCCCTC ATTGCGATCT 600
AACAAAGGAA CTGCGCCCCA GAGAGTCCCG GGAGCGCGC CGGTGCGTGC CCGCGCGGCC 660
GGGCCATGCA GCGACGCGCG CCGCGGAGCT CCGAGCAGCG GTAGCGCCCC CCTGTAAAGC 720
GGTTCTGCTAT CGCGGGGCCA CTGTGAACCC TGCCGCGCTGC CGGAACACTC TTCGCTCCGG 780
ACCAAGCTCAG CCTTGTGATAA CTGGACTCG GCACGCGCGC AACCAAGCAC GAGGAGTTAA 840
GAGAGCCGCA AGCGCAGGGA AGGCTCTCCC GCACGGGTGG GGGAAAGCGG CCGGTGCAGC 900
CGCGGGACAG GCACCTCGGC TGCGACTGGC TGCTAGGGAT GTCGTCTCTG ATAAGGTGGC 960
ATGGAACCGC CTGCGCGCGG TCTGCGGCT TCTGCTGGCT GGTGTGGGC TTCTGGAGGG 1020
CGCTTTTGGC CTGTCCACG TCCTGCAAAAT GCAGTGCTCT TCGGATCTGG TGCAGCGACC 1080
CTTCTCTCGG CATCGTGGCA TTTCCGAGAT TGGAGCCTAA CAGTGTAGAT CCTGAGAACA 1140
TCACCGAAAT TTTTCATCGA AACCAAGAAA GGTAGAAAT CATCAACGAA GATGATGTTG 1200
AAGCTTATGT GGGACTGAGA AATCTGACAA TTGTGGATTC TGGATTAAAA TTTGTGGCTC 1260
ATAAAGCATT TCTGAAAAAC AGCAACCTGC AGCAGATCAA TTTTACCCGA AACAACTGA 1320
CGAGTTTGTG TAGGAACAT TTCCGTACCC TTGACTTGTC TGAACCTGAT CTGTGGGGCA 1380
ATCCATTATC ATGCTCTCTG GACATATGT GGATCAAGAC TCTCCAAGAG GCTAAATCCA 1440
GTCCAGACAC TCAGGATTTG TACTGCTGA ATGAAAGCAG CAAGAATATT CCCCTGGCAA 1500
ACCTGCAGAT ACCCAATTGT GGTTTGCCAT CTGCAAACTC GGCGCGACCT AACCTCACTG 1560
TGGAGGAAGG AAGTCTATC ACATTATCCT GTAGTGTGGC AGGTGATCCG GTTCTTAATA 1620
TGATTTGGGA TGTGTGTAAC CTGGTTTCCA AACATATGAA TGAACAACAG CACACACAGG 1680
GCTCCTTAAG GATAACTAAC ATTTATCCCG ATGACAGTGG GAAGCAGATC TCTGTGTGG 1740
CGGAAAAATC TGTAGAGGAA GATCAAGATT CTGTCAACCT CACTGTGCAT TTTGACCAA 1800
CTATCACATT TCTCGAATCT CCAACCTCAG ACCACCTG GTGCATTCCA TTTACTGTGA 1860
AAGGCAACCC CAAACACGCG CTTCAGTGGT TCTATAACGG GCAATATTG AATGAGTCCA 1920
AATACATCTG TACTAAAAA CATGTTACCA ATCACACGGA GTACCACGGC TGCCTCCAGC 1980
TGGATAATCC CACTCACTG AACCAATGGG ACTACACTCT AATAGCCAAG AATGAGTATG 2040
GGAAGGATGA GAAACAGATT TCTGCTCACT TCTAGGGCTG GCCTGGAATT GACGATGGTG 2100
CAAAACCCAA TTATCTGTAT GTAATTTATG AAGATTATGG AACTGCAGCG AATGACATCG 2160
GGGACACACG GAACAGAAAT AATGAAATCC CTTCACAGA CGTCACTGAT AAAACCGGTC 2220
GGGAACATCT CTGGTCTAT GCTGTGGTGG TGATTGCGTC TGTGGTGGGA TTTTGCCCTT 2280
TGGTAATGCT GTTCTGCTT AAGTTGGCAA GACACTCCAA GTTGGCATG AAAGGTTTGG 2340
TTTGTGTTCA TAAGATCCCA CTGGATGGGT AGCTGAAATA AAGGAAAAAG CAGAGAAAGG 2400
GGCTGTGGTG CTGTGTGGTT GATGCTGCCA TGTAAGCTGG ACTCCTGGGA CTGCTGTGG 2460
CTTATCCCGG GAAGTGTGTC TTATCTGGGG TTTTCTGGTA GATGTGGGCG GTGTTGGAG 2520
GCTGTACTAT ATGAAGCCTG CATATACTGT GAGCTGTGAT TGGGGAACAC CAATGCAGAG 2580
GTAACCTCTA GGCAGCTAAG CAGCAGCTCA AGAAAAATG TTAATTAAT GCTTCTCTTC 2640
TTACAGTAGT TCAATACAA AACTGAAATG AAATCCCATG GGATTGTACT TCTCTTCTGA 2700
AAAGTGTGCT TTTGACCCCT ACTGGACATT TATTGACTTA ATTGCTTCTG TTTATTAAAA 2760
TTGACCTGCA AAGTTAAAAA AAAATTAAG TTGAGAACAG GTATAAGTGC ACACGTGAATA 2820
GTCTAATCTA CATGTAACAC ATATTTTAGT GTGATTTTCT ATACTCTAAT CAGCACTGAA 2880
TTACAGAGGT TTGACTTTT CATCTATAAC ACAGTGACTA AAAGAGTTAA GGGTATATAT 2940
ACCATCACTT TGGGACTTGG TAGTATTAT AAAAGGTTAT TTCCTTCACT GTCATATAAA 3000
GTCCAAATGT TTAGCTTAGG TCTGAGAGTC AAACAATGTT AAGGATTGTC TTAAGATTCC 3060
TTAGCCAGCA AAACAAACA AAACAAACA AACAAATGAA AACGTTTAA AAAGAAGAAG 3120
AAGAAAAAAA ACAAGAACAA GCAGCAACAG CTGTTTGTG GGGGCTATAG ATTTAAGTTA 3180
GGCAGATGCA ATTTCAAGAT AACTAAGAGT GGAATATATG CATATGGTGA AATTATAACC 3240
TTGCCCTTTT TATTTGCCCT TCTGCGATCC ACCTGCTTTT TAGAAGTCTG CCGAGTGAGA 3300
AGGCCACAGT ATCTCATGCT GTTTGCATTA CAGAACTGCA GCTTTTCTAC TCTGAAAAGG 3360
CCTGGGAGCA GAATGGCTGG CCGTGTGTGA GCAGGAGAGG AGATTCTAAG AAGGATAGTC 3420
CCCCCTACAA CATAGTCTCA TACTGCTGGG TTTTCATGGG TAGGAAAGCT TGTCTCTGACC 3480
CCAGCAGCAA AGAGGTGGCA GGTGCTAAT GAATATATGC TTTATAATGT CCTTCTCTAT 3540
TGCTGAGAGG GCAGCCTTAG AGCTGTGGAT TTCTGCATCC CCCCTGAGTC TGACCCATGG 3600
ACACCTGTTT CATTCACCTT AGCATCACAG TGACCTTTGT ATGCTCTGTT CAGTCTGTGT 3660
CAGGCAGTAT GCTTGTCTG AAGAGAGGTT TGGCTATCCC CACCCACCC CACCCACCC 3720
TGTTCTCTTT TTATCAGGAG GACTTCAGAG CCAGGCTGTC AGCATTTTGT TTGAAAACAC 3780
AATCAGCTCT GACAGTTAGA CATGCACACA GACGCCATAG CTGGATTGGA AACATTGATG 3840
TTTTAAAAAT TATTTTGTG TTGAAAATAG TGCACAAATG CTGCAATTTA GCTTTAAGGT 3900
TCTATAGATT TTTAACTAGT CCAACACAGT CAGAAACATT GTTTTGAATC CTCTGTAATC 3960
CAAGGCATTA ATCTTAATAA ACCAGGATCC ATTTAGGTAC CACTTGATAT AAAAAGGATA 4020
TCCATAATGA ATATTGTATA CTGCATCCTT TACATTAGCC ACTAAATACG TTATTGCTTG 4080
ATGAAGACCT TTCACAGAA CTCTATGATT GCAGCATTTT ACTTGGCTAC TTCATACCCA 4140

TGCCTTAAAG AGGGGCAAGT TCTCAAAGC AGAAACATGC CGCAGTTCT CAAGTTTTC 4200
 TCCTAACTCC ATTTGAATGT AAGGGCAGCT GGGCCCCAAT GTGGGGAGGT CCGAACATTT 4260
 TCTGAATCC CATTTCTCTG TFCGGGCTA AATGACAGTT TCTGTCTATTA CTTAGATTCC 4320
 GATCTTTCCC AAAGGTGTTG ATTTACAAAG AGGCCAGCTA ATAGCAGAAA TCATGACCCT 4380
 5 GAAAGAGAGA TGAAATTCAG GCTGTGAGCC AGGCAGGAGC TCAGTATGGC AAAGGTTCCT 4440
 GAGAATCAGC CATTTGTTAC AAAAAGATT TTTAAAGCTT TTAGTTTATA CCATGGAGCC 4500
 ATAGAAAGGC TATGGATTGT TTAAGAACTA TTTTAAAGTG TTCCAGACCC AAAAAGGAAA 4560
 AATAAAAAAA AAGGAATATT TGTACCCAAC AGCTAGAAGG ATTGCAAGGT AGATTTTGT 4620
 10 TTTAAATGG AGAGAAGTGG ACAGATAAGG CCATTTAATA TATCAAAGAT CAGTTGACAT 4680
 CTCCTAGGGA ATGATGAAAA CAGCAGGCTA T

Seq ID NO: 18 Protein sequence:
 Protein Accession #: CAA53571

15 1 11 21 31 41 51
 MSSWIRWHP AMARLWGF CW LVVGFWRAP ACPTSCCKSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLITVD SGLKPVAKHA FLKNSNLQHI 120
 20 NPTRNKLTSL SRKHFRLDL SELILVGNPF TCSCDIMWIK TLQEKSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLP SAN LAAPNLTVEE GKSTLSCSV AGDPVFNMYW DVGNLVSXHM 240
 NETSHTQSSL RITNISSDDS GKQISCV AEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPTVKGN PKPALQWYFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIEDY GTAANDIGDT TNRSEIPST 420
 25 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG

Seq ID NO: 19 DNA sequence
 Nucleic Acid Accession #: NM_000228
 Coding sequence: 82-3600

30 1 11 21 31 41 51
 GCTTTCAGGC GATCTGGAGA AAGAACGGCA GAACACACAG CAAGGAAAGG TCCTTTCTGG 60
 GGATCACCCC ATTGGCTGAA GATGAGACCA TTCTTCTCTT TGTGTTTTC CCTGCCTGGC 120
 35 CTCCTGCAAT CCCAACACGC CTGCTCCCGT GGGGCCTGCT ATCCACCTGT TGGGGACCTG 180
 CTTGTTGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240
 ACCTACTGCA CCCAGATATGG CGAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCCAGGCAG 300
 CCTCACAAC ACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCCG CCCCATGCGC 360
 TGGTGGCAGT CCCAGAAATGA TGTGAACCTT GTCTCTCTGC AGCTGGACCT GGACAGGAGA 420
 40 TTCCAGCTTC AAGAAGTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCCCG CATGCTGATT 480
 GAGCGCTCCT CAGACTTCGG TAAGACCTGG CGAGTGTACC AGTACCTGGC TGCCGACTGC 540
 ACCTCCACCT TCCCTCGGGT CCGCCAGGGT CGGCCTCAGA GCTGGCAGGA TGTTCGGTGC 600
 CAGTCCCTGC CTCAGAGGCC TAATGCACGC CTAAATGGGG GGAAGGTCCA ACTTAACCTT 660
 ATGGATTAG TGCTCGGATG TCCCACTACT CAAAGTCAAA AAATTCAGGA GGTGGGGGAG 720
 45 ATCACTAACT TGAGAGTCAA TTTACCCAGG CTGGCCCTCG TGCCCAAG GGGCTACAC 780
 CCTCCACGCG CTTACTATGC TGTGTCCAG CTCGCTCTGC AGGGGAGCTG CTTCTGTAC 840
 GGCATGCTG ATCGCTGCGC ACCCAAGCCT GGGGCCTCTG CAGGCCCTTC CACCGCTGTG 900
 CAGTCCACG ATGTCTGTGT GTGCCAGCAC AACACTGCCG GCCCAATTTG TGAGCGCTGT 960
 GCACCCCTCT ACAACAACCG GCCCTGGAGA CCGCGCGAGG GCCAGGACGC CCATGAATGC 1020
 50 CAAAGGTGCG ACTGCAATGG GCACTCAGAG ACATGTCACT TTGACCCCGT TGTGTTTGGC 1080
 GCGAGCCAGG GGGCATGTGT AGGTGTGTGT GACAATTGCC GGGACACAC CGAAGGCAAG 1140
 AACTGTGAGC GGTGTACGCT GCACTATTTC CGGAACCGGC GCCCGGAGC TTCCATTGAG 1200
 GAGACCTGCA TCTCCTGCGA GTGTGATCCG GATGGGGCAG TGCCAGGGGC TCCCTGTGAC 1260
 CCAGTGACCG GCGATGTGTG GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320
 55 AAGCGGGCT TCACTGGACT CACCTACGCC AACCCGAGG GCTGCCACCG CTGTGACTGC 1380
 AACATCTCG GGTCCCGGAG GGACATGCCG TGTGACGAGG AGAGTGGCG CTGCCTTTGT 1440
 CTGCCCAACG TGTGGGTGCC CAAATGTGAC CAGTGTGCTC CTAACACTG GAAGCTGGCC 1500
 AGTGGCCAGG GCTGTGAACC GTGTGCCCTG GACCCGCACA ACTCCCTCA GCCCACAGTG 1560
 CAACCAATTC ACAGGCGAGT GCCCTGTCTG GAAGGCTTTG GTGGCCTGAT GTGACGCT 1620
 60 GCAGCCATCC GCCAGTGTCC AGACCGGACC TATGGAGACG TGGCCACAGG ATGCCGAGCC 1680
 TGTGACTGTG ATTTCCGGGG AACAGAGGGC CCGGGCTGCG ACAAGGCATC AGGCCGCTGC 1740
 CTCTGCCGCC CTGGCTTGAC CCGGCCCGCG TGTGACCAAT GCCAGGAGG CTACTGCAAT 1800
 CGTACCCGG TGTGCGTGGC CTGCCACCTT TGCTTCCAGA CCTATGATGC GGACCTCCGG 1860
 GAGCAGGGCC TGCGCTTTGG TAGACTCCGC AATGCCACCG CCAGCTGTG GTACGGGCTT 1920
 65 GGGCTGGAG ACCGTGGCCT GGCCTCCCGG ATCCTAGATG CAAAGAGTAA GATTGAGCAG 1980
 ATCCGAGCAG TTCTCAGCAG CCCCAGCAGT ACAGAGCAGG AGGTGGCTCA GGTGGCCAGT 2040
 GCCATCTCTT CCTCAGGCG AACTCTCAG GGCCTGCAGC TGGATCTGCC CCTGGAGGAG 2100
 GAGACGTTGT CCTCTCCAG AGACCTGGAG AGTCTTGACA GAAGCTTCAA TGGTCTCCTT 2160
 ACTATGTATC AGAGGAAGAG GGAGCAGTTT GAAAAATTA GCASTGCTGA TCCTTCAGGA 2220
 70 GCCTTCGGGA TGCTGAGCAC AGCCTACGAG CAGTCAGCCC AGGCTGCTCA GCAGGTCTCC 2280
 GACAGCTGCG GCCTTTTGGG CCAGCTCAGG GACAGCCGGA GAGAGGCAGA GAGGCTGGTG 2340
 CCGCAGGCGG GAGGAGGAGG AGGCACCGGC AGCCCCAGC TTGTGGCCCT GAGGCTGGAG 2400
 ATGTCTTGTG TGCTGACCT GACACCCACC TTCAACAAGC TCTGTGGCAA CTCCAGGCAG 2460
 75 ATGGCTTGCA CCCCAATATC ATGCCCTGGT GAGCTATGTC CCCAAGACAA TGGCACAGCC 2520
 TGTGCTCCC GCTCAGGGG TGTCTTCCC AGGGCCGGTG GGGCCTTCTT GATGGCGGGG 2580
 CAGGTGGCTG AGCAGCTGCG GGGCTTCAAT GCCCAGCTCC AGCGGACCAG GCAGATGATT 2640
 AGGGCAGCGG AGGAATCTCG CTCACAGATT CAATCCAGTG CCCAGCGCTT GGAGACCCAG 2700
 GTGAGCGCCA GCGCTCCCA GATGGAGGAA GATGTGAGC GCACACGGCT CCTAATCCAG 2760
 CAGGTCCGGG ACTTCTTAAC AGACCCCGAC ACTGATGCAG CCACTATCCA GGAGGTGAGC 2820
 80 GAGGCCGTGC TGGCCCTGTG GCTGCCACA GACTCAGCTA CTGTTCTGCA GAAGATGAAT 2880
 GAGATCCAGG CCAATGAGC CAGGCTCCCC AACGTGGACT TGTGCTGTC CCAGACCAAG 2940
 CAGGACATTG CCGCTGCCCG CCGTTGCGG GCTGAGGCTG AGGAAGCCAG GAGCCGAGCC 3000
 CATGCAATGG AGGCCAGGT GGAAGATGTG GTTGGGAACC TGGGCGAGG GACAGTGGCA 3060
 CTCAGGAGAG CTCAGGACAC CATGCAAGGC ACCAGCCGCT CCTCTCGGCT TATCCAGGAC 3120
 85 AGGTTGCTG AGGTTGAGCA GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180
 AAGCAGCTGG GTGACTCTG GACACGAGT GAGGAGCTCC GCCACCAAG CCGGACGAGC 3240
 GGGGACAGG CAGTCCAGGC CCAGCAGCTT GCGGAAGGTG CCAGCGAGCA GGCATTGAGT 3300
 GCCCAAGAGG GATTGTAGAG AATAAACAA AAGTATGCTG AGTTGAAGGA CCGTTGGGT 3360

CAGAGTTCCA TGCTGGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG 3420
 GAGCTGTTTG GGGAGACCAT GGAGATGATG GACAGGATGA AAGACATGGA GTTGGAGCTG 3480
 CTGCGGGGCA GCCAGGCCAT CATGCTGCGC TCGGCGGACC TGACAGGACT GGAGAAGCGT 3540
 5 GTGGAGCAGA TCCGTGACCA CATCAATGGG CGCGTGCTCT ACTATGCCAC CTGCAAGTGA 3600
 TGCTACAGCT TCCAGCCCGT TGCCCCACTC ATCTGCCGCC TTTGCTTTTG GTTGGGGGCA 3660
 GATTGGGTTG GAATGCTTTC CATCTCCAGG AGACTTTCAT GCAGCCTAAA GTACAGCCCTG 3720
 GACCACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCCAAT 3780
 GGGACAGTTA CACTTGACAG ACAAAGATGG TGGAGATTGG CATGCCATTG AAACCTAAGAG 3840
 10 CTCTCAAGTC AAGGAAGCTG GGCTGGGCAG TATCCCCCGC CTTTAGTTCT CCACCTGGGA 3900
 GGAATCTGG ACCAAGCACA AAAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960
 AAAATCTTTG G

Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_000219

1 11 21 31 41 51
 MRPFLLCPA LPGLLHAQQA CSRGACYPPV GDLLVGRTRF LRASSTCGLT KPETYCTQYG 60
 20 ENQMKCKCKD SRQPHNYSH RVENVASSG PMRWWSQND VNPVSLQLDL DRRFQLQEVN 120
 MEFQGPMPAG MLIERSSDFG KTWRVYQYLA ADCTSTFFRV RQGRPQSWQD VRCQSLPQRP 180
 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQRLRLQGS FCHGHADRC PKPGASAGPS TAVQVHVCV CQHNTAGPNC ERCAPFYNNR 300
 PWRPAEGQDA HECQRCDCNG HSETCHFDPA VFAASQGAAYG GVCNDCRDHT EGKNCERCQL 360
 25 HYFRNRNPGA SIQETCISCE CPDPAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPQGCHR CDNLILGSRD DMPCEESGR CLCLPNVVG P KCDQCAPYHW KLASQGCEP 480
 CACDPHNSFQ PTVQPVHRAV PCREGFGGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG 540
 TEGPGCDKAS GRCLCRPGLT GPRCDQCQRG YCNRYPVCAV CHPCFQTYDA DLREQALRFG 600
 RLNRNATASLW SGPGLEDRLG ASRILDAKSK IEQIRAVLSS PAVTEQEVAV VASAILSLRR 660
 30 TLQGLQLDL LEEETLSLPR DLESLDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720
 AYEQSAQAQA QVSDSSRLLD QLRDSRREAE RLVQAGGGG GTGSPKLVAL RLEMSSLPDL 780
 TPTFNKLCGN SRQMACTPIS CPGELCPQDN GTACGSRCRG VLPRAGGAFI MAGQVAEQLR 840
 GFNAQLQRTQ QMIRAAEESA SIQSSAQRLL ETQVSASRSQ MEEDVRRTRL LIQQVRDFLT 900
 DEDTDAAITQ EVSEAVLALW LPTDTSATVLQ KMNEIQAIQA RLPNVLDVLS QTKQDIARAR 960
 35 RLQAEAEAR SRAHAVEGVQ EDVVGNLRQ TVALQEAQDT MQGTSRSLRL IQDRVAEVQQ 1020
 VLRPAEKLVT SMTKQLGDFW TRMEELRHQA RQQAEEAVQA QQLAEGASEQ ALSAQEGFER 1080
 IKQKYAEKLD RLQSSMLGE QGARIQSVKT EABELFGETM EMDRMKDM E LELLRGSQAI 1140
 MLRSADLTQL EKRVEQIRDH INGRVLYAT CK

Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_003722
 Coding sequence: 145-1491

1 11 21 31 41 51
 45 TCGTTGATAT CAAAGACAGT TGAAGGAAAT GAATTTTGAA ACTTCACGGT GTGCCACCCT 60
 ACAGTACTGC CCTGACCCTT ACATCCAGCG TTTCTAGTAA ACCCAGCTCA TTTCTCTTGG 120
 AAAGAAAGTT ATTACCGATC ACCCATGTCC CAGAGCACAC AGACAAATGA ATTCTCTAGT 180
 CCAGAGGTTT TCCAGCATAT CTGGGATTTT CTGGAACAGC CTATATGTTT AGTTCAGCCC 240
 50 ATTGACTTGA ACTTTGTGGA TGAACCATCA GAAGATGGTG CGACAAACAA GATTGAGATT 300
 AGCATGGACT GTATGCCCAT GCAGGACTCG GACCTGAGTG ACCCCATGTG GCCACAGTAC 360
 ACGAACCTGG GGCTCCTGAA CAGCATGGAC CAGCAGATTG AGAACGGCTC CTCGTCCACC 420
 AGTCCTCTATA ACACAGACCA CGCGCAGAAC AGCGTCACGG CGCCCTCGCC CTACGCACAG 480
 CCCAGCTCCA CCTTCGATGC TCTCTCTCCA TCACCCGCCA TCCCCTCCAA CACCGACTAC 540
 55 CCAGGCCCGC ACAGTTTCGA OGTGTCTTTC CAGCAGTCGA GCACCGCCAA GTCCGCCACC 600
 TGGACGTATT CCACTGAACT GAAGAAACTC TACTGCCAAA TTGCAAGAC ATGCCCATC 660
 CAGATCAAGG TGATGACCCC ACCTCCTCAG GGAGCTGTGA TCCGCGCCAT GCCTGTCTAC 720
 AAAAAGCTG AGCAGCTCAC GGAGGTGGTG AAGCGGTGCC CCAACCATGA GCTGAGCCGT 780
 GAATTCACG AGGACAGAT TGCCCCCTCT AGTCATTGTA TTCGAGTAGA GGGGAACAGC 840
 60 CATGCCAGT ATGTAGAAGA TCCCATCACA GGAAGACAGA GTGTGCTGGT ACCTTATGAG 900
 CCACCCAGG TTGCACATGA ATTCACGACA GTCTTGATCA ATTTTATGTG TAACAGCAGT 960
 TGTGTTGAGG GGATGAACCG CCGTCCAATT TTAATCATTG TTAATCTGGA AACCAGAGAT 1020
 GGGCAAGTCC TGGGCCGAGC CTGCTTTGAG GCCCGGATCT GTGCTTGCCC AGGAAGAGAC 1080
 AGGAAGGCGG ATGAAGATAG CATCAGAAAG CAGCAAGTTT OGGACAGTAC AAAGAACGGT 1140
 65 GATGATACGA AGCGCCGTT TCGTCAGAAC ACACATGGTA TCCAGATGAC ATCCATCAAG 1200
 AAACGAAGAT CCCAGATGA TGAACGTGTA TACTTACCAG TGAGGGGCCG TGAGACTTAT 1260
 GAAATGCTGT TGAAGATCAA AGAGTCCCTG GAACATATGC AGTACCTTCC TCAGCACACA 1320
 ATTGAAACGT ACAGGCAACA GCAACAGCAG CAGCACCAGC ACTTACTTCA GAAACATCTC 1380
 CTTTCAGCCT GCTTCAGGAA TGAGCTTGTG GAGCCCCGGA GAGAACTCC AAAACAATCT 1440
 70 GACGCTCTTC TTAGACATTC CAAGCCCCCA AACCGATCAG TGTACCCATA GAGCCCTATC 1500
 TCTATATTTT AAGTGTGTGT GTTGATTTT CATGTGTATA TGTGAGTGTG TGTGTGTGTA 1560
 TGTGTGTGCG TGTGTATCTA GCCCTCATAA ACAGGACTTG AAGACACTTT GGCTCAGAGA 1620
 CCCAAGTGT CAAAGGCACA AAGCCACTAG TGAGAGAATC TTTTGAAGGG ACTCAAACCT 1680
 75 TTACAGAAA GATGTTTTTC TGCAGATTTT GTATCCTTAG ACCGGCCATT GGTGGGTGAG 1740
 GAACCACTGT GTTTGTCTGT GAGCTTTCTG TTGTTTCTGT GAGGGGAGGG GTCAAGTGGG 1800
 GAAAGGGGCA TTAAGATGTT TATTGGAACC CTTTTCTGTC TTCTTCTGTT GTTTTCTTAA 1860
 AATTACAGG GAAGCTTTTG AGCAGGTCTC AAACCTAAGA TGTCTTTTAA AGAAAGAGGAG 1920
 AAAAAGTTG TTAATGTCTG TGATAAGTA AGTTGTAGGT GACTGAGAGA CTCAGTCAGA 1980
 CCCTTTTAA GCTGGTCATG TAATAATATT GCAAGTAGTA AGAAACGAAG GTGTCAAGTG 2040
 80 TACTGCTGGG CAGCGAGGTG ATCATTACCA AAAGTAATCA ACTTTGTGGG TGGAGAGTTC 2100
 TTTGTGAGAA CTTGCATTAT TTTGTCTCTC CCCTCATGTG TAGGTAGAAC ATTTCTTAAT 2160
 GCTGTGTACC TGCCTCTGCC ACTGTATGTT GGCATCTGTT ATGCTAAAGT TTTTCTGTGA 2220
 CATGAAACCC TGGAGACCTT ACTACAAAAA AACTGTTGTT TGGCCCCCAT AGCAGGTGAA 2280
 CTCATTTTGT GCTTTTAAAT GAAAGACAAA TCCACCCAG TAATATTGCC CTTACGTAGT 2340
 85 TGTTTACCAT TATTCAAGC TCAAAATAGA ATTTGAAGCC CTCTCAGAAA ATCTGTGATT 2400
 AATTTGCTTA ATTAGAGCTT CTATCCCTCA AGCCTACCTA CCATAAAACC AGCCATATTA 2460
 CTGATACTGT TCAGTGCATT TAGCCAGGAG ACTTACGTTT TGAGTAAGTG AGATCCAAGC 2520
 AGACGTGTTA AAATCAGCAC TCCTGGACTG GAAATTAAG ATTGAAAGGG TAGACTACTT 2580

TTCTTTTTTT TACTCAAAAG TTTAGAGAAT CTCTGTTTCT TTCCATTTTA AAAACATATT 2640
 TTAAGATAAT AGCATAAAGA CTTTAAAAAT GTTCTTCCCC TCCATCTTCC CACACCCAGT 2700
 CACCAGCACT GTATTTTCTG TCACCAAGAC AATGATTTCT TGTATTAGAG GCTGTGTGCT 2760
 TTGTGGATGT GTGATTTTAA TTTTCAATAA ACTTTTGTCAT CTTGGTTTAA AAGAAA

Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

1 11 21 31 41 51
 MSQSTQTNF LSPEVFQHIW DFLEQPICSV QPIDLNFVDE PSEDGATNKI EISMDCIRMQ 60
 DSDLSDPMPW QYTNLGLLNS MDQQIQNGSS STSPYNTDHA QNSVTAPSPY AQPSSTFDAL 120
 SPSPAIPSNT DYPGPHSFDV SFQSSSTAKS ATWTYSTELK KLYCQIAKTC PIQIKVMTFP 180
 PQGAVIRAMP VYKAEHVTE VVKRCPNHEL SREFNEGQIA PPSHLIRVEG NSHAQYVEDP 240
 ITGRQSVLVP YEPPQVGTEF TTVLYNFMEN SSCVGGMNRR PILIIVTLET RDGQVLGRRC 300
 FEARICACPG RDRKADSDSI RKQQVSDSTK NGDGTKRPPR QNTHGIQMTS IKKRRSPDDE 360
 LLYLPVRGRE TYEMLLKIKE SLELMQYLPQ HTIETYROQQ QQQHQHLLQK HLLSACFRNE 420
 LVEPRRETEK QSDVFFRHSH PPNRSVYP

Seq ID NO: 23 DNA sequence
 Nucleic Acid Accession #: NM_001944.1
 Coding sequence: 84-3083

1 11 21 31 41 51
 TTTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCACGGGCTC ACTTGGACTT 60
 TTTACACAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGGTCATA TTGGTTTCATG GAGAAATTGCG AATAGAGACT AAAGGTCAAT 180
 ATGATGAGAA AGAGATGACT ATGCAACAAG CTAAAAGAAG GCAAAAACGT GAATGGGTGA 240
 AATTGGCCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAAA AAGAAACCCA ATTGCCAAGA 300
 TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCGGCC TTTTGGAAATC TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCCCC 480
 AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCTTCCAGT ATTTTCAACA CAAATTTTCA TGGGTGAAAT TGAAGAAAT AGTGCTCAA 600
 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCCAC TTGAATTCTA 660
 AAATTCGCTT CAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCCTAAGCA 720
 GAAACACTGG GGAATCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT 780
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
 GTAATATTAA AGTGAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCAGGTAT TGAAGAAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAAATGAG 1020
 GAAATTTGGT TGAATATACA ACTGATCCTA GAACATAATGA AGGCATCTGT AAAGTGGTGA 1080
 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAACCTTAG TATTGCTGTC AAAACAAAG 1140
 CTGAATTTCA CCAATCAGTT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200
 AGGTAATAAA TGTAAAGAGAA GGAATTGCAT TCCGTCCCTG TCCCAAGACA TTTACTGTGC 1260
 AAAAAGGCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGGAAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAATATGT CATGGGACGT AACGATGGTG 1380
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAATT TGTCAAAAAT ATGAACCGAG 1440
 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CCGGTAAAC TTTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAAT GACAATTGTC 1560
 CAACAGCTGT CCTCGAAAAA GATGCAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCG 1620
 CTAGAACTAT GAATAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680
 TAAAGTTGCC TGCCGTATGG AGTATCAAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG 1740
 CCCAGGAACA GACACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCACTGT GACAACAGGG 1860
 GCATCTGTGG AACTTCTTAC CCAACCAAA GCCCTGGGAC CAGGTATGGC AGGCCGCACT 1920
 CAGGGAGGCT GGGGCTCGCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT 1980
 TGGCCCCCTT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040
 TGTGTTTTAT CCCAGTTTCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100
 GAGCCCATCC TGAAGACAAG GAAATCAAA ATATTGTGT GCCTCCTGTA ACAGCCAATG 2160
 GAGCCGATTT CATGGAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220
 TGGAGGCCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280
 GTGCTGCAGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340
 CTGGAGTTGG CATCTGTTC TCAGGGCAGT CTGGAACCAT GAGAACCAAG CATTCCACTG 2400
 GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460
 TTTCTCAGAA ASCATTGTCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520
 TGTGTATCTA TGATAATGAA GGGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580
 GTTGCACTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640
 TTAATAAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700
 CCTCTAAGA CAGCGGTTAT GGGATTGAAT CCTGTGCCA TCCCATAGAA GTCCAGCAGA 2760
 CAGGATTTGT TAAGTGCCAG ACTTTGTCAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCT 2820
 CTGGGTCTGT CCAGCCAGCT GTTTCATCC CTGACCTCT GCAGCATGGT AACTATTAG 2880
 TAAOGGAGAC TACTCGGCT TCTGGTTCCC TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940
 CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000
 CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060
 ATCCTTGCTC CCGTCTAATA TGACCAGAA GAGCTGGAAT ACCACCTGA CCAATCTGG 3120
 ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180
 TGGCACTTAT TAGCTTCTCT CATAAATCGA TCACGATTAT AAATTAATG TTTGGGTCA 3240
 TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA 3300
 TCTTAAAGTT TTTCAAAACC CTAATATCAT ATTCCG

Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

1 11 21 31 41 51

	MMGLFPRTTG	ALAIFFVVIL	VHGLRIETK	QGYDEEEMTM	QQAARRQKRE	VWPKAPPCRE	60
	GEDNSKRNPI	AKITSDYQAT	QKITYRISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
5	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIEENS	ASNSLVMILN	180
	ATDADEFNHL	NSKIAFKIVS	QEPAGTBMFL	LSRNTGVEVRT	LTSNLDREQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIKVKDV	NDNPPMFRDS	QYSARIEENI	LSSELLRFQV	TDLDEEYTDN	300
	WLAIVYFPTSG	NEGNWFBIQT	DPRTNIEGILK	VVKALDYEQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRVRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQY	AIDEDTNKAA	420
10	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
	VYVRVPDPND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNRY	TGPYTFALD	QPVKLPVWS	540
	ITTLNATSAL	LRAGEQIPFG	VYHISLVLT	SQNNRCMFR	SLTLEVQCQD	NRIGCTSYF	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPLLLLT	CDCGAGSTGG	VTGGFIFVFD	660
	GSEGTIHQWG	IEGAHPEDKE	ITNICVFPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSME	720
15	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	QSGTMRTRH	STGGTNKYA	780
	DGAISMNPLD	SYFSPQAFAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIAAD	840
	LDDSFLLSLG	PKFKLLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGSASL	SASGSVQPAV	SIPDPLQHGN	YLVETETYSAS	GSLVQPSLAG	FDPLLTQNV	960
	VTERVICPIS	SVPGNLGAPT	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

25	1	11	21	31	41	51	
	AGTATCCAG	GAGGAGCAAG	TGGCAGCTCT	TCGGACCTAG	GCTGCCCTG	CCGTATGTC	60
	GCAAGGGATC	CTTTCTCCG	CAGCGGGCTT	GCTGTCCGAT	GACGATGTC	TAGTTTCTCC	120
	CATGTTTGA	TCCACAGCTG	CAGATTGGG	GTCTGTGTA	CGCAAGAACC	TGCTATCAGA	180
	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
30	GGAGAAGGTG	AAATATATACT	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAACGACA	300
	GGAAGATCAG	GGTGTGTGCC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCACAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCAG	ATCTTTGGGC	CAGAAGTGGG	ACAGGCATCC	TTCTTCAACC	TAACGTGTAA	480
	GGAGATGTA	AAGGATGTAC	TCAAAGGGCA	GAACTGGCTC	ATCTATACAT	ATGGAGTCAC	540
35	TAACCTCAGG	AAAACCCACA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCCTCA	AGGCCCACTT	CATCCAACAC	CTGATCTGAA	660
	GCCCTTGCTC	TCCAATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGTCTA	ATGGAGGCCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGAA	780
40	GAGGAGTGTG	TACATCGAAA	GTCCGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTGC	840
	TGGGCTCTCT	TCTATCAGTC	AGTGTACCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGACATG	CCCCACTACC	TGTCCCGGCA	AACATTGCT	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAAC	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
45	AGATCTCAA	TGGATTCACT	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAAGTGGG	1140
	TCGTAAGAAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCAG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAAC	CTCTCTACAC	ACCCTGGGCC	GCTGTATTGC	1380
50	TGCCCTTCGT	CAAAACCCAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
	CAAGTTGAAT	CGAGTGTTC	AAAGTTTCTT	CACAGGCCGA	GGCGGTTCC	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGCTAGC	CAGGTGACTT	GTGCATGCCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTTAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTGTATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
	AGGAGCTCCT	ACAAGTTGTG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GGAGATGCAT	CTCCGAGATG	AAATTGTCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGTGTC	AGTGAACATT	TGGACACCCA	AAAGGAACCTA	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACCTAAAT	ATCTCAAGG	AGTCACTGAC	AAAGTTTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTGACAGGAA	GCCAGACAAC	2040
	AGTCAGTGGC	CCATCAGCAA	TCAGGGTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAAATGTTA	GAACCAACCAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAATT	AGAAGAGGGC	CAGAAGAATA	2280
	TAAAGCTGTT	GCGGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
65	CTTGTGTGCA	CAGCACTGGG	GCAGGAAAAC	TTCTGCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATCTGTG	TTGAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAATCAG	CAACCAAAACC	2580
70	AACAACCAAC	AGGGAAGAAA	CCATTCTCTC	GAAATTTACT	TCCCCGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCCTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTGACGT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTGTAT	2880
75	TATAACCAAC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTCTTAT	2940
	GCACACAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATTG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAAAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

80	1	11	21	31	41	51	
	MSQGILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSTSL	EDKQVPSSE	60
	SMEKVKVYLR	VRPLLPSELE	ROEDQGCVR	ENVETLVLA	PKDSFALKSN	ERIGQATHR	120
85	PTPSQIFGPE	VQQAASFNL	VKEMVKDVLK	GQNWLYTYG	VTNSGKTHTI	QGTIKDGGIL	180
	PRSLALIFNS	LQGLHPTPD	LKPLLSNEVI	WLDKSKIRQE	EMKLSLLNG	GLQEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLEDETS	HRWAQPDATP	LPVPANIRFS	300

IWISFFEIYN ELLVDLLEPP SQQRKRQTLR LCEDQNGNYP VKDLNWIHVQ DAEAEWKLLK 360
VGRKNQSPAS THLNQNSRRS HSIPIRILH LQEGGDIVPK ISELSLCDLA GSERCKDQKS 420
GERLKEAGNI NTSLHTLGRC IAALRQNNQN RSKQNLVPPR DSKLTRVFPQ PFTGRGRSCM 480
IVNVNFCAS YDETLHVAKF SAIASQVTC APTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 13-1424

1 11 21 31 41 51
TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
CTTCCCTGGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTGG TGAAAGATAC 120
TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCCGAT 300
GTCCATCATT TCAGGGGAAA GGCAGGGGGG CCGGTATGGA GGAACATTA TATCACTAC 360
AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAA 420
GCTTTCCAAG TATGGAGTAA TGTATCCCCC TTGAAATTCA GCAAGATTAA CACAGGCATG 480
GCTGACATTT TGGTGGTTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTTGTATGG 540
AAAGGTGGAA TCCTAGCCCA TGCTTTTGGA CTGGGATCTG GCATTGGAGG GGATGCACAT 600
TTGATGAGG ACGAATTCTG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT 660
GTTCACGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAAATG 720
TTCCCACTCT ACAATATGT TGACATCAAC ACATTTGCGC TCTCTGCTGA TGACATACGT 780
GGCATTCACT CCGTGTATGG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT 840
TCAGAACGAG CTCTCTGTGA CCCCATTGTT AGTTTTGATG CTGTCACTAC CGTGGGAAAT 900
AAGATCTTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAAG TTTCTGAGAG ACCAAAGACC 960
AGTGTTAATT TAATTTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATGTA AGCTGCTTAT 1020
GAAATTGAAG CAGAGAAATCA AGTTTTTCTT TTTAAAGATG ACAAATACTG GTTAATTAGC 1080
AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGTGTTT TCCTAACTTT 1140
GTGAAAAAAA TTGATGCAGC TGTTTTAAAC CCACGTTTTT ATAGGACCTA CTTCTTTGTA 1200
GATAACCACT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCCCTG TTATCCCAAA 1260
CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380
CGTATCACCA AACCACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAATG GTGTAATTA 1440
TGGTTTGTG TAGTTCCTT CAGCTTAATA AGTATTTATT GCATATTGTC TATGTCCTCA 1500
GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAACCA TAGGTAATGA 1560
TTATATAAAA TACATAATAT TTTTCAATTT TGAAACTCT AATTGTCCAT TCTTGCTTGA 1620
CTCTACTATT AAGTTTGAAG ATAGTTACCT TCAAGCAAG ATAATTCTAT TTGAAGCATG 1680
CTCTGTAAGT TGCTTCTCAA CATCCTTGGA CTGAGAAAT ATACTTACTT CTGGCATAAC 1740
TAAATTAAG TATATATATT TTGGCTCAA TAAATTG

Seq ID NO: 28 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MKFLILLLLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTQQLD TSTLEMMHAP RCGVPDVHFP REMPGGPVWR KHYITYRINN 120
YTFDNMRDED DYAIRKAFQV WSNVTPKFS KINTGMADIL VVPARGAHGD FHAFDGGKGI 180
LAHAFPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMPPTY 240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VITVGNKIPF 300
KFDPRFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
EPNPKSIHS FGFNPFVKKI DAAVFNPRFY RTYFPVDNQY WRVDERRQMM DPGYPKLITK 420
NFGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRTK TLKSNWFGC

Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_006115.1
Coding sequence: 236..1765

1 11 21 31 41 51
GCTTCAGGTT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCCCTC AGCACCCTC 60
CGGACACCCC CACCGCTTTC CAGGCGTGA CCTGTCAACA GCAACTTCG GGTGTGGTGA 120
ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT 180
GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
ACGAAGGCGT TTGTGGGGTT CCATTGAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
CCCACGGAGA CTTGTGGAGC TGGCAGGCA GAGCCTGCTG AAGATGAGG CCCTGGCCAT 360
TGCCCGCCCTG GAGTGTCTGC CCAGGAGGCT CTTCCTCCCA CTCTTCATGG CAGCCTTTGA 420
CGGAGAGCAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
GGATTACGG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAGAAGAGC GAAAGTAGA 720
TGGTTTGAGC ACAGAGGCG AGCAGCCCTT CATTCCAGTA GAGGTGCTCG TAGACCTGTT 780
CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
GAAAAATGTA CTACGCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
TATCAAGATG ATCCTGAAAA TGGTGAGCT GGACTCTATT GAAGATTGG AAGTGACTTG 960
TACCTGGAAG CTACCCACCT TGGCGAAAT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
CGGTAGACTC CTCTCTCTCC ACATCCATGC ATCTTCTTAC ATTTCCCCCG AGAAGGAAGA 1080
GCAGTATATC GCCCAGTTCA CCTCTCAGT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
TGTGGACTCT TTATTTTCTC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGTATGA 1200
CCCTTGGGAA ACCCTCTCAA TAACTAACTG CCGGCTTTG GAAGGGGATG TGATGCATCT 1260
GTCCAGAGT CCCAGGCTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
CCTGGTCTTT GATGAGTGTG GGATCAGGGA TGATCAGCTC CTGCCCCTCC TGCCCTTCCC 1440
GAGCCACTGC TCCAGCTTA CAACCTTAAG CTCTACGGG AATTCCATCT CCATATCTGC 1500

CTTGACAGGT CTCTGCAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
TGTCCTCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCTTA 1620
TCTGCTACGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
TAGTGCCAAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
5 GTGCCCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
ACAAATGTTT AGTGTAGTG AGGAAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
GTTCACTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGA AGGAGTTAAT 1980
GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
10 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
TGTTGAAAAA AAAGAGAAGC AATGTGAAGC AAAAAAATA AAAAAAAA

Seq ID NO: 30 Protein sequence:
Protein Accession #: NP_006106.1

1 11 21 31 41 51
GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCTT GCAGCGCTCT AGCACCCTCT 60
CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
20 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGCCA ACAAGTGACT 180
GAGACCTAGA AATCCRAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
ACGAAGGCGT TGTGTGGGTT CCATTTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
CCCAAGGAGA CTGTGTGGAG TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
TGCGCCCTCG GAGTTGCTGC CCAGGAGGCT CTTCCTGCTG CAGCCTTTGA 420
25 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
TCTGGGAGTG CTGATGAAGG GACACATCTC TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
GGATTACGG AAGAATCTCT ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
TCTGTACTCA TTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAAGAAGC GAAAAGTAGA 720
30 TGGTTTGAGC ACAGAGGCGC AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
GAAAAATGTA CTACGCTGTG GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
TATCAAGATG ATCCTGAAAA TGGTGACGCT GGACTCTATT GAAGATTGGG AAGTGACTTG 960
TACCTGGAAG CTACCCACCT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA TGATTAATCT 1020
35 GCGTAGACTC CTCTCTCCC ACATCCATGC ATCTTCTTAC ATTTCCCGG AGAAGGAAGA 1080
GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCTCTC AGGCTCTCTA 1140
TGTGGACTCT TTATTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGGC ACGTGATGAA 1200
CCCTTGGAA ACCCTCTCAA TAACTAAGT CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260
40 GTCCAGAGT CCAGCGTCA GTCAAGTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
CGATGTAAGT CCGGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTGCGCTTCC TGCCTTCCCT 1440
GAGCCACTGC TCCAGCTTA CAACCTTAAG CTCTACGGG AATTCATCT CCATATCTGC 1500
CTTGAGAGT CTCTGACAG ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
45 TGTCCCTCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCTTA 1620
TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
TAGTGCCAAAC CCTGTCTCTC ACTGTGGGGA CAGAACCTTC TATGACCCGG AGCCCATCCT 1740
GTGCCCCGTG TTCTGCTCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTCAG 1860
50 ACAAATGTTT AGTGTAGTG AGGAAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
GTTCACTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGA AGGAGTTAAT 1980
GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
TGTTGAAAAA AAAGAGAAGC AATGTGAAGC AAAAAAATA AAAAAAAA

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 64-2754

1 11 21 31 41 51
GGCAGGTCTC GCTCTCGGCA CCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC 60
CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCCT GCATCTGCTG 120
65 CTGACCCCTCG TGATCTTCAG TCGTATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCACTG 300
TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
70 TCGAAGACAA GACACACTAG AGAACTGTT CTGAGGCGTG CCAAGAGGAG ATGGGCACCT 480
ATTCTTGTCT CTATGCAAGA GAATTCCTTG GGCCTTTTCC CATTTGTTCT TCAACAAGTT 540
GAATCTGATG CAGCAGAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600
AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTGTATTG CTTATGCGTC AACTGCAGAT 720
75 GGATATTGAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
CACCCTGTTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAAT GCATACGCGC 900
CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACTTG GGTCTTTTC TGTGCATCCC 960
AGCAGAGGCG TAATCACCAC AGTCTCTCAT TATTGGACA GAGAGGTTGT AGACAAGTAC 1020
80 TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGATTGAT AGGCACATCA 1080
ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCATTTTCAG ACAAATGCT 1140
TATGAAGCAT TTGTAGAGGA AATGTCATTC AATGTGGAAT TCTTACGAAT ACCTATAGAA 1200
GATAAGGATT TAATTAACAC TGCCCAATTG AGAGTCAATT TTACCATTTT AAAGGGAAT 1260
GAAAATGGAC ATTTCAAAT CAGCAGAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
85 GTAAAGCCAC TGAATATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAAT 1380
GAAGCGCCAT TTGCTAGAGA TATTCACAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
GTTCTATGTA GGGATCTGGA TGAGGGGCTT GAATGCACTC CTGACGCCCA ATATGTGCGG 1500
ATTAAGAGAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

AATAGAAATG GCAATGGTTT AAGGTACAAA AAATTCGATG ATCCTAAAGG TTGGATCACC 1620
ATTGATGAAA TTTACGGGTC AATCATAACT TCCAAAATCC TGGATAGGGA GGTGAAACT 1680
CCCAAAATAG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAGATGA TAGATCATGT 1740
ACTTGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
GAATATGTAG TCATTTCGAA ACCAAAAATG GGGTATACCG ACATTTTAGC TGTGTATCCT 1860
GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCGTCTTTC ATATCAGAAA 1980
AATGCTGGAT TTCAAGAATA TACCATTCTT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040
GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCGTGGG 2100
ACTTCAAGGA GTACAGGAGT AATACCTGGA AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
ATAGCACTGC TCTTTTCTGT ATTGCTAACT TTAGTATGTG GAGTTTTTGG TGCAACTAAA 2220
GGGAAACGTT TTCTCGAAGA TTTAGCACAG CAAAACTTAA TTATATCAA CACAGAAGCA 2280
CCTGGAGACG ATAGAGTGTG CTCTGCCAAT GGATTTATGA CCAAACTAC CAACAACTCT 2340
AGCCAAGGTT TTTGTGGTAC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCAT 2400
GAAATGATGA AAGGAGGAAA CCAGACCTTG GAATCTGCCC GGGGGGCTGG GCATCATCAT 2460
ACCTCGAGCT CCGTGGGGT CTGCAAGTGA AAGCAGGAGG AGATGGCCCT TGACTTTTAA 2520
GAGTGGCACA GTTTTACTCA ACCCGCTCTC GGTGAAAAAT TGCATCGATG TAATCAGAA 2580
GAAGACCGCA TGCCATCCCA AGATTATGTC CTCACITATA ACTATGAGGG AAGAGGATCT 2640
CCAGCTGGTT CTGTGGGGT CTGCAAGTGA AAGCAGGAGG AGATGGCCCT TGACTTTTAA 2700
AATAATTGGG AACCCAAAT TATTACATTA GCAGAAGCAT GCACAAAGAG ATAATGTCAC 2760
AGTGCTACAA TTAGGCTCTT GTCAGACATT CTGGAGGTTT CCAAAAAATA TAITGTAAAG 2820
TCAATTTCAT ACATGTATGT ATATGATGAT TTTTCTCTCA ATTTGAATT ATGCTACTCA 2880
CCAATTATTA TTTTAAAGC CAGTTGTGTC TTAGTCTTTC CAAAAGTGA AAAATGTTAA 2940
AACAGACAAC TGGTAAATCT CAAACTCCAG CACTGGAATT AAGGTCTCTA AAGCATCTGC 3000
TCTTTTTTTT TTTTACGGAT ATTTTAGTAA TAAATATGCT GGATAAATAT TAGTCCAAAC 3060
ATAGCTAAGT TAGTCTAATA TCACATTATT ATGTATTAC TTTAAGTATG AGTTTAAAAA 3120
ATAACACAAG AATATTGAGT ATCACTATGT GAAGAAAGTT TTGGAAGAAGA AACAATGAAG 3180
ACTGAATTAAT ATTTAAAAATG TTGCAGCTCA TAAAGAATTG GGACTCACCC CTACTGCACT 3240
ACCAAAATCA TTGACCTTTG GAGGCAAAAT GTGTGGAAGT GCCCTATGAA GTAGCAATTT 3300
TCTATAGGAA TATGATTTGA AATAAATGTG TGTGTGTATA TTATTATTAA TCAATGCAAT 3360
ATTTAAAAATG AATGAGAAC AAAGAGGAAA ATGGTAAAAA CTGAAATGA GGCTGGGGTA 3420
TAGTTTGTCC TACAAATAGAA AAAAGAGAGA GCTTCCTAGG CCGTGGGCTCT TAAATGCTGC 3480
ATTATACTG AGCTATAGAG GAAATAGTTC CTGTCCAATT TGTGTAATT GTTTAAAAAT 3540
GTAAATAAAT TAACTTTTC TGGTTTCTGT GGAAGGAAA TAGGGAATCC AATGGAACAG 3600
TAGCTTTGCT TTGCAGTCTG TTTCAAGATT TCTGCATCCA CAAGTTAGTA GCAAACCTGGG 3660
GAATACTGCG TGCAGCTGGG TTTCCTGCTT TTTTGGTAGC AAGGGTCCAG AGATGAGGTG 3720
TTTTTTTCGG GGAGCTAATA ACAAAAACAT TTTAAAACTT ACCTTTACTG AAGTTAAATC 3780
CTCTATTGCT GTTCTATTTC TCTCTTATAG TGACCAACAT CTTTAAATG TAGATCCAAA 3840
TAACCATGTC TCCTCTAGAT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTACTGAAA 3900
GCACCCTGGG GAGATTGATT GTCCCTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG 3960
GTCTGGGAGC TACAAAATTT CATTTTCTC CTCACCTGCC TTCTCTGAG TGGCATTGGC 4020
CTGAATCAAG GAAAGCCAGG CCTGTGGGGC CCCCTTCTTT CGGCTTTCTG CTAAGCAAC 4080
ACCTCCAGCA GAGATTCCCT TAAGTGATC CAGGTTTTC ACCATCCTTC AGCGTGAATT 4140
AATTTTTAAT CAGTTTGCTT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAAT 4200
TTGAATGTAT AAAAGAAAAA GATCAAGTTG TCATTTTAGA ACAGAGGGAA CTTTGGGAGA 4260
AAGCAGCCCA AGTAGGTTAT TGTACAGTC AGAGGGCAAC AGGAAGATGC AGGCCTTCAA 4320
GGGCAAGGAG AGGCCAAG GAAATGGGT GGGAGTAAAA GCAACATCGT CTGCTTCATA 4380
CTTTTCTCTA GGCTTGGCAC TGCCCTTTCC TTTCTCAGGC CAATGGCAAC TGCCATTGGA 4440
GTCCGGGTAG GATCAGCCA ACCTCTCTC TATGGCTCAC CTTATTGGA GTGAGAAATC 4500
AAGGAGACAG AGCTGATCG ATGATGAGTC TGAAGGCATT TGCAGATGA CCCTGAACTG 4560
GTTGTGCAGA ACAACAAGG CATTATGCG AATTGTTGTA TTCTTCTGC AGCCTCCTT 4620
CTGGGCACTA AGAAGGTCTA TGAATTAAT GCCTATCTAA AATCTGATG TATTCTTACA 4680
TTTTCTGTTT TCTAATTTGA CCTTAAATC TATGTGTTT AGACTTAGAC TTTTATTGC 4740
CCCCCCCCC TTTTTTTTG AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG 4800
GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCGGGGT CATGCCATTC TCCTGCCTCA 4860
GCCTCTGAG TAGCTGGGAC TACAGGCGCC CACCACCAAG CCGGCTAAT TTTTGTATT 4920
TTTAATAGAG ACGGGGTTT ACTGTGTTAG CAGGATGGT CTGATCTCC TGACCTCGTG 4980
ATCCGCTGCT CTGGGCTCC CAAAGTCTG GATTACAGG CATGACCCAC CGCTCCCGGC 5040
CTTGTTTCTT GTTTAAAGTC GTCTCTTTT AATGTAATCA TTTTGAACAT GTGTGAAAGT 5100
TGATCATACG AATTGATCA ATCTGAAAT ACTCAACCA AAGACAGTCG AGAAGCCAGG 5160
GGGAGAAAGA ACTCAGGCA CAAATATTG GTCTGAGAA GTCAAGCTCT GTAAGCCTAG 5220
TTGCTGAAAT TTCTGCTGT AACCAGAGC CAGTTTATC TAACGGCTAC TGAAACACCC 5280
ACTGTGTTT GCTCACTCC TCACTCACG ATCAAAACCT GCTACCTCCC CAAGACTTTA 5340
CTAGTCCGA TAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTT ATAAAACCTC 5400
TAACCATCTC TTTGTTCTT GAACATGCTG AAAACCACCT GGTCTGCATG TATGCCGAA 5460
TTTGTAAATC TTTTCTCTA AATGAAATTA TAATTTTAGG GATTCATTC TATATTTTCA 5520
CATATGTAGT ATTATTATT CCTTATATG GTAAGGTGAA ATTTATGTTA TTTGAGTGTG 5580
CAAGAAAAA TATTTTTTAA GCTTTCATT TTCCCCAGT GAATGATTTA GAATTTTTTA 5640
TGTAATATA CAGAATGTT TTTCTTACT TTATAAGGAA GCAGCTGTCT AAAATGCAGT 5700
GGGGTTTGT TTGCAATGTT TTAACAGAG TTTTAGTATT GCTATTAAAA GAAGTTACTT 5760
TGCTTTTAAA GAACTTGGC TGCTTAAAT AAGCAAAAT TGGATGCATA AAGTAATATT 5820
TACAGATGTG GGGAGATGTA ATAAACAAT ATTAACCTGG TTCTTGTGTT TTGCTGTATT 5880
TAGAGATTAA ATAATTCTAA GATGATCACT TTGCAAAAT ATGCTTATGG CTGGCATGGA 5940
AATAGAAATA CTCAATTATG TCTTGTGTT ATTAATGGG AATATTGTTG ACAATGTTTC 6000
ATTATCAAT TGTCGATC ATTAAATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT 6060
GAAGCACAGC TTTAGATATG ATATCTATG ATATAAATTT TTGATCGGGT 6120
ATTAAGGATA TTAGAAGGTG GTTATAATG CAGAGTATTC CATGAATAGT ACATGACAC 6180
AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGAAAAAC ATGAGTTAAA AAGAAAAACA 6240
GGCAATATTG CAGTCTTGAT TCTGCCACT TTGCAAAAT ATGCTTATGG CTGGCATGGA 6300
CAAGATGATC CAACCAATAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
AGTGTGCTCC CCTACAAACG TTAAGACTGA TCAATTCAAA AATCTATTAG CTATATCAAA 6420
AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACCT CTATTGTAAC 6480
CATTATTTT GTGTATGCT TCAAGAAATG TCATTTGATT TTTGTTTGA ATAGTAAAA 6540
ACCGGATACA TTTCAGTGT CCTTCAGTAT TGATTTGGT GAATATTGGG TCATAATGGT 6600
TGAGAAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACCTAC 6660
TTCTGTGTA CCTTGAAAG GCTACTTAT TCCTCTCTTA GCTTCTCAT TAAATCAAT 6720
GAACAATGCC AGCCTCATGG GGTGTTGAA TGATTAATTA AGTTAATATA CCTAAGTAC 6780

ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAAATTAT 6840
GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAAATAA AGTTTGTGCA 6900
TATATATAAT CCGGAACAT G

Seq ID NO: 32 Protein sequence:
Protein Accession #: NP_001932.1

1	11	21	31	41	51	
MAAAGPRRSV	RGAVCLHLLL	TLVIFSRDGE	ACKKVILNVP	SKLEADKIIG	RVNLEECFRS	60
ADLIRSSDPD	FRVLNDGSVY	TARAVALSDK	KRSFTIWLSD	KRKQTQKEVT	VLLHQQKKVS	120
KTRHRETVL	RRAKRRWAPI	PCSMQENSLG	PFPLFLQQVE	SDAAQNYTVF	YSISGRGVDK	180
EPLNLFYIER	DTGNLFCTRP	VDREYDVDFD	LIAYASTADG	YSADLPLPLP	IRVEDENDNH	240
PVFTEAIYNF	EVLESSRPGT	TVGVVCATDR	DEPDTMHTRL	KYSILQQTFR	SPGLFSVHPS	300
TGVITTVSHY	LDREVVDKYS	LIMKVQDMDG	QFFGLIGTST	CIITVTDSDN	NAPTFRQNAV	360
EAFVEENAFN	VEILRIPIED	KDLINTANWR	VNFTILKGNE	NGHFKISTDK	ETNEGVLSSV	420
KPLNYEENRQ	VNLEIGVNNE	AFFARDIPRV	TALNRLVTV	HVRDLDEGPE	CTPAQYVRI	480
KENLAVGSKI	NGYKAYDPEN	RNGNGLRYKK	LHDPKGWITI	DEISGSIITS	KILDREVETP	540
KNELYNITVL	AIDKDRSCT	GTLAVNIEDV	NDNPPEILQE	YVVICKPKMG	YTDILAVDPD	600
EFVHGAPFFY	SLPNTSPEIS	RLWSLTKVND	TAARLSYQKN	AGFOEYTIPI	TVKDRAGQAA	660
TKLLRVLNCE	CTHPTQCRAT	SRSTGVILGK	WAILAILLGI	ALLFSVLLTL	VCGVFGATKG	720
KRFPEDLAQV	NLIISNTEAP	GDDRVCSSANG	FMTQTNNSS	QGFCGTMGSG	MKNGGQETIE	780
MMKGGNQTL	SCRGAGHHHT	LDSCRGGHTE	VDNCRYTYSE	WHSFTQPRLG	EKLHRCNQNE	840
DRMPSQDYVL	TYNBYGRGSP	AGSVGCCSEK	QEEDGLDPLN	NLEPKFITLA	EACTKR	

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: Eos sequence.
Coding sequence: 64-2583

1	11	21	31	41	51	
GGCAGGTCTC	GCTCTCGGCA	CCCTCCCGGC	GCCCGCGTTC	TCCTGGCCCT	GCCCGGCATC	60
CCGATGGCCG	CCGCTGGGCC	CCGGCGCTCC	GTGCGCGGAG	CCGTCTGCCT	GCATCTGCTG	120
CTGACCCCTG	TGATCTTCAG	TGCTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTTAATGTA	180
CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGAAGA	GTGCTTCAGG	240
TCTGCAGACC	TCATCCGGTC	AAGTGATCCT	GATTTCAGAG	TTCTAAATGA	TGGGTCAGTG	300
TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
ATTCTTGTCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
GAATCTGATG	CAGCAGACAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
AAAGAACCTT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAAATCTATT	TTGCACTCGG	660
CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AACCTGCAGT	720
GGATATTTCG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
CACCTCTGTT	TCACAGAAGC	AATTTATAAT	TTTGAAAGTT	TGGAAGTAG	TAGACCTGGT	840
ACTACAGTGG	GGGTGGTTTT	TGCCACAGAC	AGAGATGAAC	CGGACACAA	GCATACGCGC	900
CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTACACCTG	GGCTCTTTTC	TGTGCATCCC	960
AGCAGAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
ACTTGTATCA	TAACAGTAAC	AGATTCAAA	GATAATGCAC	CCACTTTCAG	ACAAAATGCT	1140
TATGAAGCAT	TTGTAGAGGA	AAATGCATTC	AATGTGGAAA	TCTTAGCAAT	ACCTATAGAA	1200
GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAT	1260
GAAAATGGAC	ATTTCAAAAT	CAGCAGACAC	AAAGAACTA	ATGAAGGTGT	TCTTCTGTGT	1320
GTAAGCCAC	TGAATATGTA	AGAAAACCGT	CAAGTGAACC	TGGAATTGG	AGTAAACAA	1380
GAAGCGCCAT	TTCTCTGAAG	TATTCCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGTTTACA	1440
GTTCAATGTA	GGGATCTGGA	TGAGGGGCCCT	GAATGCACTC	CTGCAGCCCA	ATATGTGCGG	1500
ATTAAGAAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCAATG	ATCTTAAAGG	TTGGATCACC	1620
ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
CCCAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAATGATA	ATCCACCAGA	AATACTTCAA	1800
GAATATGTAG	TCATTGTCAA	ACCAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
AGTAGACTGT	GGAGCCTCAC	CAAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
AATGCTGGAT	TTCAAGAATA	TACCATTCTC	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
ACTTCAAGGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
ATAGCACTGC	TCCTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
GGGAAACGTT	TTCTCTGAAG	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGTA	CCCAAACTAC	CAACAACCTC	2340
AGCCAAAGTT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCAAT	2400
GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
ACCTGGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACTTACTCG	2520
GAGTGGCACA	GTTTACTCTA	ACCCCGTCTC	GGTGAAGAAT	CCATTAGAGG	ACACACTGGT	2580
TAAAAATTAA	ACATAAAGAA	ATTGTCATCG	ATGTAATCAG	AATGAAGACC	GCATGCCATC	2640
CCAAGATTAT	GTCTCTCACT	ATAACTATGA	GGGAAGAGGA	TCTCCAGCTG	GTTCTGTGGG	2700
CTGCTGCAGT	GAAAGCAGG	AAGAAGATGG	CCTTGACTTT	TTAAATAATT	TGGAACCCAA	2760
ATTTATTACA	TTAGCAGGAG	CATGCACAAA	GAGATAATGT	CACAGTGCTA	CAATTAGGTC	2820
TTTGTGACAG	ATTCTGGAGG	TTTCCAAAAA	TAATATTGTA	AAGTTCAAAT	TCAACATGTA	2880
TGTATATGAT	GAITTTTTTT	TCAATTTTGA	ATTATGCTAC	TCACCAATTT	ATATTTTTAA	2940
AGCCAGTTGT	TGCTTATCTT	TTCCAAAAAG	TGAAAAATGT	TAAAAACAGC	AACTGGTAAA	3000
TCTCAAACTC	CAGCACTGGA	ATTAAGGTCT	CTAAAGCATC	TGCTCTTTTT	TTTTTTTACG	3060
GATATTTTAT	TAATAAATAT	GCTGGATAAA	TATTAGTCCA	ACAATAGCTA	AGTTATGCTA	3120
ATATCACATT	ATTATGTATT	CACCTTAAGT	GATAGTTTAA	AAAATAAACA	AGAAATATTG	3180
AGTATCACTA	TGTGAAGAAA	GTTTTGGAAA	AGAAACAATG	AAGACTGAAT	TAAATTAAAA	3240
ATGTTGCAGC	TCATAAAGAA	TTGGGACTCA	CCCCTACTGC	ACTACCAAA	TCATTTGACT	3300

TTGAGGCAAA AATGTGTGTA AGTGCCCTAT GAAGTAGCAA TTTTCTATAG GAATATAGTT 3360
 GGAAATAAAT GTGTGTGTGT ATATTATTAT TAATCAATGC AATATTATAA ATGAAATGAG 3420
 AACAAAGAGG AAAATGGTAA AAACCTTGAA TGAGGCTGGG GTATAGTTTG TCCTACAATA 3480
 GAAAAAGAGG AGAGCTTCCT AGGCTGGGCT TCCTAAATGC TGCAITATAA CTGAGTCTAT 3540
 5 GAGGAAATAG TTCTGTGCCA ATTTGTGTAA TTTGTTTAAA ATGTATAATA AATTAAACTT 3600
 TTCTGGTTTC TGTGGGAAGG AAATAGGGAA TCCAATGGAA CAGTAGCTTT GCTTTGCAGT 3660
 CTGTTTCAAG ATTTCTGCAT CCACAAGTTA GTAGCAAACT GGGGAATACT CGCTGCAGCT 3720
 GGGGTTCCCT GCTTTTGTGT AGCAAGGGTC CAGAGATGAG GTGTTTTTTT CGGGGAGCTA 3780
 10 ATAACAAAAA CATTTTAAAA CTACCTTTA CTGAAGTTAA ATCCTCTATT GCTGTTTCTA 3840
 TTCTCTCTTA TAGTGACCAA CATCTTTTAA ATTTAGATCC AAATAACCAT GTCCTCCTAG 3900
 AGTTTAGAGG CTAGAGGGAG CTGAGGGGAG GATCTTACTG AAAGCACCTT GGGGAGATTG 3960
 ATTTGCTCTA AACCTAAGCC CCACAAACTT GACACCTGAT CAGGCTCTGGG AGCTACAAAA 4020
 TTCTATTTTT TTCTCTCTCT CCCTCTCTCT GAGTGGCATT GGCCTGAATC AAGGAAAGCC 4080
 15 AGGCTTGTGT GGGCCCTCTT TTTCGGCTTT CTGCTAAAGC AACACCTCCA GCAGAGATTG 4140
 CCTTAAGTGA CTCCAGGTTT TCCACCATCC TTCAGCGTGA ATTAATTTTT AATCAGTTTG 4200
 CTTTCTCCAG AGAAATTTTA AAATAATAGA AGAAATAGAA ATTTTGAATG TATAAAAGAA 4260
 AAAGATCAAG TTGTCATTTT AGAACAGAGG GAACCTTGGG AGAAAGCAGC CCAAGTAGGT 4320
 TATTGTGACA GTCCAGAGGC AACAGGAAGA TGCAGGCCTT CAAGGGCAAG GAGAGGCCAC 4380
 20 AAGGAATATG GGTGGGAGTA AAAGCAACAT CGTCTGCTTC ATACTTTTTT CTAGGCTTGG 4440
 CACTGCCTTT TCCTTTCTCA GGCCTAATGGC AACTGCCATT TGAGTCCGGT GAGGGATCAG 4500
 CCAACCTCTT CTCTATGGCT CACCTATTAT GGAGTGAGAA ATCAAGGAGA CAGAGCTGAC 4560
 TGCATGATGA GTCTGAAGGC ATTTGCAGGA TGAGCCTGAA CTGGTGTGTC AGAACAAACA 4620
 AGGCATTTCAT GGGAAATGTT GTATTCTCTC TGCAGCCCTC CTTCTGGGCA CTAAGAAAGT 4680
 CTATGAATTA AATGCTATC TAAATTCCTG ATTTATTCTT ACATTTCCTG TTTTCTAATT 4740
 25 TGACCTTAAA ATCTATGTGT TTTAGACTTA GACTTTTTAT TGCCCCCCCC CCCTTTTTTT 4800
 TTGAGACGGA GTCTCGCTCT GACGCACAGG CTGGAGTGCA GTGGCTCCGA TCTCTGCTCA 4860
 CTGAAAGCTC CGCCTCCCGG GTTCATGCCA TTCTCTGCC TCAGCCTCCT GAGTAGCTGG 4920
 GACTACAGGC GCCCACCACC AGCCCGGCT AATTTTTTGT ATTTTATAA GAGACGGGGT 4980
 30 TTCCTGTGT TAGCCAGGAT GGTCTCGATC TCCTGACCTC GTGATCCGCC TGCCCTCGGC 5040
 TCCCAAAGTG CTGGGATTAC AGGCATGACC CACCGCTCCC GGCCTGTGTT TCCGTTTAAA 5100
 GTCGCTCTCT TTTAATGTAA TCATTTTGAA CATGTGTGAA AGTTGATCAT ACGAATTGGA 5160
 TCAATCTTGA AATACTCAAC CAAAGACAG TCGAGAAGCC AGGGGGAGAA AGAAGCTCAG 5220
 GCACAAATAA TTGCTCTGAG AATGGAAATC TCTGTAAGCC TAGTTGCTGA AATTCTCTGC 5280
 35 TGTAACAGCA AGCCAGTTTT ATCTAACGGC TACTGAAACA CCCACTGTGT TTTGCTCACT 5340
 CCCACTCACC GATCAAAACC TGCTACCTCC CCAAGACTTT ACTAGTCCCG ATAAACCTTC 5400
 TCAAGAGGCA ACCAGTATCA CTCCCTGTT TATAAAACCT CTAACCATCT CTTTGTCTCT 5460
 TGAACATGCT GAAACCCACC TGGCTCGCAT GTATGCCCGA ATTTGTAATT CTTTCTCTC 5520
 AAATGAAAAA TTAATTTTAG GGATTCATT CTATATTTT ACATATGTAG TATTATTATT 5580
 40 TCCTTATATG TGTAAGGTGA AATTTATGGT ATTTGAGTGT GCAAGAAAA ATATTTTAA 5640
 AGCTTTTCTT TTTCCCCCAG TGAATGATTT AGAATTTTT ATGTAAATAT ACAGAAATGT 5700
 TTTTCTTACT TTTATAAGGA AGCAGCTGTC TAAATGCAG TGGGGTTTGT TTTGCAATGT 5760
 TTTAAACAGA GTTTTAGTAT TGCTATTAAA AGAAGTTACT TTGCTTTTAA AGAACTTGG 5820
 CTGCTTAAAA TAAGCAAAAA TTGGATGCAT AAAGTAATAT TTACAGATGT GGGGAGATGT 5880
 45 AATAAAACAA TATTAACCTG GCTGCTTAAA ATAAGCAAAA ATTGGATGCA TAAAGTAATA 5940
 TTTACAGATG TGGGGAGATG TAATAAAACA ATATTAACCT GTTTCTCTGT TTTTCTGTGA 6000
 TTTAGAGATT AAATAATTCT AAGATGATCA CTTTGCAAAA TTATGCTTAT GGCTGGCATG 6060
 GAAATAGAAA TACTCAATTA TGTCTTTGTT GTATTAATGG GGAATATTTT GGCAATGTT 6120
 TCAITATCAA ATTTGTGACA TCATTAATAT ATATTGTAAT GTTGGGAAGA GATCACTATT 6180
 50 TTGAAGCACA GCTTTACAGA TGAGTATCTA TGATACATAT GTATAATAA TTTTGATCGG 6240
 GTATTAAAAA TTTATAAGG TGTTATAAT TGCAGAGTAT TCCATGAATA GTACACTGAC 6300
 ACAGGGGTTT TACTTTGAGG ACCAGTGTAG TCAAGGGAAG ACATGAGTTA AAAAGAAAAG 6360
 CAGGCAATAT TGCAGTCTTG ATCTGCCAC TTACAGGATA GATAATGCCT GAACTTTAA 6420
 GACAAGATGA TCCAACCATTA AAGGTGCTCT GTGCTTCACA GTGAATCTTT TCCCATGCA 6480
 55 GGAGTGTGCT CCCTTACAAA CGTTAAGACT GATCATTTCA AAAATCTATT AGCTATATCA 6540
 AAAGCCTTAC ATTTTAAAT AGGTTGAACC AAAATTTCAA TTCCAGTAAC TTCTATTGTA 6600
 ACCATTATTT TTGTGTATGT CTTCAAGAA GTTCATTGGA TTTTGTGTTG TAATAGTAAA 6660
 ATACCGGATA CATTTCACTG GTCCTTCAGT ATTGATTGG TTGAATATTG GGTCTAATG 6720
 GTTGAGAAGC ATGGACACTA AGCCAGAAAT GCTTGATAT GAATCCTGGA TCTGTCACTT 6780
 60 ACTTCTGTGT GACCTTTGAA AGGCTACTTA TTTCTCTCT TAGCTTTCTC ATTAATAATCA 6840
 ATGAACAAAT CCAGCCTCAT GGGGTGTTG AATGATTAAT TTAGTATAA TACCTAAAGT 6900
 ACATAGAACAT CTGCTGACAT ATAGTAAAAG AATTATAAGT GTGAGTAGT TGGTAAAT 6960
 ATGTAGTTGG ATATACTACC GAACAATATC TAATCTCTTT TTAGGGAAAT AAAGTTTGTG 7020
 CATATATATA ATCCGAAAC ATG

Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_077741.1

1 11 21 31 41 51
 70 MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLEHQKKVS 120
 KTRHRTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQOVE SDAAQNYTVF YSISGRGVDK 180
 EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240
 75 PVFTEALYNF EVLESSRPGT TVGVVCATDR DEPDTHMTRL KYSILQQTFR SPGLFSVHPS 300
 TGVITTVSHY LDREVQDMG QFFGLIGTST CIITVDSND NAPTFRQNAV 360
 EAPVEENAFN VEILRIPIED KDLINTANWR VNFTILKNE NGHFKISTDK ETNEGVLVSV 420
 KPLNYEENRQ VNLEIGVNE AFFARDIPRV TALNRLVTV HVRDLDEGPE CTPAAQVYRI 480
 KENLAVGSKI NGYKAYDPEN RGNGLRYKK LHPKGNITI DEISGSIITS KILDREVETP 540
 80 KNELYNITVL AIDKDRSCT GTLAVNIEDV NDNPPILQE YVVICKPKMG YTDILAVDPD 600
 EPVHGAPYPF SLNTPSPETS RLWSLTQVND TAARLSYQKN AGFQETIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHTPTCRAT SRSTGVILGK WAILAILGI ALLFSVLLTL VCGVFGATKG 720
 KRFPEDLAQQ NLIISNTEAP GDDRVCASANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGNGQTLK SCRGAGHHHT LDCRGGHTE VDNCRYTYSE WHSFTQPRLG EESIRGHTG

Seq ID NO: 35 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 146-1273

	1	11	21	31	41	51	
	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCC	AGACACGGTC	60
5	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCTGTT	CCTTTTCCAC	GCATTTTCCA	120
	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAAAT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACTTGC	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
	TGAAATTGGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCCTTG	GATTTCAAAC	360
10	AGTAACATCG	GATGTAAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTCTTAC	AGAGTTTATC	AGCTCTACGA	AGAGACCCTA	480
	TGCAAGAGAA	TTGGAACCTG	TTGACTTCAA	AGATAAATG	GAAGAAACGA	AAGGTCAGAT	540
	CAACAACCTA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAACAG	600
	TGTGAACGAC	CAGACCAAAA	TCCTTGTGGT	TAAATGCTGCC	TACTTTGTTG	GCAAGTGGAT	660
15	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAACCACTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAACAA	TTGACAGTAT	780
	CAATGTGAAG	ATCATAGAGC	TTCTTTTCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGGAGAAG	ATTGAAAAAC	AACTCAACTC	900
	AGAGTCACTG	TCACAGTGGG	CTAATCCAG	CACCATGGCC	AATGCCAAGG	TCAAACCTCT	960
20	CATTCCAAAA	TTTAAGGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTTAGG	1020
	GCTGAAACAT	ATCTTCAGTG	AAGACACATC	TGATTTCTCT	GGAATGTGAG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAAATGTTA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGTTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACAAG	GATGAATTGA	ATGCTGACCA	1200
	TCCTTTTATT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAATT	1260
25	CTGTTCTCCT	TAAGTGGCAT	AGCCCATGTT	AAGTCCTCCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAAT	GCTAATGTTG	1380
	CTGATCAGG	AAGCCGCCAG	TACTTGTCT	ATGTAGCCTT	CACACAGATA	GACCTTTTCT	1440
	TTTTTCCAAT	TCTATCTTTT	GTTTCCTTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
	TGAAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCGGGGGT	1560
30	AGTTGGCAGA	AAATGAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCAGC	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTCCAGACA	TCTCGCTTC	1680
	CCTGAAAGAG	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAGTC	CTTATGTTAA	GCCCTGGCAG	1800
	GCAGGTGTTT	ATTAAATTC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
35	CTGTATGTTA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAAATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTTG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGAGAGC	TTTTAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTGATA	2160
	GCTGTCCCAT	CTGGTCATGT	GGTTGGCACT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGGAT	TCTACAATA	GCCGATATCA	GAATTTGTGT	TGAAGGAAC	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAAGTAAAGT	2340
	GATTAAGGTG	CTCAGCTTAC	CTTGACACAT	AGTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATGGCAAG	CATGTAACTT	ATATTAATAG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTTGCCG	GTTCATGGAT	TACTTCTCTA	TAAAAAATAT	ATATTTACCA	AAAAATTTTG	2520
	TGACATTCCT	TCTCCCATCT	CTTCTTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAAATTTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

	1	11	21	31	41	51	
	MDALQLANSA	FAVDLPKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
55	ENVKDIPPGF	QVTSDVNKL	SSFYSLKLIK	RLYVDKSLNL	STEFISSTKR	PYAKELETVD	120
	FKDKLEETKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAYFVKG	WMKKFPESET	180
	KECPERLNKT	DTKPVQMMNM	EATFCMGNID	SINCKIIELP	FQNKHLSMFI	LLPKDVEDES	240
	TGLEKIEKQL	NSESLSQWNT	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIPSED	300
60	TSDFSGMSET	KGVALSNIH	KVCLEITEDG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFFG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

	1	11	21	31	41	51	
	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
70	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TGATGTCTTT	CTACGGGCTG	TAGCCGAGA	120
	CCATGGCCCA	GTTTGGAGGC	CTGCCGTGTC	CCCTGGACCA	GACCCGTCCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCCTGCT	GTCGCGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
	TGAAGCTTGG	AGGAGGTACT	TCTGTTGGCC	TCCTTGGGGG	ACTGCTTGA	AAAGTGACGT	360
75	CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CAGTGACCCC	CAGCTGCTGG	420
	AACTTGGCCT	TGTGAGAGGC	CCTGATGGCC	ACCGTCTCTA	TGTACCATC	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATAAG	CCCTGGTTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	TTGGTGACTG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
	CCCTCCCAT	TCAAGGTCTT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCCTGCTG	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCCTCCA	GGAGGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAGTGCTCA	CAGATGGCTG	900
85	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCCTT	960
	TCCCACCAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      MFQTGGLIVF YGLLAQTMQA FGGLPVPLDQ TLPLNVNPFAL PLSFTGLAGS LTNALSNGLL 60
      SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
      VQSPDGHRLY VTITPLGKIQ VNTPLVGASL LRLAVKLDIT AEILAVRDQK ERIHLVLGDC 180
10     THSPGSLQIS LLDLGLPLPI QGLLDSLITGI LNKVLPPLVQ GNVCPVLNVEV LRGLDITLVH 240
      DIVNMLIHGL QFVIKV
```

Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

```
15      1      11      21      31      41      51
      |      |      |      |      |      |
      CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAAAGT 60
20     TCCTGGAAGT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
      TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCCCTGGC AGAGGCTCCT GCTCACAGCC 180
      TCACTTCTAA CCTTCTGGAA CCGGCCCAACC ACTGCCAAGC TCACATTGGA ATCCACGCCG 240
      TTCAATGTCT CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT 300
      TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
25     GTAATAGGAA CTCACAAGC TACCCAGGG CCGCATACA GTGGTCGAGA GATAATATAC 420
      CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAAATG ACACAGGATT CTACACCCTA 480
      CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTCCG GGTATACCCG 540
      GAGCTGCCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
      GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
30     CAGAGCCTCC CGTCTAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
      TTCAATGTCA CAGAAATGGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAAT 780
      GCCAGGCGCA GTGATTCAGT CATCTGAAT GTCTCTATG GCCCGGATGC CCCACCAATT 840
      TCCCCTCTAA ACATCATCTT CAGATCAGGG GAAATCTGGA ACCTCTCCTG CCACGAGGCC 900
35     TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
      GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
      AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
      CCAAACCCCT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
      TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
      CTCCCGGTCA GTCCGAGCT GCAGCTGTCC AATGACAACA GGACCCCTAC TCTACTCAGT 1260
40     GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAAT AAGTGTGAC 1320
      CACAGCGACC CAGTATCTCT GAATGTCTCT TATGGCCCGC ACGACCCAC CATTTCCCCC 1380
      TCATACACCT ATTACGCTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
      CCACCTGCAC AGTATTCTTG GCTGATTGAT GGAACATCC AGCAACACAC ACAAGAGCTC 1500
      TTTATCTCCA ACATCTCTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
45     GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCAAG 1620
      CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
      TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
      GTCACTCCCA GGCTGCAGCT GTCCAAATGGC AACAGGACCC TCACTCTATT CAATGTCACA 1800
      AGAAATGACG CAGAGCCCTA TGTATGTGGA ATCCAGAAGT CAGTGAGTGC AAACCGCAGT 1860
50     GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
      TCGTCTTACC TTTGGGAGG GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC 1980
      CCGCAGTATT CTGGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
      GCCAAATCAA CGCAAAATAA TAAACGGACC TATGCCTGTT TTGTCTCTAA CTGGCTACT 2100
      GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160
55     CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
      TAGCAGCCTT GGTGTAGTTT TTTCAATTTC GGAAGACTGA CAGTTGTTTT GCTTCTTCTT 2280
      TAAAGCATTG GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
      AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
      AAATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCCAAGTTA CTCGGGAGGC 2460
60     TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
      ACTGCATCCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580
      TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
      AACTTTAATG AACTAATCGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
      TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTTCTTA AATGCTTGT 2760
65     TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTTACAG CAATTGATA 2820
      AAATATACCT TTGTGAACAA AATTTAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
      AGACTTGGGA AACTATTTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
      TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA
```

Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

```
70      1      11      21      31      41      51
      |      |      |      |      |      |
      MESPSAPPHR WCIPWQRLLT TASLLTFWNP PTTAKLTIES TFPNVAEGKE VLLLVHNLPO 60
75     HLEFGYSWYRG ERVDGNRQII GYVIGTQOAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
      TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPFVEDK DAVAFTEPE TQDATYLVWV 180
      NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 240
      TISPLATSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQQS TQELFIPNIT VNNSGSYTCQ 300
80     AHNSTDTGLNR TTVTITIVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLVWVNN 360
      QSLPVSPRLQ LSNDRNLTLT LSVTRNDVGP YECGIONELS VDHSDPVILN VLYGPDPTI 420
      SPSYTYRFG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN 480
      NSASGHSRTT VKTITVSSEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
85     LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLVL VYGPDPPIISF 600
      PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPOQHTQVL FIAKITPNNN GTYACFVSNL 660
      ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
```

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

```
1      11      21      31      41      51
|      |      |      |      |      |
AATCCCGACA ATGGCGAAGG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT 60
10 TGGAATGTG ATTATTGGTT GTTGC GGCCAT TGCCTGACT GCGGAGTGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTTCATT TGATGTTTAT 300
AGTATATGCC TTGGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
15 ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GCGTAAATG GTCCATCAGA CTGGCAAAA TACACATCTG CCTTCCGGAC 540
TGAGAAATAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACTCTC AACCTGAGG CTGTGAACT AGGCGTGCTT GGTTTTATAT ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
20 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA
```

Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

```
1      11      21      31      41      51
|      |      |      |      |      |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
30 IGIFVIGICLF CLSVLGIUVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TORDFFTPNL 120
FLKQMLERYQ NNSPPNDDQ WKNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
DADYFWPRQC CVMNMLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVANWFGFAI 240
LCWTFWVLLG TMFYWSRIEY
```

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

```
1      11      21      31      41      51
|      |      |      |      |      |
GCCGGACAGA TCTGCGCGTA TCCTGGAGCC GGCCCAAGTTG TGAAGTAGGA GAGCTTTGGG 60
40 ACCTCTGTCC CAAGCAAGAG AGATGAATGG AGAGTATAGA GGCAGAGGAT TTGGACGAGG 120
AAGATTTCAA AGCTGGAAGAA GGGGAAGAGG TGGTGGGAAC TTCTCAGGAA AATGGAGAGA 180
AAGAGAACAC AGACCTGATC TGAGTAAAC CACAGGAAAA CGTACTTCTG AACAAACCCC 240
45 ACAGTTTTTG CTCTCAACAA AGACCCCA CA GTCAATGCAG TCAACATTGG ATCGATTCA 300
ACCATATAAA GGCCTGAAGC TTTATTCTC TGAAGTTTAC AGCGATAGCT CTCCTTTGAT 360
TGAGAAGATT CAAGCATTTG AAAAATTTT CACAAGGCAT ATTGATTGTG ATGACAAGGA 420
TGAAATAGAA AGAAAGGGA GTATTTTGGT AGATTTTAAA GAACTGACAG AAGGTGGTGA 480
AGTAACTAAC TTGATACCAG ATATAGCAAC TGAAGTAAAG GATGCACCTG AGAAAACTCT 540
50 GGCTTGCAATG GGTTCGGCAA TACATCAGGT GTTAACTAAG GACCTTGAAA GGCATGCAGC 600
TGAGTTACAA GCCCAGGAAG GATTGTCTAA TGATGGAGAA ACAATGGTAA ATGTGCCACA 660
TATTCATGCA AGGCTGTACA ACTATGAGCC TTGACACAG CTCAAGAAATG TCAGAGCAAA 720
TTACTATGGA AATATCATTTG CTCTAAGAGG GACAGTGGTT CGTGTCACTA ATATAAGCC 780
55 TCTTTGCACC AAGATGGCTT TTCTTTGTGC TGCATGTGGA GAAATTCAGA GCTTTCTCT 840
TCCAGATGGA AATACAGCT TTCCCAACAA GTGTCCTGTG CCTGTGTGTC GAGGCAGGTC 900
ATTACTGCT CTCCGAGCT CTCTCTCAC AGTTACGATG GACTGGCAGT CAATCAAAAT 960
CCAGGAATTG ATGCTGTGAT ATCAGAGAGA AGCAGGTCGG ATTCCACGAA CAATAGAATG 1020
TGAGCTTGT CATGATCTTG TGGATAGCTG TGTCCCGGGA GACACAGTGA CTATTACTGG 1080
60 AATTGTCAA GTCTCAAAAT CGGAAGAGG TTCTCGAAAT AAGAATGACA AGTGTATGTT 1140
CCTTTGTAT ATTGAAGCAA ATTCTATTAG TAATAGCAAA GGACAGAAA CAAAGAGTTC 1200
TGAGGATGGG TGTAAGCATG GAATGTTGAT GGAGTTCTCA CTTAAAGACC TTTATGCCAT 1260
CCAAGAGATT CAAGCTGAAG AAAACCTGTT TAAACTCATT GTCAACTCGC TTTGCCCTGT 1320
CATTTTGGT CATGAACCTG TTAAGCAGG TTTGGCATT GCACTCTTTG GAGGAAGCCA 1380
65 GAAATACGCA GATGACAAAA ACAGAATTCC AATTCGGGGA GACCCCAACA TCCTTGTGT 1440
TGGAGATCCA GGCCTAGGAA AAGTCAAAAT GCTACAGGCA GCGTGCAATG TTGCCCAAG 1500
TGGCGTGTAT GTTTGTGGTA ACACACGAC CACCTCTGGT CTGACGGTAA CTCTTCAA 1560
AGATAGTTCC TCTGGAGATT TTGCTTTGGA AGCTGGTGCC CTGTACTTTG GTGATCAAG 1620
70 TATTTGTGGA ATCGATGAAT TTGATAAGAT GGGGAATCAA CATCAAGCCT TGTGGAAGC 1680
CATGGAGCAG CAAAGTATTA GTCTTGCTAA GGCTGGTGTG GTTTGTAGCC TTCCTGCAAG 1740
AACTTCCATT ATTGCTGCTG CAAATCCAGT TGGAGGACAT TACAATAAAG CCAAAACAGT 1800
TTCTGAGAA TTAATAATGG GGAGTGCACT ACTATCCAGA TTTGATTTGG TCTTTATCCT 1860
GTAGATACT CCAATGAGC ATCATGATCA CTACTCTCT GAACATGTGA TTGCAATAAG 1920
AGCTGGAAG CAGAGAACCA TTAGCAGTGC CACAGTAGCT CGTATGAATA GTCAAGATT 1980
75 AAATACTCC GTACTTGAAG TAGTTTCTGA GAAGCCATTA TCAGAAAGAC TAAAGGTGGT 2040
TCTCGGAGAA ACAATAGATC CCATCCCCA CCAGCTATTG AGAAAGTACA TTGGCTATGC 2100
TCGGCAGTAT GTGTATCCAA GGCTATCCAC AGAAGCTGCT CGAGTTCTTC AAGATTTT 2160
CCTTGAGCTC CGGAACAGA GCCAGAGGTT AATAGCTCA CCAATCACTA CCAGGCAGCT 2220
GGAATCTTTG ATTCGTCTGA CAGAGGCAG AGCAAGGTTG GAATTGAGAG AGGAAGCAAC 2280
80 CAAAGAAGAC GCTGAGATA TAGTGGAAAT TATGAAATAT AGCATGCTAG GAACTTACTC 2340
TGATGAATTT GGGAACTAG ATTTTGAGCG ATCCAGAGT GGTCTGGA TGAAGCAACAG 2400
GTCAACAGCG AAAAGATTTA TTTCTGCTCT CAACAACGTT GCTGAAAGAA CTTATAATA 2460
TATATTTCAA TTTGATCAAC TTTCGGCAGAT TGCCAAAGAA CTAAACATTC AGGTTGCTGA 2520
TTTGAATAAT TTTATGGAT CACTAAATGA CCAGGTTTAC CTCTGAAAAA AAGGCCCAAA 2580
85 AGTTTACCAG CTTCAAACCTA TGTAAAAGGA CTTACCAAG TTAGGGCTCT CTGGGTTTAT 2640
TGCAATTAAG AGCATCTCA GTGAAGATAT CGGTGCAAGC ACAGACAGAC AGACACACAC 2700
ACACACACAC ACACACACAC ACACACACAC ACACACAGTC AAATACTGTT CTCTGAAAAA 2760
TGATGTCCCA AAGTATTAT AATAGGAAAA AAGCATTAAA TATAATAAAC TAATTTAAGA 2820
```

AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA 2880
 GGTGAGAGGA TTCTCTGAGG CCAGGGTTCC AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
 CATTTCTTAA AAAAAAAAAA AAAAAATTTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
 TAGTCTCAGC TACTTTGTAG GCTGAGGCAG GAGGATTCTT TGAGCCGAGG AGTTTGAGGT 3060
 TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
 GACTCAAAAA AATAAAAAAA ATTTAGTAGG TAGCCATGTG TTAATTGTGA AATAAATTCT 3180
 CCAAAGGGCT AAAAGTAAAT TACTTATAA TTTTATAG TTGTATTTT GACCTGCCTT 3240
 TTATATGTAT GAATATTTC A TAGTTTGTCA TATCAGATGT AGGCATACAG ACAAATACAT 3300
 AAACCAATGA ATATATTACA TATTTCTGTG TCCATAAAAA CTTTATTTAT GGCACTATAA 3360
 ATTTGAAATT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
 GCTATTTAAT AATAGGTCTC AITTTATCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
 AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTTTGAAG GAATTTTGTG TGGCTCACGG 3540
 AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATT GTAAAAACCAT 3600
 GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
 AGAAAGTGCT GCTGCTCTCC TGCCCCACCT TTGCCACTTC TGCAGCAGGA ATAGGTAGAA 3720
 GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTG TGCATGAGAT GCCTCCCTAA 3780
 ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTGA 3840
 TATGCCCTTT TCATAGGCTG CTAGGGAGTT TTCCTGGTTC TACTTTCAGG TGGTGGGATC 3900
 AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
 AACTATCAA TCATGTATAA ATCCAACAA CACTTTGTAA CATACAAGAA CTCAGGAAAT 4020
 GTGAACCAAT GTTGAGAAT CTACTAAAT ACGGCTTCCC GCAACGAAG ATGAATGGAA 4080
 AATGTAATA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
 GATGTGGAGA CTATTGCCAT AGACCACAAT GTAAATTTT AAGTGAGGAA GGAAAAATCA 4200
 GGAATCAAAA GGGGCCAGGT CCACTGGCTC ACATCTATAA TCCCAGAGCT TTGGGAGTTC 4260
 GAGGCAGGAG GATCACTTGA AGCCAGTTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
 TATCTCTACA AAAAATAGAT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
 GTGGAGGCTG AAGTAGAAAA TCACTTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
 TTATACCACT GCACTCCAGC CTGGGCAAGA GAGCAAGACC TTGTCTCTT

Seq ID NO: 44 Protein sequence:
 Protein Accession #: CAB55276.2

1 11 21 31 41 51
 MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLSTK 60
 TPQSMQSTLD RFIPYKQWKL YFSEVYSDSS PLIEKIQAPE KFFTRHIDLY DKDEIERKGS 120
 ILVDFKELTE GGEVTNLIPD IATELRDAPE KTLACMLAI HQVLTKDLER HAAELQAQEG 180
 LSNDGETMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVRVSN IKPLCTKMAF 240
 LCAACGETQS FPLPDGKYSL PTKCPVPVCR GRSPTALRSS PLVTMDWQS IKIQELMSDD 300
 QREAGRIPRT IECELVHDLV DSCVPGDVT ITGIVKVSNA EBSRNKNNDK CMFLLYIEAN 360
 SISNSKGQKT KSSEDGCKHG MLMEFSLKDL YAIQEIQAE NLFKLIVNSL CPVIFGHELV 420
 KAGLALALFG GSQKYADDDN RIPIRGDPHI LVVGDPLGLK SQMLQAACNV APRGVYVCGN 480
 TTTTSGLTVT LSKDSSSGDF ALEAGALVLG DQGICGIDEF DKMGNHQHAL LEAMEQQSIS 540
 LAKAGVVCSL PARTSIIAAA NPVGGHYNKA KTVSENLMKG SALLSRFDLV FILLDTPNEH 600
 HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVPVGETIDP 660
 IPHQLLRKYI GYARQVYVPR LSTEARVLQ DFYLELRKQS QRLNSSPITT RQLESILRLT 720
 EARARLELRE EATKEDAEDI VEIMKYSMLG TYSDEFNLD FERSQHGSGM SNRSTAKRFI 780
 SALNNVAERT YNNIFQPHQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPKVYQLQTM

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_005416.1
 Coding sequence: 149..658

1 11 21 31 41 51
 ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
 CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
 AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCTTAC CAGCAGAAGC AGACCTTTAC 180
 CCCACCACTC CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
 AATATTTGTT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAACAC 300
 AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
 GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
 CRAAGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
 ACCAGGCAGC ATCAAGTCC CTGACCAAGG CTTATCATAG TTTCTGAGC CAGGTGCCAT 540
 CAAAGTTCTC GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACACGA 600
 GCCATGTCTC TCAACGGTCA CTCCAGGCCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
 TGGTGACAGC ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC 720
 TGTCTCTGTG TCTTAATGT CTGTAGACCT TGTAATCAGC ACATTGTAC CCCAAGCCAT 780
 AGTCTCTCTC TTATTTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGT TACACACACT 840
 CTGAAGAAATC CTGTAGCCCC CTGAATTAA CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
 GGCTGCTCAG GGTTCATCTG AAGATTCCGA TGAAGAGAAA TGCATGTTTC CTGCTCTTCC 960
 CTCATTAAAT TGCTTTAAT TCCA

Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_005407.1

1 11 21 31 41 51
 MSSYQKQTF TPPQLQQQK VKQPSQPPQ EIFVPTTKEP CHSKVPQGN TKIPEPGCTK 60
 VPEPGCTKVP EPGCTKVPEP GCTKVPEPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
 GPKKFPPEGA IKVPEQGYTK VVPVGYTKLP EPCPSTVTPG PAQKQTKQK

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
	GCCTCGTGTG	CAGGCGTCCC	CGGGCTGTGG	ATAATTAGAC	ACGTTCTTCC	CTCATTGCCC	60
	AAGGCTCGTT	AGAAATCGCC	CTAGAGCTGT	ATCATGTATT	TTCTTTCAAA	TTAATTTTGC	120
5	TTGCAATTAA	GCTTAGGGAA	CCAGCAACAA	AAGCAAACCT	GGCCCGAGGT	CGTTCACCGC	180
	GAAATGGAT	TAGAGAACT	TCTTCCCGGA	TTTAAGGGGA	AAGATTCTGT	CGGCCAGCGC	240
	TTTGGGAAA	GTGCCCGGAC	CGCAGAGGCG	ACGACAGGGG	AGCAGGAAGC	TGCTCACGGT	300
	AGTCGGCGTT	GGCGGCAGCG	GTGCCCTTCC	TCATCTGGGC	GATGTGGGCT	CCTAGAAAGAG	360
	TAAGGATAAC	ATCTCGGAAA	TGACTTCTGT	ACGGTTTGAG	CCCAACTGCA	CACTCATGAC	420
10	TTGGAGCTCG	CCTGTGGAGT	TACAGTTTAC	CAAAACACAT	CATGAACATA	ATCTCATTTA	480
	CTAAAACTT	TGTGAGAATT	TTCTTTTACT	AAAATTTTTT	CTTATTACAA	A	

Seq ID NO: 48 DNA sequence:
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
	TTCCAAATTT	TTTTTTTTGT	AATAAGAAAA	AATTTTAGTA	AAAGAAAAAT	CTCACAAGAT	60
	TTTTAGTAAA	TGAGATTATG	TTTCATGAATG	TGTTTGGTAA	ACTGTAATC	CACAGGGCAG	120
20	CTCCAAGTCA	TGAGTGTGCA	GTGGGGCTCA	AACCGTACAG	AAGTCATTTC	CAGGATGTTA	180
	TCCTTACTCT	TCTCGGAGCC	CACATCGCCC	AGATGAGGAA	GGCCACCGCT	GGCCCAACG	240
	CCGACTACCG	TGAGCAGCTT	CCTGCTCCCC	TGTCGTGCGC	TCTGCGTTCG	GGGCACTTTC	300
	CCCAAGCGC	TGGCCGCGAG	AATCTTTCCT	CTTAATCGG	GGAAGAAGTT	TCTCTAATCC	360
25	ATTTTCGCGG	TGAACGACCT	CGGGCCAAGT	TTGCTTTTGT	TGCTGGTTCC	CTAAGCTTAA	420
	TTGCAAGCAA	AGTTAATTGT	AAAGAAAATA	CATGATACAG	CTCTAGGGCG	AATTCTAACG	480
	AGCCTTGGGC	AATGAGGGAA	GAACGTGTCT	AGTTATCCAC	AGCCCCGGGA	CGCCTGCACA	540
	CGACGCT						

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
35	TCCTTCTTCT	GCTGCTCGTT	TGCTCTCTCT	GTGCTCTTCT	TCCTTCTTTC	CCTCGCCGCT	60
	CCTGCGGACC	TCTGTGTCT	CTTCTCTGAT	GGCGGGGGGC	GGGAGAAGCT	GACCGGTGAG	120
	ACCGTAGACC	CGAAACCACT	GGGTGTGACA	AGCCGGTCCG	CGGCTTTTTT	GGGAGAAGCC	180
	GACACATGCA	GACCAGTTTT	CCTGGAAACG	CATGACCATG	TTATTACTAT	GGGCGCGCTC	240
	CCCAACCAAA	GTGTTTAAAA	CTTTTAGGG	CACCCCCAAA	ATTTTTTTTT	TTTTTTTTTT	300
40	TTCAATTTAA	AACTCTAAT	ATTTATATTA	AATACAAAGA	TACCCAAACC	CTTTATGCTT	360
	CTTCTCTGTA	TCTGTGTCTT	TTTTCTTGA	CAGCATCTCG	ATTTTTTTTC	TGCTGCTTCA	420
	TGCTGTAGC	CATGGGAATC	CGTTTCATTA	TTATGGTAGC	AATATGGAGT	GCTGTATTCC	480
	TAAAGAACT	GACACAGGAG	AATCACTTGA	ACTTGGGAGG	CAGAGTTTGC	AGTGAGCCGA	540
	GATTGAACCA	GTGCACCTCA	GCCTTGGCAG	CGGAGCAAGA	TTCTGTGACA	GTTCTGTAAG	600
45	TGCTGGTATC	GTCTGTCAGC	CCCATCTCTG	GTTCCATTGC	GCTGCCAGGC	AGGGTGCTGG	660
	GACGTGGGGA	GAGCTGTGCT	ATATATCCGG	GTGAAGCTCA	GCTGTGGCAC	ACCTTGGATG	720
	CGGGTCTCT	CCTGGGCCCG	GGGACCTAGT	ATTTTGGCCA	CGAGTGTACA	CCAAACAAG	780
	GAGACAGCAT	CATTATAGAG	CCTGCAGCAT	CCACCCTACT	GCTGTATCCA	GTTTCCATTG	840
	ACTG						

Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: L05187
Coding sequence: 1991..2260

	1	11	21	31	41	51	
55	CTGCAGGGAG	GCAGGTAGAA	AAGGCTTTTG	GGTTTTCAGG	TGGGGGCGAG	TCTAGCCTGA	60
	TCAGAAAGGA	GGAAAAGGCC	AGGGCAGATG	TCTGGGTGGA	GTGAAGGGAA	AAAGTGATCC	120
60	CAGAAGAAGG	ATTAGCCCTT	GAAAGTCCCT	GAAGTAGGAG	AAGGGTAAAG	GTGTGGTTGG	180
	TGAAGGAAGG	CAGGTTTTCC	CAGATTAGCA	ACCAGTCAGG	GGGAGGAAGG	TGAGAGTGGG	240
	AGAGTCATAA	GTAATTTATT	CTGAATGTGT	GTAGTTTAAT	GGAATTGGGA	AAAAGATGGG	300
	GGAAATGGAT	GGAAGGTCTT	GGACTCTGAG	ACAAGGGGTC	TATAATCAGT	CCATTTCATT	360
	ATTTCTAGCT	TCCACCTTCA	CCAAGGCAGA	CAAGGAGGGC	CCACCTCAGC	TCCTCTGCTC	420
	CCCCCTCCCT	TCCCACCTAT	TCATGTGTGC	AAGAGTGGCC	TGTCCTCACAG	AACACGGGGA	480
65	ACAACCATCT	CAATGACAAG	GACAGCAGGT	GGCAAGGCTC	AACAGGACTC	AGATGTCCCC	540
	CCAGGGTTAA	CTCATGAAAC	CCTCCATGAA	GCCTGCTGCT	CACCCCTCCC	TCAAGGCAAG	600
	CCCTGCACCT	GGGTCTGAGG	ATGAGGGTGG	CAGTGAATAA	TAGGCCAGTG	ACATCATTTT	660
	CAGCCAGCTA	GTGCCAAAAA	ATATCAGGTG	GTGTTTATCA	AATAAGCCGA	GCCAACCGGT	720
70	GATGAGGATG	GTAGTGTGAG	TCATGTGTGA	CAGGTGAGGA	ATGAAAACAG	AGTGCCCGAG	780
	AGCTTCTATT	TCCTTGAGGC	AGGGCTCATT	CATCTTATAA	AAGCCAGCTG	GCCATTGCTT	840
	TCACACCAAA	CCCAAGGGAC	CACACAGCCC	ATTCTGTCTC	GTATACCAGG	TAAGTCTCTG	900
	ATTGCAACAA	ACTGGCAATT	CTAGTGTACT	TTTTCTATT	TAGAAATTAG	CTAAAGGCAA	960
	ATATGTGTAA	GCAGGTTAAT	CCAGGGTTTC	AATGGGAGAT	AGAGAATAGT	GGAAATATCT	1020
75	TATTTTAAGT	TAAATTACAG	TCTGGATTTG	AAAGGACCTT	AGAGATGGTT	AGGGCTCCCA	1080
	CCTCAGTAGA	TAGTCATTGA	ACTGGGAGTC	CTGGAGAAGA	TTGTTCAAT	GCCCATGGGA	1140
	AGTTCATAGC	AGAACTAGAA	CTCAGGCCAG	AGCACTCTCA	GTAACACTGC	AATTTCCCCC	1200
	TGACAAGATA	TTTATAGAAA	TTTAAATTTA	TTAGATGGAT	CTCTACTGAG	CATTATATCC	1260
	ATTTAAGGCA	GTATGCTTAG	CACCTTGGAC	AAATCAATGC	CCTAACGTAC	TTACTTAACA	1320
80	AACATAAAAC	CTAGCAGGAA	GGTAATACAT	ATATATAAAT	AAATGAAATG	CAAAGTAGAT	1380
	AGTAATTGGC	ATGACGGAGA	TGGGCAGAGA	AGGGCTGTGC	ACTTTTGGGA	GACTTGCTCA	1440
	AGGAGACCTC	TAGGGTGTCA	AGTGATGTGA	GCTATGATGG	AGGGGTATTT	GGACAAGCAG	1500
	AGATGGGAAG	AAAAGCATTT	GGAAGGGACT	GTGTAAGCAC	AGACCAGAAG	CAAAACCAT	1560
	GAGGCTTAGA	TGAATATAAA	GGCATCCTAT	AAGTCACAGG	CTTTCTACAT	GGTACTAGGA	1620
85	GAGGAAAGTG	GTCTGATGCC	ATTTTCCAAA	AGACCTAATA	TGCGGACCTC	ATGTCCCTCA	1680
	GAAGCCAGCT	TTAGTAGGGC	ATTTTCCAG	AACAGATATA	AGGTGCCTTG	GGTAGGAAGG	1740
	GAGCCAAGAA	GAGAACTCCA	ATAAATGGA	GCAGAAGAAA	TTGCCTTTTA	GCTCCTCCTC	1800
	TTCAAAGGGC	CTGAAAATTA	TCCAAGCTTA	TTTCATTTT	AAATGTAATG	GGGGAGCTAA	1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTGAGCTT TCTGTCTCTA GAAAAAACA 1980
CATTTTGAGC ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
GCAGCAGCAG GTGAACAAC CTTGCCAGCC TCCACCCCAG GAACCATGCA TCCCCAAAC 2100
5 CAAGGAGCCC TGCCAAACCA AGGTGCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
CCAGCCCAG ATTCAGAGC CCGTCCAGCC CAAGGTGCTT GAGCCCTGCC CTTCAACGGT 2220
CACTCCAGCA CCAGCCCAGC AGAAGACCA GCAGAAGTAA TGTGGTCCAC AGCCATGCCC 2280
TTGAGGAGCT GCCACTGGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATTT 2340
10 GCCTATTGAC CCGTCACTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGCACCT 2400
CTAAAAAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
GTCTCACTGA CTGAGCTAGT CTTCTTGTG CTCGGGTGCA TTTGAGGATG GATTTGGGGA 2520
AGGTCAAGTG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
Protein Accession #: AAC26838

1 11 21 31 41 51
MNSQQQKQPC TPPPQPPQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
10 IPEPCQPKVP EPCFSTVTPA PAQQKTKQK

Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120-473

1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
30 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
AGGAGCTGT CACGGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCACTTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
35 TCCGGTGGCG CATGTGTAAT CCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCAGGAA 420
TCAAGAAAGT CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
CGGTCTTTCG TGCACTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG 600
40 GAGCTGCCTC TCTCATCCAC TTTCCAATAA A

Seq ID NO: 53 Protein sequence:
Protein Accession #: NP_002629.1

1 11 21 31 41 51
MRASSFLIVV VFLLIAGTLVL EAAVTGVPVK QQDVTGKRVF FNGQDPVKQ VSVKGQDKVK 60
45 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTPCPG IKKCEGSGC MACFPVQ

Seq ID NO: 54 DNA sequence
Nucleic Acid Accession #: NM_019618
Coding sequence: 75-584

1 11 21 31 41 51
GGCAGAGGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTCTCT GCCAGGTGCT 60
55 GAGACAAACA CACTATGAGA GGCACTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT 120
ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAAGTGTGA 180
CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAGTCACTG 240
60 TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATTT 300
ATTGGGAAAT CCAGATCCCA GAAATGTGTT TGTATTGTGA GAAGGTGTGA GAACAGCCCA 360
CATTGCAGCT AAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCCGTGAAAC 420
CCTTCCCTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
CGGACTGTGT CATGTGCTCC TCCAAGAGAG ACCAGCCCAT CATCTGACT TCAGAACTTG 540
65 GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAAGTCA CTAAGAGGTG 600
GCAGCTTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCTGCT ACATTTTCTT 660
AGTGTCAATT TCAGCTGCTT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
TAATGAAGAA GAAGCAATTA CTTCATAGCA ACTGAAGAAC AGGATGTGGC CTCAGAAGCA 780
GGAGAGCTGG TGGGTATAAG GCTGTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
70 CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
CTCTGTTTCT GTTTTGTCTT ATTCCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAA 1080
TAATCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATTGT AATGTGTAAT CTTAAGTTA 1140
75 AATAAACTTT GTGATTTTAT ATAATAAAAA AAAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
Protein Accession #: NP_062564

1 11 21 31 41 51
MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGG NLVAVPRSDS VTPVTVAVIT 60
80 CKYPEALEQG RGDPIYLGIG NPEMCLYCEK VGEQPTLQLK EQKIMDLYGQ PEPVKPFLFY 120
RAKTGRTSTL ESVAFPPWFI ASSKRDQPII LTSELGKSYN TAFELNIND

Seq ID NO: 56 DNA sequence
Nucleic Acid Accession #: NM_003125
Coding sequence: 65-334


```

1      11      21      31      41      51
AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTTG 60
5 CAGCATGAGT TCCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCCTCAGC TTCAGCAGCA 120
GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCCATCCCA AAACCAAGGA 180
GCCCTGCCAC CCAAGGTGCG CTGAGCCCTG CACCCCAAAA GTGCCGTGAGC CCGCCAGGCC 240
CAAGCTTCCA GAGCCATGCC ACCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
10 AGCGGCCAC CAGATCTGA ATCCCTATC CCATTCTGTG TATGAGTCCC ATTTGCCTTG 420
CAATTAGCAT TCTGTCTCCC CCAAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
TCTGAGTCTC TGAATGAAGC TGAAGGTCTT AGTACCAGAG CTAGTTTCTA GCTGCTCAGA 540
ATTCATCTGA AGAGAGACTT AAGATGAAAG CAAATGATTC AGCTCCCTTA TACCCCATTT 600
15 AAATTCACCT TCAATTCCA

```

Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

```

1      11      21      31      41      51
MSSQQQKQPC IPPPQLQQQQ VKQPCQPPPO EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
LPEPCHPKVP EPCPSIVTPA PAQKTKQK

```

Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

```

1      11      21      31      41      51
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
CTCTGAGGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCCTCTTC TCCAGGTTTG 120
CTGGCTGCAG TGGCGGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
35 CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCAA TATCTGTCCC 420
TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
40 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTCGCTGTA GAGAAAGGAG CAGGTGGTGT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAAGT 780
45 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTGT CTTACTCCAT 840
CCATAGCCAA GAACCAAGG ACCCACAGG CCTCATGTTT ACCATTACCC GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCAAC ACGGCACTGG CAGTAGTGGA 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
50 GCCTGAGAAAT GTGCGGGGCC ATGAGGTGCA GAGGCTGACG GTCACGTATC TGGACGCCCC 1140
CAACTCACA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCAATT 1200
TACCATCACC ACCCACCTCG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGA 1260
TTTTGAGGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
55 ACCTGTGTTT GTCCCACCTT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTTT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGCTACCG 1500
CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCAAGC 1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
60 ACTGATTGAT GTCAATGACC ATGGCCCATG CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAAGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTCT AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
65 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTGTGCT GTTCTCTCTG CTGGTGCTGC TTTTGTGTTG 2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
70 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
CATCATCCCG ACACCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACA GCCCGCCCTT ACGACACCTT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCGCGT TCCCTGAGCT CCCTCACCTC 2460
CTCCGCTTCC GACCAAGACC AAGATPACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
75 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCTC TGCAGGGCTG 2580
GGGACCAAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCTT TTCAGCTGAG 2640
GACTTCGGAG CTGTGTCAGG AGTGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCTAG AGGCCAAGTT TCCAGAAGCC 2820
80 TCTTACCTGC CGTAAATATG TCAACCTGTG GTCCTGGGCC TGGGCTGCTG GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCC CTGGCCGTCC TGCAATTCTG GTTTCAGAC CCCAATGCCT CCCATTGCGA 3060
TGGATCTCTG CGTTTATATA CTGAGTGTGC CTAGGTGGCC CCTTATTTT TATTTTCCCT 3120
85 GTTGGCTGCG TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTAT 3180
TAAAGAAACT TTTCCAGAA AAAAA

```

Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

	1	11	21	31	41	51	
5	MGLPRGPLAS	LLLLQVCWLQ	CAASEPCRVA	FREAETVLEA	GGAEQEPGQA	LGKVFMGCPG	60
	QBPALFSTDN	DDFTVVRNGE	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
	KGPFPPQRLN	LKSNKORDTK	IFYSITGPGA	DSPPEGVFAV	EKETGWLLEN	KPLDREEIAK	180
	YELFGHAWSE	NGASVEDPMN	ISIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSVMQVTAT	240
	DEDDAIYTYN	GVVAYSISHS	EPKDPHDLMP	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
10	TDMDGDSSTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHVPEN	AVGHEVQRLT	VTDLDAPNSP	360
	AWRATYLIMG	GDDGDHETIT	THPESNQIL	TTRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
	PTSTATIVVH	VEDVNEAPVF	VPPSKVVEVQ	BGIPTGEPVC	VYTAEDPDKE	NQKISYRILR	480
	DPAGWLAMP	DSGQVTAVGT	LDREDEQFVR	NNIYEVMLA	MDNGSPPTTG	TGTLTLLTLD	540
	VNDHGPVPEP	RQITICNQSP	VRQVLNITDK	DLSPTSPFQ	AQLTDDSDIY	WTAEVNEEGD	600
15	TVVLSLKKFL	KQDTYDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
	GAVLALLFLL	LVLLLVRKK	RKIKEPLLLP	EDDTRDNVFI	YGEEGGGEED	QDYDITQLHR	720
	GLEARPEVVL	RNDVAPTIIP	TPMYRPRPAN	PDEIGNFIIE	NLKAANTDPT	APPYDTLLVP	780
	DYEGSGSDAA	SLSSLTSSAS	DQDQDYDYLN	EWGSRPKKLA	DMYGGGEDD		

Seq ID NO: 60 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 162-428

	1	11	21	31	41	51	
25	GCGTTCCGTT	GGCGGCGGAT	TCGAACGTTT	GGACTGAGGT	TTTTCTGCCT	GAAGAAGCGT	60
	CATACGGACC	GGATTGTTTT	CGCTGGCCCA	GTGTCCCGCG	AGCTTGTGTG	CGATACAGAG	120
	AGCACTCGG	AAGCTGAGGC	AGCTGTGACT	TGACAGAGAG	GATGGCGCTG	TCGACCATAG	180
	TCTCCACAG	GAAGCAGATA	AAGCGGAAGG	CTCCCCGTGG	CTTTCTAAAG	CGAGTCTTCA	240
30	AGCGAAAGAA	GCCTCAACTT	CGTCTGGAGA	AAAGTGGTGA	CTTATTGGCT	CATCTGAAC	300
	GTTTACTGTT	TGTTTACTGA	TTAGCAGAA	AGTCCAGGAC	AAACGCTTGT	GCGAGTAAAT	360
	GTAGAGTCAT	TAACAAGGAG	CATGTACTGG	CCGCAGCAAA	GGAATTTCTA	AAGAAGAGCA	420
	GAGGTAGAAA	GTCAAAGAAC	ATATTCTTGA	AAGTTATGAT	GCATTCTTTT	GGGTGGTAAC	480
35	AGATCATAAA	GACATTTTTT	ACACATCAGT	TAATATGGGA	TTATTAAATA	TTGG	

Seq ID NO: 61 Protein sequence:

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MALSTIVSQR	KQIKRKAPRG	FLKRVFKRKK	PQLRLEKSGD	LLVHLNCLLF	VHRLAESERT	60
	NACASKCRVI	NKEHVLAAAK	VILKKSRO				

Seq ID NO: 62 DNA sequence

Nucleic Acid Accession #: NM_000094.2

Coding sequence: 99-8933

	1	11	21	31	41	51	
50	GGGCTGGAGG	GGCGTGGGCG	TCGGACCTGC	CAAGGCCACC	GCAGGGGGGA	GCAAGGGACA	60
	GAGGCGGGGG	TCCTAGCTGA	CGGCTTTTAC	TGCCTAGGAT	GACGCTGCGG	CTTCTGGTGG	120
	CCGCGCTCTG	CGCCGGGATC	CTGGCAGAGG	CGCCCGAGT	GCGAGCCGAG	CACAGGGAGA	180
	GAGTGACCTG	CACGCGCCTT	TACGCGCTG	ACATTGTGTT	CTTACTGGAT	GGCTCCTCAT	240
	CCATTGGCCG	CAGCAATTTT	CGCGAGGTCC	GCAGCTTTCT	CGAAGGGCTG	GTGCTGCCTT	300
55	TCTCTGGAGC	AGCCAGTGCA	CAGGGTGTGC	GCTTTGCCAC	AGTGCACTAC	AGCGATGACC	360
	CACGGACAGA	GTTGCGCCTG	GATGCACITG	GCTCTGGGGG	TGATGTGATC	CGCGCCATCC	420
	GTGAGCTTAG	CTACAAGGGG	GGCAACACTC	GCACAGGGGC	TGCAATTTCT	CATGTGGCTG	480
	ACCATGTCTT	CTGCCCCCAG	CTGGCCCGAC	CTGGTGTCCC	CAAGGTCTGC	ATCCTGATCA	540
60	CAGACGGGAA	GTCCAGGAC	CTGGTGGACA	CAGCTGCCCA	AAGGCTGAAG	GGGCAGGGGG	600
	TCAAGCTATT	TGCTGTGGGG	ATCAAGAAATG	CTGACCCCTG	GGAGCTGAAG	CGAGTTGCCT	660
	CACAGCCAAC	CTCCGACTTC	TCTTCTCTCG	TCAATGACTT	CAGCATCTTG	AGGACACTAC	720
	TGCCCTCGT	TTCCCGGAGA	GTGTGCACGA	CTGCTGGTGG	CGTGCTGTG	ACCCGACCTC	780
	CGATGATCTC	GACCTCTGCT	CCAAGAGACC	TGGTGTCTGC	TGAGCCAAGC	AGCCAATCCT	840
65	TGAGATAC	GTGGACAGCG	CGCAGTGGCC	CTGTGACTGG	CTACAAGGTC	CAGTACACTC	900
	CTCTGACGGG	GCTGGGACAG	CCACTGCCGA	GTGAGCGGCA	GGAGGTGAAC	GTCACAGCTG	960
	GTGAGACCA	TGTGCGGCTG	CGGGGTCTCC	GGCCACTGAC	CGAGTACCAA	GTGACTGTGA	1020
	TTGCCCTCTA	CGCCAACAGC	ATCGGGGAGG	CTGTGAGCGG	GACAGCTCGG	ACCACTGCC	1080
	TAGAAGGGCC	GGAAGTGAAC	ATCCAGAATA	CCACAGCCCA	CAGCCTCCTG	GTGGCCTGGC	1140
70	GGAGTGTGCC	AGGTGCCACT	GGTACCGTGG	TGACATGGCG	GGTCCCTCAG	GGTGGGCCCA	1200
	CACAGCAGCA	GGAGCTGGGC	CCTGGGCAGG	GTTTCACTGT	GCTGCGTGAC	TTGGAGCCTG	1260
	GCACGGACTA	TGAGGTGACC	GTGAGCACCC	TATTGTGGCG	CAGTGTGGGG	CCCCCACTT	1320
	CCCTGATGGC	TGCACTGAC	GCTTCTGTGG	AGCAGACCC	GCGCCCGGTC	ATCCTGGGCC	1380
	CCACATCCAT	CCTCTTTTCC	TGGAACCTGG	TGCCCTGAGG	CGGTGGCTAC	CGGTGGGAAT	1440
	GGCGGCGTGA	GACTGCTCTG	GAGCCACCGC	AGAAGGTGGT	ACTGCCCTCT	GATGTGACCC	1500
75	GCTACCAATT	GGATGGGCTG	CAGCCGGGCA	CTGAGTACCG	CCTCACACTC	TACACTCTGC	1560
	TGGAGGGCCA	CGAGGTGGCC	ACCCCTGCAA	CCGTGGTTC	CACTGGACCA	GAGCTGCCTG	1620
	TGAGCCCTGT	AACAGACCTG	CAAGCCACCG	AGCTGCCCGG	GCAGCGGGTG	CGAGTGTCTT	1680
	GGAGCCAGT	CCCTGGTGCC	ACCCAGTACC	GCATCATTTG	GCGCAGCACC	CAGGGGGTTG	1740
	AGCGGACCTT	GCTGCTTCTT	GGGAGTCAGA	CAGCATTCGA	CTTGGATGAC	GTTTCAAGCTG	1800
80	GGCTTAGCTA	CATGTGCTGG	GTGTCTGTCT	GAGTGGGTCC	CCGTGAGGGC	AGTGCCAGTG	1860
	TCTCACTGT	CCGCGGGGAG	CCGGAAACTC	CACCTTGTCT	TCCAGGGCTG	CGGGTGTGG	1920
	TGTCAAGATC	AACGCGAGTG	AGGGTGGCCT	GGGGACCCGT	CCCTGGAGCC	AGTGGATTTC	1980
	GGATTAGCTG	GAGCACAGGC	AGTGGTCCGG	AGTCCAGCCA	GACACTGCCC	CCAGACTCTA	2040
	CTGCCACAGA	CATGACAGGC	CTGCAGCCTG	GAACCACTTA	CCAGGTGGCT	GTGTCCGTAC	2100
85	TGCGAGGCG	AGAGGAGGGC	CCTGCTGCAG	TCATCGTGGC	TCCAACGGAC	CCACTGGGCC	2160
	CAGTGAGGAC	GGTCCATGTG	ACTCAGGCCA	GCAGCTCATC	TGTCAACATT	ACCTGGACCA	2220
	GGGTTCCTGG	CGCCACAGGA	TACAGGGTTT	CCTGGCACTC	AGCCACGGC	CCAGAGAAAT	2280

	CCCAGTTGGT	TTCTGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
	AGTATACGGT	GCACTGTGAGG	GCCCCATGTG	CTGGCGTGGA	TGGGCCCCCT	GCCCTCTGTG	2400
	TTGTGAGGAC	TGCCCTCTGAG	CCTGTGGGTC	GTGTGTGAG	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGAGCT	TCTACGGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CCTGGGGCCG	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGCTACTC	AGTGGAGTGG	ACTGCACTTG	2640
	TGGGGGACCG	GAGGGGCACA	CCTGTCTCCA	TTGTTGTAC	TACGCGCCT	GAGGCTCCG	2700
	CAGCCCTGGG	GAGCCTTCAC	GTGGTGCAGC	GCGGGGAGCA	CTGCTGAGG	CTGCGCTGGG	2760
10	AGCCGGTGCC	CAGAGCGCAG	GGCTTCTTTC	TGCACTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTGAGGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGCCC	TCTGCAGAGG	2940
	TGACTGCGCG	CACCTGAGTCA	CCTCGTGTTC	CAAGCATTGA	ACTACGTGTG	GTGGACACCT	3000
	CGATCGACTC	GGTGACTTTG	GCCTGGACTC	CAGTGTCCAG	GGCATCCAGC	TACATCCTAT	3060
15	CCTGGCGGCC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCCGAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCCAGCGG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCCCTGT	CCTGGATGGT	GTGCGGGGTC	CTGAGGCATC	TGTACACAG	ACGCCAGTGT	3240
	GCCCCCGTGG	CCTGGCGGAT	GTGGTGTTC	TACCACATGC	CACCTAAGAC	AATGCTCACC	3300
	GTGCGGAGGC	TACGAGGAGC	GTCTGGAGC	GTCTGGTGT	GGCACTTGGG	CCTCTTGGGC	3360
20	CACAGGAGT	TCAGGTTGGC	CTGCTGTCTT	ACAGTTCATG	GGCCTCCCCA	CTGTTCCAC	3420
	TGAATGGCTC	CCATGACCTT	GGCATATCT	TGCAAAAGAT	CCGTGACATG	CCCTACATGG	3480
	ACCCAAGTGG	GAAACAACCTG	GGCAGCCG	TGGTCAAGC	TCACAGATAC	ATGTTGGCAC	3540
	CAGATGCTCC	TGGGCGCCCG	CAGCAGCTAC	CAGGGGTGAT	GGTTCGTCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATTC	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
	TGATGTTGGG	AATGGCTGGA	GGGACCCAG	AGCAGCTGCG	TGCTTGGCG	CCGGGTATGG	3720
25	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCTC	TCATCTACTA	GGCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAGGGG	CAGAAGGGGG	AACCTGGAGA	GATGGGCTTG	AGAGGACAAG	3900
	TTGGGCTCTC	TGGCGACCTC	GGCCTCCCGG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
30	CCCCTGGAAG	TGCCACTTGC	AAGGGCGAGA	GGGGCTTCCC	TGGAGCAGAT	GGGCGTCCAG	4020
	GCAGCCCTGG	CCGCGCCGGG	AATCTTGGGA	CCCCTGAGAC	CCCTGGCCTA	AAGGGCTCTC	4080
	CAGGGTTGCC	TGGCCCTCTG	GGGGACCCGG	GAGAGCGAGG	ACCTCGAGGC	CCAAAGGGGG	4140
	AGCCGGGGGC	TCCCGGACAA	GTCACTGGAG	GTGAAGGACC	TGGGCTTCTT	GGGCGGAAAG	4200
	GGGACCCCTG	ACCATCGGGC	CCCCCTGGAC	CTCGTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
	GTGGCCCCCC	AGGGCTTCTC	GGAACAGCCA	TGAAGGGTGA	CAAAGGCGAT	CGTGGGGAGC	4320
35	GGGGTCCCCC	TGGACCAAGT	GAAGGTGGCA	TTGCTCTTGG	GGAGCCTGGG	CTGCCGGGTC	4380
	TTCCCGGAAG	CCCTTGAGACC	CAAGGCCCGG	TTGGCCCCCC	TGGAAAGAAA	GGAGAAAAG	4440
	GTGACTCTGA	GGATGGAGCT	CCAGGCCTCC	CAGGACCAAC	TGGGTCTCCG	GGTGAGCAGG	4500
	GCCCCACGGG	ACCTCTTGGA	GCTATTGGCC	CCAAAGGTGA	CCGGGGCTTT	CCAGGGCCCC	4560
40	TGGGTGAGGC	TGGAGAGAAG	GGCGAACGTG	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
	TGCCAGGGGT	TGCTGAGCGT	CCTGGAGCCA	AGGGTCTCTA	AGGGCCACCA	GGACCCACTG	4680
	GCCGCCAAGG	AGAGAAGGGG	GAGCCTTGTC	GCCCTGGGGA	CCCTGCAGTG	GTGGGACCTG	4740
	CTGTTGCTGG	ACCCAAGGGA	GAAAAGGGAG	ATGTTGGGGC	CGCTGGGCCC	AGAGGAGCTA	4800
	CCGGAGTCCA	AGGGGAACGG	GGCCCAACCG	GCTTGGTTCT	TCCTGGAGAC	CCTGGCCCCA	4860
45	AGGGAGACCC	TGGAGACCGG	GTCTCCATTG	GCCTTACTGG	CAGAGCAGGA	CCCCAGGTG	4920
	ACTCAGGGCC	TCTTGAGAGG	AAGGGAGACC	CTGGGCGGCC	TGGCCCCCCA	GGACCTGTTG	4980
	GGCCCGGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGTCTT	CCGGGTGACC	5040
	CGGGTTTGCC	TGGAAGAGCA	GGCGAGCGTG	GCCTTCCGGG	GGCACTTGGA	GTTCGGGGGC	5100
	CTGTGGGTGA	AAAGGGAGAC	CAGGGAGATC	CTGGAGAGGA	TGGAACGAAT	GGCAGCCCTG	5160
50	GATCATCTGG	ACCCAAGGGT	GACCTGTTGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACCGG	5220
	TGGTAGACAC	AGGACCTTGA	CCAGAGAGGA	AGGGAGAGCC	TGGGGACCCG	GGACAAGAGG	5280
	GTCTCTGAGG	GCCCAAGGGT	GATCTTGCCG	TCCCTGGAGC	CCCTGGGGAA	AGGGGCATTG	5340
	AAGGGTTTCC	GGGACCCCCA	GGCCACACAG	GGGACCCAGG	TGTCGAGGCG	CCAGCAGGAG	5400
55	AAAAGGGTGA	CCGGGGTCCC	CCTGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACCTG	5460
	GAGCCGCTGG	GGCCTCTGGG	CCGAATGGTG	CTGCAGGCAA	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCCTCCGT	GGAGAACCAAG	GCCTCCCTGG	CCCTCTGGT	CCCCCTGGAT	5580
	TACCCGGAAA	GCCAGGCGAG	GATGGGAAAC	CTGGCCTGAA	TGGAAAAAAC	GGAGAACCTG	5640
	GGGACCTTGG	AGAAGACCGG	AGGAAGGGAG	AGAAAGGAGA	TTCAAGGCGC	TCTGGGAGAG	5700
	AAGGTCGTGA	TGGCCCCCAA	GTTGAGCCTG	GAGCTCCTGG	TATCCTTGGA	CCCCAGGGGC	5760
60	CTCCAGGCTC	CCCAAGGCCA	GTGGGCCCTC	CTGGCCAGGG	TTTTCTTGGT	GTCCCAAGGAG	5820
	GCACGGGCCC	CAAGGGTGAC	CGTGGGGAGA	CTGGATCCAA	AGGGGAGCAG	GGCCTCCCTG	5880
	GAGAGCGTGG	CCTGCGAGGA	GAGCCTGGAA	GTGTGCCGAA	TGTGGATCGG	TTGCTGGAAA	5940
	CTGCTGGCAT	CAAGGCATCT	GCCCTGCGGG	AGATCGTGGG	GACCTGGGAT	GAGAGCTCTG	6000
	GTAGCTTCTC	GCCTGTGCCC	GAACGGCGTC	GAGGCCCCAA	GGGGGACTCA	GGCGAACAGG	6060
65	GCCCCCAGG	CAAGGAGGGC	CCCATCGGCT	TTCCTGGAGA	ACCGGGGCTG	AAGGGCGACC	6120
	GTGGAGACCC	TGGCCCTCAG	GGGCCACCTG	GTCTGGCCCT	TGGGGAGAGG	GGCCCCCCCG	6180
	GGCCTTCCGG	CCTTGCCCGG	GAGCCTGGAA	AGCCTGGTAT	TCCCGGGCTC	CCAGGCAGGG	6240
	CTGGGGGTGT	GGGAGAGGCA	GGAAGGCCAG	GAGAGAGGGG	AGAACGGGGA	GAGAAAAGGAG	6300
	AACGTGAGGA	ACAGGGCAGA	GATGGCCCTC	CTGGACTCCC	TGGAACCCCT	GGGCCCCCCG	6360
70	GACCCCTTGG	CCCCAAGGTT	TCTGTGGATG	AGCCAGGTCC	TGGACTCTCT	GGAGAACAGG	6420
	GACCCCTTGG	ACTCAAGGGT	GCTAAGGGGG	AGCCGGGCAG	CAATGGTGC	CAAGGTCCCA	6480
	AAGGAGACAG	GGGTGTGCCA	GGCATCAAAG	GAGACCGGGG	AGAGCCTGGA	CCGAGGGGTC	6540
	AGGACGGCAA	CCCGGGTCTA	CCAGGAGAGC	GTGGTATGGC	TGGGCTTGAA	GGGAAGCCGG	6600
	GTCTGCAGGG	TCCAAGAGGC	CCCCCTGGCC	CAGTGGGTGG	TCATGGAGAC	CCTGGACCAC	6660
75	CTGGTGGCCC	GGGTCTTGCT	GGCCTGCGAG	GACCCCAAGG	ACCTTCTGGC	CTGAAGGGGG	6720
	AGCCTGGAGA	GACAGGACCT	CCAGGACGGG	GCCTGACTGG	ACCTACTGGA	GCTGTGGGAC	6780
	TTCTTGGACC	CCCCGGCCCT	TCAGGCCTTG	TGGGTCCACA	GGGGTCTCCA	GGTTTGCCTG	6840
	GACAAGTGGG	GGAGACAGGC	AAGCCGGGAG	CCCCAGGTGG	AGATGGTGCC	AGTGAAAAG	6900
	ATGGAGACAG	AGGGAGCCCT	GGTGTGCCAG	GGTCAACAGG	TCTGCTGGC	CCTGTGGGAC	6960
80	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGGCC	CTGGACAGGC	TGTGGTGGG	CTCCCTGGAG	7020
	CAAAGGGAGA	GAAGGGAGCC	CTTGGAGGCC	TTGCTGGAGA	CCTGGTGGGT	GAGCCGGGAG	7080
	CCAAAGGTGA	CCGAGGACTG	CCAGGGCCCG	GAGGCGAGAA	GGGTGAAGCT	GGCCGTGCAG	7140
	GGGAGCCCGG	AGACCTTGGG	GAAGATGGTC	AGAAAGGGGC	TCCAGGACCC	AAAGGTTTCA	7200
	AGGGTGACCC	AGGAGTCCGG	GTCCCGGGCT	CCCCGGGGCC	TCCTGGCCCT	CCAGGTGTGA	7260
85	AGGGAGATCT	GGGCTCTCCT	GGCCTGCCCC	GTGCTCTTGG	TGTTGTGGG	TTCCCGGGTC	7320
	AGACAGGCCC	TGAGGAGAGG	ATGGGTGAGC	CAGGCCCTAG	TGGAGAGCGG	GGTCTGGCAG	7380
	GCCCCCAGG	GAGAGAAGGA	ATCCAGGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGTGCTG	7440
	TGGGACACAC	TGGGGCTCTT	GGACTCAAAG	GAGACAAGGG	AGACCCCTGA	GTAGGGCTGC	7500

5 CTGGGCCCCG AGGCGAGCGT GGGGAGCCAG GCATCCGGGG TGAAGATGGC CGCCCCGGCC 7560
 AGGAGGGACC CCGAGGACTC ACGGGGCCCC CTGGCAGCAG GGGAGAGCGT GGGGAGAAGG 7620
 GTGATGTTGG GAGTGCAGGA CTAAAGGGTG ACAAGGGAGA CTCAGCTGTG ATCCTGGGGC 7680
 10 CTCCAGGCCC ACGGGGTGCC AAGGGGGAACA TGGGTGAACG AGGGCCTCGG GGCTTGGATG 7740
 GTGACAAAGG ACCTCGGGGA GACAATGGGG ACCCTGGTGA CAAGGGCAGC AAGGGAGAGC 7800
 CTGGTGACAA GGGCTCAGCC GGTTTGCCAG GACTGCGTGG ACTCCTGGGA CCCCAGGGTC 7860
 AACCTGGTGC AGCAGGGATC CCTGGTGACC CGGATCCCC AGGAAAGGAT GGAGTGCCTG 7920
 GTATCCGAGG AGAAAAAGGA GATGTTGGCT TCATGGGTCC CCGGGGCTC AAGGGTGAAC 7980
 GGGAGTGAA GGGAGCCTGT GGCTTGTATG GAGAGAAGGG AGACAAGGGA GAAGCTGGTC 8040
 15 CCCCAGGCCG CCCCAGGGCTG GCAGGACACA AAGGAGAGAT GGGGGAGCCT GGTGTGCCGG 8100
 GCCAGTCGGG GGGCCCTGGC AAGGAGGGCC TGATCGGTCC CAAGGGTGAC CGAGGCTTTG 8160
 ACGGGCAGCC AGGCCCCAAG GGTGACCAGG GCGAGAAAGG GGAGCGGGGA ACCCCAGGAA 8220
 TTGGGGGCTT CCGAGGGCCC AGTGGAAATG ATGGCTCTGC TGGTCCCCCA GGGCCACCTG 8280
 GCAGTGTGGG TCCAGAGGCC CCGAAGGAC TTCAGGGCCA GAAGGGTGAG CGAGGTCCCC 8340
 20 CCGGAGAGAG AGTGGTGGGG GCTCTGGGG TCCCTGGAGC TCCTGGCGAG AGAGGGGAGC 8400
 AGGGGCGCGC AGGCGCTGCC GGTCTCGAG GCGAGAAGGG AGAAGCTGCA CTGACGGAGG 8460
 ATGACATCCG GGGCTTTGTG CCGCAAGAGA TGAGTCAGCA CTGTGCTGTC CAGGGCCAGT 8520
 TCATGCTATC TGGATACGCA CCCCTCCCTA GTTATGCTGC AGACACTGCC GGCTCCACG 8580
 TCCATGCTGT GCCTGTGCTC CGCTCTCTC ATGCAGAGGA GGAAGAGCGG GTACCCCTCTG 8640
 AGGATGATGA GTACTCTGAA TACTCCGAGT ATTCTGTGGA GGAGTACCAG GACCTCTGAA 8700
 25 CTCCTTGGGA TAGTGATGAC CCTGTCTCC TGCCTCTGGA TGAGGGCTCC TGCCTGCTCT 8760
 ACACCTCTGG CTGTTACCAT CCGGCTGTGA CAGGCAGCAC AGAGGCTGT CACCTTTTGT 8820
 TCTATGTTGG CTGTGGAGGG AATGCCAACG GTTTTGGGAC CCGTAGGGCC TGCGAGCGCC 8880
 GCTGCCACC CCGGCTGGTC CAGAGCCAGG GGACAGGTAC TGCCCGAGAC TGAGGCCAG 8940
 30 ATAATGAGCT GAGATTACG ATCCCTCTGA GGAGTCGGGG TCTCAGCAGA ACCCCACTGT 9000
 CCTCTCCCTT GGTGCTAGAG GCTTGTGTGC ACGTGAGCGT GCGAGTGCAC GTCCGTTATT 9060
 TCAGTGAATG GTTCCCGTGG GTCTAGCCTT CCCCCCTGTG GACAAACCCC CATTTGGGCT 9120
 CCTGCCACCC TGGCAGATGA CTCACTGTGG GGGGGTGGCT GTGGGCAGTG AGCGGATGTG 9180
 ACTGGCGTCT GACCCGCCCC TTGACCCAAAG CCTGTGATGA CATGGTGTCT ATTCGTTGGG 9240
 GCATTAAAGC TGCTGTTTTA AAGGCCAAAA AA

Seq ID NO: 63 Protein sequence:
 Protein Accession #: NP_000085.1

35 1 11 21 31 41 51
 MTLRLVAAL CAGILAEAPR VRAQHRERV CTRLYAADIV FLDDGSSSIG RSNFREVRSF 60
 LEGLVLPFSG AASAQGVRFV TKQYSDDPRT EFGLDALGSG GDVIRAIREL SYKGNTRTGT 120
 40 AAILHVADHV FLPLQARPGV PKVCILITDG KSQDLVDTAA QRLKGGVVKL FAVGIKNADP 180
 EELKRVAQSP TSDFFFVND FSILRTLLFL VSRVCTTAG GVPVTRPPDD STSAPRDLVL 240
 SEPSQSRLV QWTAASGPTV GYKVQYPLT GLGQPLPSER QEVNVPAJET SVRLRGLRPL 300
 TEYQVTIAL YANSIGEAVS GTARTTALEG PELTIQNTTA HSLLVAVRSV PGATGYRVTV 360
 RVLSGGPTQQ QELGPGQGSV LLRLDEPGTD YEVTVSTLFG RSVGPATSLM ARTDASVEQT 420
 45 LRPVILGPTS ILLSNLVEPE ARGYLEWRR ETGLEPPQKV VLPDVTTRYQ LDGLQPGTEY 480
 RLTLTYLLEG HEVATPATVV PTGPELPVSP VTDLQATELP QQRVRVSWSP VPGATQYRII 540
 VRSTQGVERT LVLPQSGTAF DLDDVQAGLS YTVRVSVARVG PREGSASVLT VRREPETPLA 600
 VPGLRVVVD ATRVRVWAGP VPGASGFRIS WSTGSGPESS QTLPPDSTAT DITGLQPGTT 660
 YQVAVSVLRG REEGPAIVIV ARTDPLGPVR TVHVTAQASS SVTITWTRVP GATGYRVSWH 720
 50 SAHGPEKSQL VSGEATVAEL DGLEPDTETV VHVRAHVAGV DGPPASVVVR TAPEPVGRVS 780
 RLQILNASSD SVTLTAVGVT GATAYRLAWG RSEGGPMRHQ ILPGNTDSAE IRGLEGGVSY 840
 SVRVTAIVGD REGTPVSIIV TTPPEAPPAL GTLHVVRQGE HSLRLRWEVP PRAQGFLLHW 900
 QPEGQEQSR VLGPESLSYH LDGLEPATQY RVRLSVLGP GEGPSAEVTA RTSEPRVPSI 960
 ELRVVDTSID SVTLTAVGVT RASSYILSWR PLRGPQGEVP GSPQTLPGIS SSQRTVLEP 1020
 55 GVSIFSLTP VLDGVRGPEA SVTQTPVCFR GLADVVLPH ATQDNHRAE ATRRVLERLV 1080
 LALGPLPQA VQVGLLSYSH RPSPLFPLNG SHDLGIIQR IRDMPYMDPS GNNLTAVVT 1140
 AHRYMLAPDA PGRRPVHGV MVLVDDEPLR GDI FSPAREA QASGLNVVML GMAGADPEQL 1200
 RRLAPGMDSV QTFFAVDGSP SLDQAVSGLA TALQASFTT QPRPEPCPVY CPGKQKGEPP 1260
 60 EMGLRGQVGP PGDPGLPGRT GAPGPGQPGP SATAKGERGF PGADGRPGSP GRAGNPGTPG 1320
 APGLKGSPL PGPRGDPGER GPRGPKGEPG APGQVIGGEG PGLPGRKGDG GPSGPPGPRG 1380
 PLGDPGPRGP PGLPGTAMKG DKGRDGERGP PGPGEGGIAP GEPGLPGLPG SPFGPPGVP 1440
 PGKKEKEDS EDGAPGLPGQ PGSPGEQGR GPPGAIGPKG DRGFPGLGE AGEKGERGPP 1500
 GPAGSRGLPG VAGRPKAGKP EGPPGPTGRQ GEKGEPRGP DPAVVGPAVA GPKKEKGDVG 1560
 65 PAGPRGATGV QGERGPPGLV LPGDGPKGDG PGDRGPGLT GRAGPPGDSG PPGKGDGPR 1620
 FGPPGVPGR GRDGEVGEKG DEGPDPGLP PGKAGERGLR GAPGVRGFVG EKGDQGDGPE 1680
 DGRNGSPSS GPKDRCEPG PPGPPGRLVD TGPAREKGE PGDRGQEGPR GPKGDGGLPG 1740
 APGERGIEGF RGPFGPQGDG GVRGPAGEKG DRGPPGLDGR SGLDGKPGAA GPSGPNAG 1800
 70 KAGDPGRDGL PGLRGEQGLP GPSGPPGLPG KPGEDGKPL NGKNGEPGDG GEDGRKKEKG 1860
 DSGASGREGR DGPKGERGAP GILGPQPPG LEPVGPVPGG GPPGVPGGTG PKGDRGETGS 1920
 KGEQGLPGER GLRGEPSVP NVDRLLTAG IKASALREIV ETWDESSGSF LPVPERRRGP 1980
 KGDSGEQGP GKBPICFP ERGLKGRGD PGPPGPPGLA LGERGPPGPG GLAGEPGKPG 2040
 IPGLPGRAGG VGEAGRGER GERGEKGERG EQGRDGPPL PGTPGPPGPF GPKVSVDEPG 2100
 75 PGLSGEQGP GLKGAKEGEP SNGDQPKGD RGVPGIKGDR GEPGPRQDG NPGLPGERGM 2160
 AGPEKPLGL GPRGPPGPGV GHGDPGPPGA PGLAGPAGP GPSGLKGEPP ETGPPGRLT 2220
 GPTGAVLPG PPGPSGLVGP QGSPGLPGQV GETGKPGAP RDGASGKGDG RGSPPVPGSP 2280
 GLPFPVPGK EPGPAGPQ AVVGLPGAAG EKAGPGLAG DLVGEPAKAG DRGLPGRGE 2340
 KGEAGRAGEP APGPKGPKGD PGVGVPGSP PPGPPGVKGD LGLPGLPAG 2400
 80 GVVGFPGGT PRGEMQPGP SGERGLAGP GREGIPGLG PPGPPGSPV PGASGLKGDG 2460
 GDFGVGLPG RGRGERGIR GEDRPGQEG PRGLTGPPGS RGERGEKGDV GSAGLKGDG 2520
 DSAVILPFP PRGAKGDMGE RGRGLDGDG GPRGDNDPG DKSGKEPGD KGSAGLPGLR 2580
 GLLGPGQGP AAGIPGDPGS PKDGVPGIR GEKGDVFGM PRGLKGERGV KGACGLDGEK 2640
 85 GDKGEAGPFP RGLAGHKE MGEPPVPGQS GAPKEGLIG PKDGRGFDG PGPKDQGEK 2700
 GERGTPGIG PPGPSGNDGS AGPPGPPGSP GPRGPEGLQ QKGERGPPGE RVVGPVPG 2760
 APGERGQGR PGAPGRGEK GEALTEDDI RGFVRQESQ HCACQGFIA SGSRPLPSYA 2820
 ADTAGSQLHA VPLRVSHAE EERVPEDD EYSEYSESV EYQDPEAPV DSDPCSLPL 2880
 85 DEGSCTAYTL RWHYRAVTGS TEACHPFVYG CGGNANRFG TREACERRCP PRVQSQGTG 2940
 TAQD

	1	11	21	31	41	51	
25	TAGTCCGAGC	GAGGTGGCGA	GTCGCTGAGC	CCGCGCGCGC	CCCAGAGAGC	GCTGCAGCCG	60
	CCGCGCGCGG	GAAGGAGAGG	GCGAGGCGCG	CCCGAGCCGC	CGCGCGCCGC	GCCACCGCCG	120
	CCGCGCCGCA	CACCGCCACC	GGAGTCCGCG	GCCAGCCCGG	CAGCTCCCGC	GGGCCCCGGC	180
	CGGGGCGGGG	GAGGCGGGCC	ACAGGCCCCC	GCTCCGGCGG	TCGTTTTCAG	ACCGCGGGCG	240
30	CCGATGTCGC	CCGCGCCCCG	TTAGGATGAG	TCTCGGGTCG	GGGAGGAGGC	CGCCCGCAGC	300
	GCGCGCGCGG	GAGCGCGGGG	CAGGAGCTTC	GCGCGCGCGC	GCGCGCGCGC	CGCGCGCCCG	360
	GCGCGGCCCC	GAGCGCGGCC	GCGCGCCCCC	GGGCCCCCGA	CACACATGAG	ATTCTTCAGG	420
	CTCATTCTCA	AGTGTCTCGT	GGACTGCTTC	TGACTGCGCC	CGCCGCGCCG	CGCACCCCGC	480
	CGTTCGCGCG	CGCCGCCGTC	CCCGCGCGCG	GCGCGCCCCC	GGCCCGCGCC	GGCCCGCGCG	540
35	CCTCGGGGCC	CTCCCCGGTG	CCGCGCGGTG	CCCCCGCCTG	ACCGCCGCCC	CCCGTGAGGC	600
	GCGCGGACCC	CGGCGCGCCC	GTGCGCGAGG	CGCGGGCCAT	CGCGAGAAG	AGCGCCCGAG	660
	ACGGCATCTA	TAGCGTGTCC	GGGAGCGAGA	AGAAAGGCCC	CCTCATCGCG	CCCGGCGCCG	720
	ACGGGGCCCC	GGCCAAGGGC	GACGGCCCCG	TGGGGCTGGG	GACACCGGGC	GGCGCGCTGG	780
	CCGTGCGCGC	GCGCGAGACC	TGGAGCGGCC	AGATGGACTT	CATCATGTGC	TGCGTGGGCT	840
40	TCGCGGTGGG	CTTGGGCAAC	GTGTGCGCGT	TCCCTTACTT	GTGCTACAAG	AACGGCGGAG	900
	GTGTGTTCTT	TATTCCCTAC	GTCTGTATCG	CCCTGGTTGG	AGGAATCCCG	ATTTTCTTCT	960
	TAGAGATCTC	GCTGGGCGAC	TTTCAATGAG	GCGCGAGACT	CAATGTCTGG	AACATCTGTC	1020
	CCCTGTTCAA	AGGCTTGCGC	TACGCTTCCA	TGGTGTACTG	CTTCTACTGC	AACACCTACT	1080
45	ACATCATGAT	GCTGGGCTGG	GGCTTCTATT	ACCTGGTCAA	GTGCTTTTAC	ACACGCTGTC	1140
	CTTGGGCGAC	ATGTGGCCAC	AGCTTGAACA	TCCCGACTAG	CGTGAGAGTC	TTCCGCAATG	1200
	AAGACTGTGC	CAATGCCAGC	CTGGCCCAAC	TCACCTGTGA	CCAGCTTGCT	GACCGCCGGT	1260
	CCCTCTGCAT	CGAGTCTGCG	GAGAAACAAG	CTTGAAGGCT	CTGCTGGGGA	CTGAGGAGTG	1320
	CAGGGGCGCT	CAACTGGGAG	TGAGCCTTTT	GTCTGCTGGC	GTGCTGGGTC	TGTGTTACTT	1380
50	TCTGTGTCG	GAAGGGGGTC	AAATCCACGG	GAAAGATCGT	GTACTTCACT	GCTACATTCC	1440
	CTTACGTTGT	CTTGGTCTGT	CTGCTGGTGC	TGTGAGTGCT	GTCGCTCGGC	GCCCTGATTC	1500
	GCATCATTTA	CTATCTCAAG	CTTGACTTGT	CAAAAGCTGG	GTCCCTTACG	GTGTGGATAG	1560
	ATGCGGGGAC	CCAGATTTTC	TTTTCTTAGG	CCATTGGGCT	GGGGGCCCTC	ACAGCCCTGG	1620
	GCAAGTACAA	CCGCTTCAAC	AAACAATGCT	ACAAGGAAGC	CATCATCCCT	GCTCTCATCA	1680
55	ACAGTGGGAC	CAGCTTCTTT	GCTGGCTTCG	TGGCTTCTTC	CATCTTGGGC	TTATGCTGCT	1740
	CAGAGCAGGG	CGTGCAATC	TCCAAGGTGG	CAGAGTCAGG	GCGGGGCGCT	GCCCTTCATG	1800
	CCTACCCCGG	GGCTGTCAAG	CTGATGCCAG	TGGCCCCACT	CTGGGCTGCC	GTGTTCTTCT	1860
	TCATGCTGTT	GCTGCTTGCT	CTCGACAGCC	AGTTTGTAGG	TGTGGAGGGC	TTTATCACCG	1920
	GCTCTCTCGA	CCTCCTCCCG	GCTCTCTACT	ACTTCCGTTT	CCAAAGGGAG	ATCTCTGTGG	1980
60	CCCTCTGTGG	TGCCCTTGCG	TTTGTCAATG	ATCTCTCATG	GGTGAAGTGT	GGCGGGATGT	2040
	ACGTCTTTCA	GCTGTTTGAC	TACTACTCGG	CCAGCGGCAC	CACCTTGCTC	TGGCAGGCCCT	2100
	TTTGGGAGTG	CGTGGTGGTG	GCTTGGGTTG	ACGGAAGTGA	CGGCTTTCAT	GACGACATTT	2160
	CTGTATATGT	CGGGTACCGA	CGCTGCCCTG	GAGTAAATGT	GTGCTGGTCT	TCTTTCATCC	2220
	CGCTGTGCTG	CATGGGCATC	TTTATCTTCA	ACGTTGTGTA	CTACGAGCGC	CTGTGTTACT	2280
65	ACAAACCTTA	CGTGTACCCG	TGGTGGGGTG	AGGGCCATGG	CTGGGCGCTT	GCCCTGTCTC	2340
	CCATGCTGCT	GCTGCGGCTG	CACCTCTGCG	GCTGCTCTCT	CAGGGCCCAAG	GGACCATATG	2400
	CTGAGACGTC	GCAGCACCTG	ACCCAGGCCA	TCTGGGGCCT	CCACCACTTG	GAGTACCGAG	2460
	CTCAGGACGC	AGATGTCCAG	GGCCTGACCA	CCCTGACCCC	AGTGTCCGAG	AGCAGCAAGG	2520
	TCGTGCTGTT	GAGAGAGTGC	ATGTGACAAC	TACAGTCACT	TACACAGCTC	ACCTCTGGTA	2580
70	GGCATAGACG	CCCCGTCTTC	AGGCCACGCG	CACCCCTCCA	GGGGGCTGCT	CTTTTCCCTGA	2640
	CACTTTGTGG	GTCTGCTTGG	GGAGGAGGGG	GAGAAAGCAC	GAGAGTGCTC	CACATAAACA	2700
	ACTTTTTCCT	TTTTTAATAA	AAAGCCAAAA	ATATCAACAAC	CCACCAAAAA	TAGATGCCTC	2760
	TCGCCCTCTCA	GCCCTAGCCG	AGCTGTGCTCT	AGGCCGCCGC	TAGTGCCCCA	CCCCCACCAC	2820
	CAGTGTCTGA	CTCTCTCTGC	CCCTGCCACG	CCACCCCTCT	CCCAAGCTCT	CAGAGCTCTG	2880
	CTCTGCAGCA	CACCCGTGGG	TGACCCCTCA	CCCCAGAAGC	AGCAGTGGCA	GCTTGGGAAA	2940
75	TGTGAGGAGG	GAGAGGAGGG	AGAGACGGGA	AGGAGGAGAG	AGAGGAGAAG	GGAGGACGGG	3000
	GAGGGGACAG	AGAACCAAGG					

CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTACGT CCAGTCCCGA GACGGCTGAG 3780
 TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA 3840
 GGGTGGCGGG CCTGCGGGGA CATTCTACTG TGCTAAAAAG CCAGTGCAGA CATAGCAATA 3900
 AAAACATGTC ATTTTCC

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

10 1 11 21 31 41 51
 | | | | | |
 MAKKSANENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD 60
 FIMSCVGFV GLGNVWRFPY LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQFMKAGS 120
 INWNICPLP KGLGYASMVI VFYCNYYIM VLAWGFYYLV KSFTTLPWA TCGHTWNTPD 180
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLRLSGGLEVPGA LNWEVTLCLL 240
 15 ACWVLVYFCV WKGVKSTGKI VYFTATFPYV VLVLVLRGV LLPGALDGI IYLLKPDWSKL 300
 GSPQWIDAG TQIPFSYAIG LGALTALGSY NRFNNNCYKD AIIILALINSG TSFFAGFVVF 360
 SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMPVAP LWALFFFML LLLGLDSQFV 420
 GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTDGMVYF QLFDYYSASG 480
 20 TLLWQAFWE CVVWVWYGA DRFMDDIACM IGYRCPWMK WCNWFFPLV CMGIFIFNVV 540
 YVEPLVYNT YVYFWGEAM GWAPALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600
 LHHLEYRAQD ADVRLGTLTL PVSSESKVVV VESVM

Seq ID NO: 68 DNA sequence
 Nucleic Acid Accession #: NM_021953.1
 Coding sequence: 178-2469

30 1 11 21 31 41 51
 | | | | | |
 GGACAGAGGG GGACCCGGCC GGTCCGGCGC GAGCCCCCGT CCGGGGCCCT GGCTCGGCC 60
 CCAGGTTGGA GGAGCCCGGA GCCCGCCTTC GGAGCTACGG CCTAACGGCG GCGGCGACTG 120
 CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAACGCGAG ATTCATAATG 180
 AAAGCTAGCC CCGCTCGGCC ACTGATTCTC AAAAGACGGA GGCTGCCCTC TCCTGTTCAA 240
 35 AATGCCCAA GTGAACATC AGAGGAGGAA CCTAAGAGAT CCCTGCCCA ACAGGAGTCT 300
 AATCAAGCAG AGGCCCTCAA GGAAGTGGCG GAGTCCAAC CTTCGAAGT TCCAGCTGGG 360
 ATCAAGATTA TTAACACACC ACCATGCCC AACACGCAAG TAGTGGCCAT CCCCACCAAT 420
 GCTAATATTC ACAGCATCAT CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT 480
 GGGCCCAACA AATTCATCCT CATCAGCTGT GGGGGAGCCC CAACTCAGCC TCCAGGACTC 540
 40 CGGCTCAAA CCAACACAG CTATGATGCC AAAAGGACAG AAGTGACCTT GGAGACCTTG 600
 GGACCAAAAC CTCGAGCTAG GGATGTGAAT CTCTCTAGAC CACTGGAGC CTTTGGGAG 660
 CAGAAACGGG AGACCTGTGT AGATGGTGAG GCAGCAGGCT GCATATCAA CAATAGCCTA 720
 TCCAACATCC AGTGGCTTGG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
 CAAGAGATGG AGGAAAAGGA GAATGTGCAC CTGGAGCAGC GACAGGTTAA GGTGTAGGAG 840
 45 CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGGCCACC CTACTCTTAC 900
 ATGGCCATGA TACAATTCGC CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC 960
 ATCTATACGT GTATTGAGGA CCACTTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
 AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGCTGCCC 1080
 AATGGCAAGG TCTCCTTCTG GACCATTCAC CCCAGTGCCA ACCGCTACTT GACATTGGAC 1140
 50 CAGGTGTTTA AGCCACTGGA CCCAGGGTCT CCACAATTGC CCGAGCACTT GGAATCACAG 1200
 CAGAAACGAC CGAATCCAGA GCTCGCCCGG AACATGACCA TCAAAACCGA ACTCCCCCTG 1260
 GCGCGACCGG GGAAGATGAA GCCACTGCTA CCACGGGTCA GCTCATACCT GGTACCTATC 1320
 CAGTTCCCGG TGAACCAATC ACTGGTGTGG CAGCCCTCGG TGAAGGTGCC ATTGCCCTG 1380
 CGGGCTTCCC TCATGAGCTC AGAGCTTGCC CGCCATAGCA AGCGAGTCCG CATTGCCCCC 1440
 55 AAGGTGCTGC TAGCTGAGGA GGGGATAGCT CCTCTTTCTT CTGCAGGACC AGGGAAGAG 1500
 GAGAAATCC TGTTTGGAGA AGGGTTTCT CCTTTGCTTC CAGTTCAGAC TATCAAGGAG 1560
 GAAGAAATCC AGCTGGGGA GGAAATGCCA CACTTAGGCA GACCCATCAA AGTGGAGAGC 1620
 CCTCCTCTGG AAGAGTGGCC CTCGCCGGCC CCATCTTTCA AAGAGGAATC ATCTCACTCC 1680
 TGGGAGGATT CGTCCCAATC TCCCACCCCA AGACCAAGA AGTCTACAG TGGGCTTAGG 1740
 60 TCCCAACCCC GGTGTGTCTC GGAAATGCTT GTGATTCAAC ACAGGGAGAG GAGGGAGAGG 1800
 AGCCGGTCTC GGGAGAAACA GCATCTACTG CTCCCTGTG TGGATGAGCC GGAGCTGCTC 1860
 TTCTCAGAGG GGCCAGTAC TTCCCGCTGG GCCGAGAGC TCCGTTCCC AGCAGACTCC 1920
 TCTGACCCTG CCTCCAGCT CAGCTACTCC CAGGAAGTGG GAGGACCTTT TAAGACACCC 1980
 ATTAAGGAAA CGCTGCCCAT CTCTCCACC CCGAGCAAT CTGTCTCTCC CAGAACCTCC 2040
 65 GAATCTCGA GGTATCGCC CCGAGCCAAA GTAGGGGAGC TGGATTTCAG CCCAGTACAA 2100
 ACCTCCAGG GTGCTCTGA CCCCTTGCCT GACCCCTTGG GGCTGATGGA TCTCAGCACC 2160
 ACTCCCTTGC AAGTGTCTCC CCCCCTTGAA TCACCGCAAA GGCTCTCAG TTCAGAACCC 2220
 TTAGACCTCA TCTCGTCCC CTTTGGCAAC TCTTCTCCCT CAGATATAGA CGTCCCCAAG 2280
 CCAGGCTCCC CGGAGCCACA GGTTCCTGCG CTTGCAGCCA ATCGTTCTCT GACAGAAGGC 2340
 70 CTGGTCCCTG ACACAATGAA TGACAGCCTC AGCAAGATCC TGCTGGACAT CAGCTTTCTC 2400
 GGCTGGAGC AGGACCCACT GGGCCCTGAC AACATCAACT GGTCCAGTT TATTCTGAG 2460
 CTACAGTAGA GCGCTGCCCT TGCCCTGTG CTCAGCTGT CCACCATCCC GGGCACTCCA 2520
 AGGCTCAGTG CACCCCAAGC CTCTGAGTGA GGACAGCAGG CAGGGACTGT TCTGCTCCTC 2580
 75 ATAGCTCCCT GCTGCTGAT TATGCAAAAG TAGCAGTCAC ACCCTAGCCA CTGCTGGGAC 2640
 CTTGTGTTC CCAAGATAT CTGATTCCTC TGCTGTCCCT GCCAGGAGCT GAAGGGTGGG 2700
 AACAAACAA GCAATGGTGA AAAGAGATTA GGAACCCCCC AGCCTGTTTC CATTCCTGTC 2760
 CCAGCAGTCT CTACCTTCC CTGATCTTTG CAGGGTGGTC CGTGTAATA GTATAAATTC 2820
 TCCAAATTAT CCTCTAATTA TAAATGTAAG CTTATTCTCT TAGATCATT TCCAGAGACT 2880
 GCCAGAAGGT GGTAGGATG ACCTGGGGTT TCAATTGACT TCTGTTCCTT GCTTTTAGTT 2940
 80 TTGATAGAAG GGAAGACCTG CAGTGCAAGG TTTCTCCAG GCTGAGGTAC CTGGATCTTG 3000
 GGTCTCTCAC TGACGGGACC CAGACAAGTG GATCTGCTTG CCAGAGTCTC TTTTGCCCTC 3060
 CCTCGCCACC TCCCGGTGTT TCCAAGTCAG CTTTCTGCA AGAAGAAATC CTGGTTAAAA 3120
 AAGTCTTTTG TATTGGGTCA GGAGTTGAAT TTGGGGTGGG AGGATGGATG CAACTGAAGC 3180
 AGAGTGTGGG TGCCAGATG TGCGCTATTA GATGTTCTC TGATAATGTC CCAATCATTA 3240
 85 CCAGGAGAC TGCCATTGAC GAGAACTCAG GTGGAGGCTT GAGAAGGCCG AAAGGGCCCC 3300
 TGACCTGCCT GGTCTCCTTA CTTTGCCTCT CAGCTTGCA AAGAGCCACC CTAGGCCCCA 3360
 GCTGACCGCA TGGGTGTGAG CCAGCTTGAG AACACTAAT ACTCAATAA AGCGAAGGTG 3420
 GACCNAAAAA AAAAAAAAAA AAAA

Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

5
10
15
20

1	11	21	31	41	51	
MKASPRRLPI	LKRRRLPLPV	QNAPSETSEE	EPKRSQAQBE	SNQAEASKEV	AESNSCKFFA	60
GKIINHPMT	ENTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
LRPQTQTSYD	AKRTEVILET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
LSNIQWLRRM	SSDGLGSRSI	KQEMEKEKNC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240
YNAMIQFAIN	STERKRMTLK	DIYTNIEDHF	PYFKHIAKPG	WKNRSIRHNS	LHDMFVRETS	300
ANGKVSFWTI	HPSANRYLTL	DQVFKPLDPG	SPQLPEHLES	QKRPNPPELR	RNMTIKTELP	360
LGARRMKPL	LPRVSSYLVP	IQFPVNQSLV	LQPSVKVPLP	LAASLMSEEL	ARHSKRVRIA	420
PKVLLAEBGI	APLSSAGPGK	EKKLLFEGEP	SPLLPVQTIK	EEBIQPGEEM	PHLARPIKVE	480
SPPLEEWSP	APSPKEBSSH	SWEDSSQSPT	PRPKKSYSL	RSPTRCVSEM	LVIQHRERRE	540
RSRRRKQHL	LPPCVDEPEL	LFSEGFSTSR	WAAELPPPAD	SSDPASQLSY	SQEVGGPFKT	600
PIKETLPISS	TPSKSVLPRT	PESWRLTPFA	XVGGLDSPV	QTSQGASDPL	PDPLGLMDLS	660
TIPLQSAFPL	ESQRLLSSE	PLDLISVFPF	NSSPSDIDVP	KPGSPPEQVS	GLAANRSLTE	720
GLVLDTMNS	LSKILLDISP	PGLDEDPLGP	DNINWSQFIP	ELQ		

Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
CCAGGTTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAACACGCAG	ATTTCATAATG	180
AAAACCTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCCC	TCCTGTTCAA	240
AATGCCCCAA	GTGAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCCA	ACAGGAGTCT	300
AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAACT	CTTGCAAGTT	TCCAGCTGGG	360
ATCAAGATTA	TTAACACACC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
GCTAATATTC	ACAGCATCAT	CACGACACTG	ACTGCCAAGG	GAACAGAGAG	TGGCAGTAGT	480
GGGCCCAACA	AAITCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
CGGCCCTCAA	CCCAAAACCG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
GGACCAAAAC	CTGCAGCTAG	GAGTGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
CAAGAGATGG	AGGAAAGGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
CCTTGAGAC	CATCAGCTGC	CTGGCAGAAC	TCTGTGCTGT	AGCGGCCACC	CTACTCTTAC	900
ATGGCCATGA	TACAATTGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAC	960
ATCTATAGCT	GGATTGAGGA	CACATTTCCT	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
AAGAATCCA	TCCGCCACAA	CCTTTCCTCG	CACGACATGT	TTGTCCGGGA	GACGTCTGCC	1080
AATGGCAAGG	TCTCTTCTGT	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
CAGGTGTTTA	AGCAGGAGAA	ACGACCGAAT	CCAGAGCTCC	GCGGGAACAT	GACCATCAAA	1200
ACCGAATCC	CCCTGGGCGC	ACGGCGGAAG	ATGAAGCCAC	TGCTACCACG	GGTCAGCTCA	1260
TACCTGGTAC	CTATCCAGTT	CCCGGTGAAC	CAGTCACTGG	TGTTGCAGCC	CTCGGTGAAG	1320
GTGCCATTGC	CCCTGGCGGC	TTCCTCATG	AGCTCAGAGC	TTGCCCGCCA	TAGCAAGOGA	1380
GTCCGATTG	CCCCAAGGT	GCTGCTAGCT	GAGGAGGGGA	TAGCTCCTCT	TTCTTCTGCA	1440
GGACCAGGGA	AAGAGGAGAA	ACTCCTGTTT	GGAGAAGGGT	TTTCTCCTTT	GCTTCCAGTT	1500
CAGACTATCA	AGAGGAGAGA	AATCCAGCCT	GGGGAGGAAA	TGCCACACTT	AGCGAGACCC	1560
ATCAAAGTGG	AGAGCCCTCC	CTTGAAGAG	TGGCCCTCCC	CGGCCCCATC	TTTCAAAGAG	1620
GAATCATCTC	ACTCTGGGA	GGATTCTGCC	CAATCTCCCA	CCCCAAGACC	CAAGAAGTCC	1680
TACAGTGGGC	TAGGTCCTCC	AACCGGTGT	GTCTCGGAAA	TGCTTGTGAT	TCAACACAGG	1740
GAGAGGAGGG	AGAGGAGCCG	GTCTCGGAGG	AAACAGCATC	TACTGCCTCC	CTGTGTGGAT	1800
GAGCCGGAGC	TGCTTCTCT	AGAGGGGCC	AGTACTTCCC	GCTGGGCCCG	AGAGCTCCCG	1860
TTCCAGCAGC	ACTCCTCTGA	CCCTGCCTCC	CAGCTCAGCT	ACTCCCAGGA	AGTGGGAGGA	1920
CCTTTTAAGA	CACCCATTAA	GGAAACGCTG	CCCATCTCCT	CCACCCCGAG	CAAACTGTCT	1980
CTCCCAAGAA	CCCTCTGAAT	CTGGAGGCTC	ACGCCCCCAG	CCAAAGTAGG	GGGACTGGAT	2040
TTCAGCCAGC	TACAAACCCC	CCAGGGTGCC	TCTGACCCTT	TGCTGACCC	CCTGGGGCTG	2100
ATGGATCTCA	GCACCACTCC	CTTGCAAAAT	GCTCCCCCCC	TTGAATCACC	GCAAGGCTC	2160
CTCAGTTAG	AAOCCTTAGA	CTCATCTCC	GTCCCTTTTG	GCAACTCTTC	TCCCTCAGAT	2220
ATAGACGTCC	CAAAGCCAGG	CTCCCGGAG	CCACAGGTTT	CTGGCCTTGC	AGCCCAATGT	2280
TCTCTGACAG	AAGGCCCTGT	CCTGGACACA	ATGAATGACA	GCCTCAGCAA	GATCCTGTCTG	2340
GACATCAGCT	TTCCTGCCCT	GGACGAGGAC	CCACTGGGCC	CTGACAACT	CAACTGGTCC	2400
CAGTTTATTC	CTGAGCTACA	GTAGAGCCCT	GCCCTTGCCC	CTGTGCTCAA	GCTGTCCACC	2460
ATCCCGGGCA	CTCCAAGGCT	CAGTGACCCC	CAAGCCTCTG	AGTGAGGACA	GCAGGCAGGG	2520
ACTGTTCTGC	TCCCTCATAGC	TCCCTGCTGC	CTGATTATGC	AAAAGTAGCA	GTACACCCCT	2580
AGCCACTGCT	GGGACCTTGT	GTTCCTCAAG	AGTATCTGAT	TCTCTGTCTG	TCCCTGCCAG	2640
GAGCTGAAGG	GTGGGAACAA	CAAGAGCAAT	GGTGAAAAGA	GATTAGGAAC	CCCCCAGCCT	2700
GTTCCTATTC	TCTGCCCAGC	AGTCTCTTAC	CTTCCCTGAT	CTTTCAGGGG	TGGTCCGTGT	2760
AAATAGTATA	AAITCTCCAA	ATTATCTCT	AATTATAAAT	GTAAGCTTAT	TTCCTTAGAT	2820
CATTATCCAG	AGACTGCCAG	AAGTGGGTA	GGATGACCTG	GGGTTTCAAT	TGACTTCTGT	2880
TCTTGTCTTT	TAGTTTGTAT	AGAAGGGAAG	ACCTGCAGTG	CACGGTTTCT	TCCAGGCTGA	2940
GGTACCTGGA	TCTTGGGTCT	TTCACTGCAG	GGACCCAGAC	AAGTGGATCT	GCTTGCCAGA	3000
GTCTTTTGTG	CCCTCTCCTG	CCACTCCCC	GTGTTTCCAA	GTCAGCTTTC	CTGCAAGAAG	3060
AAATCTCGT	TAAAAAGTC	TTTTGTATTG	GGTCAGGAGT	TGAATTTGGG	GTGGGAGGAT	3120
GGATGCAACT	GAAGCAGAGT	GTGGGTGCCC	AGATGTGCGC	TATTAGATGT	TTCTCTGATA	3180
ATGTCCCCAA	TATACACAGG	GAGACTGGCA	TGACGAGAA	CTCAGGTGGA	GGCTTGAGAA	3240
GGCCGAAAGG	GCCCTGACC	TGCCTGGCTT	CCTTAGCTTG	CCCCTCAGCT	TTGCAAGAG	3300
CCACCTTAGG	CCCCAGCTGA	CCGATGGGT	GTGAGCCAGC	TTGAGAACAC	TAACACTCA	3360
ATAAAGCGA	AGGTGGAAAA	AAAAAAAAAA	AAAAAAA			

Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

	1	11	21	31	41	51	
5	MKTSPPRLPI	LKRRRLPLPV	QNAPSETSEE	EPKRSQAQBE	SNQAEASKEV	AESNSCKFPA	60
	GIKIINHPTM	ENTQVVAIPN	NNIHSIITA	LTAKGKESGS	SGPNKFIILS	CGGAPTQPPG	120
	LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
	LSNIQWLRLM	SSDGLGSRSI	KQEMEKEKNC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240
	YNAMIQFAIN	STERKMTLTK	DIYTWIEDHF	PYFKHIAKPG	WKNISIRHNL	LHDMFVRETS	300
10	ANGKVSFWTI	HPSANRYLTL	DQVFKQKQRP	NPELRNMTI	KTELPLGARR	KMKPLLPRVS	360
	SYLVPIQFPV	NQSLVLPQSV	KVPLPLAASL	MSELARHSK	RVRIAPKVL	AEEGIAPLSS	420
	AGPGKEEKL	FGEGFSPLLP	VQTIKEEEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPSPSPFK	480
	EESSHSWEDS	QSPTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSR	RKQHLPPCV	540
	DEPELLFSEG	PSTSRWAAEL	PPFADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISSTPSKS	600
15	VLPRTPESWR	LTPPAKVGG	DFSPVQTPQG	ASDPLDPLG	LMDLSTPLQ	SAPPLESPQR	660
	LLSSEPLDLI	SVPPGNSSPS	DIDVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLSKIL	720
	LDISFPGLDE	DPLGPDNINW	SQFIPELQ				

Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

	1	11	21	31	41	51	
25	GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTGGGCC	60
	CCAGGTTGGA	GGAGCCCGGA	GCCCCGCTTC	GGAGCTACGG	CCTAACGGCG	GCGGCGACTG	120
	CAGTCTGAG	GGTCCCACT	TGTGATTCTC	AATGGAGAGT	GAAAACGCG	ATTCCATAATG	180
	AAAACCTAGCC	CCCGTCGGCC	ACTGATTCTC	AAAAGACGGA	GGCTGCCCT	TCCTGTTCAA	240
	AATGCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCCTGCCCA	ACAGGAGTCT	300
30	AATCAAGCAG	AGGCTGCCAA	GGAAGTGGCA	GAGTCCAAC	CTTGCAAGTT	TCCAGTGGG	360
	ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
	GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
	GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
	CGGCCTCAAA	CCCAAAACCG	CTATGATGCC	AAAAGGACAG	AAGTGACCCT	GGAGACCTTG	600
35	GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
	CAGAAACGGG	AGACCTGTGC	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
	TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
	CAAGAGATGG	AGGAAAGGA	GAATTGTCAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
40	CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGCTG	AGCGGCCACC	CTACTCTTAC	900
	ATGGCCATGA	TACAATTGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAAGAG	960
	ATCTATAGCT	GGATTGAGGA	CACATTTCCT	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
	AAGAATCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGTCTGCC	1080
	AATGGCAAGG	TCTCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
45	CAGGTGTTTA	AGCCACTGGA	CCCAGGCTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
	CAGAAACGAC	CGAATCCAGA	GCTCCGCCGG	AACATGACCA	TCAAAACCGA	ACTCCCTCTG	1260
	GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCATACACCT	GGTACCTATC	1320
	GACTTCCCGG	TGAACACGTC	ACTGCTGTTG	CAGCCCTCGG	TGAAGTGCC	ATTGCCCTG	1380
	GGGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCTC	1440
50	AAGGTTTTTG	GGGAACAGGT	GGTGTGTTGG	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
	CGAGATTTTG	GTCACCCCAT	CACCAGCTTG	TTTAATTGTA	TCTTTCTTTG	TTTATCAGTG	1560
	CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
	CTCTCTTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
	ATCCAGCCTG	GGGAGGAAAT	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
	TTGGAAGAGT	GGCCCTCCCC	GGCCCATCTT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
55	GATTGCTCCC	AATCTCCAC	CCCAAGACCC	AAGAAGTCTT	ACAGTGGGCT	TAGGTCCCCA	1860
	ACCCGGTGTG	TCTGGGAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
	TCTCGGAGGA	AAACAGCATCT	ACTGCTCTCC	TGTGTGATG	AGCCGGAGCT	GCTCTTCTCA	1980
	GAGGGGCCCA	GTACTTCCCG	CTGGGCGGCA	GAGCTCCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
60	CCTGCTCTCC	AGCTCAGCTA	CTCCAGGAA	GTGGGAGGAC	CTTTAAGAC	ACCCATTAA	2100
	GAAACGCTGC	CCATCTCTCT	CACCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
	TGGAGGCTCA	CGCCCCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCCACT	ACAAACCTCC	2220
	CAGGGTGCTC	CTGACCCCTT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
	TTGCAAAAGT	CTCCCCCTCT	TGAATCACCG	CAAAGGCTCC	TCAGTTTCAG	ACCCTTAGAC	2340
65	CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
	TCCCGGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAATCGTT	CTCTGACAGA	AGGCCTGGTC	2460
	CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCCTGTCTG	ACATCAGCTT	TCCTGGCCTG	2520
	GACGAGGACC	CACCTGGGCC	TGACAAATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
	TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
70	AGTGACACCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTTCTGCT	CCTCATAGCT	2700
	CCCTGCTGCG	TGATTATGCA	AAAGTAGCAG	TCACACCTTA	GCCACTGCTG	GGACCTTGTG	2760
	TTCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
	AAAGGCAATG	GTGAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
	GTCTCTTACC	TTTCCAGGAT	TTTGAGGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
75	TTATCTCTTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
	AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCGTGT	CCTTGCTTTT	AGTTTGTATA	3060
	GAAGGGAAGA	CCTGCAGTGC	ACGGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
	TCACTGCAGG	GACCCAGACA	AGTGGATCTG	CTTGCCAGAG	TCCTTTTTCG	CCCTCCCTGC	3180
	CACCTCCCGG	TGTTTCCAAG	TGACGTTTCC	TGCAAGAAGA	AATCCTGGTT	AAAAAGTCT	3240
80	TTTGATTGGG	GTCAGGAGTT	GAATTTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
	TGGGTGCCCA	GATGTGCGCT	ATTAGATGTT	TCTCTGATAA	TGTCCCAAT	CATACAGGG	3360
	AGACTGGCAT	TGACGAGAAC	TACAGTGGAG	GCTTGAGAAG	GCGGAAAGGG	CCCCTGACCT	3420
	GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAGAGAC	CACCTAGGC	CCCAGCTGAC	3480
85	CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAGCGAA	GGTGACACAA	3540
	AAAAAAAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1

1 11 21 31 41 51
 MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AENSNSCKFPA 60
 5 GIKIINHPTM PNTQVVAIPN NANIHSIITA LTARGKESGS SGNPKPILIS CGGAPTQPPG 120
 LRPTQTQSYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
 LSNIQWLRQM SSDGLGSRSI KQEMEKEKENC HLEQRQVKVE EPSRPSASWQ NSVSEPPFYS 240
 YNAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNL LDMFVRETS 300
 10 ANGKVSFWTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QQKRPNPELR RNMTIKTELP 360
 LGARRKMKPL LPRVSSYLVP IQPPVQNQSLV LQPSVKVPLP LAASLMSSSEL ARHSKRVRIA 420
 PKVFGQVVFV GYMSKFFSGD LRDFGTPIITS LFNPIFLCLS VLLAEEGIAP LSSAGPGKEE 480
 KLLFGEQFSP LLFVQTIKEE EIQPGGEEMPH LARPIKVESP PLEEWPSAP SFKESSSHSW 540
 EDSSQSPTPR PKKSYSGLRS PTRCVSEMLV IQHRERRERS RSRRKQHLIP PCVDEPELLF 600
 15 SEGPFSTRWA AELFFPADSS DPASQLSYSQ EVGGPFKTP I KETLPISSSTP SKSVLPRTPE 660
 SWRLTPPARV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
 DLISVFFGNS SPSPDIDVPK GPSEPQVSGL AANRSLTEGL VLDTMNDSL S KILLDISFPG 780
 LDEDPLGPDN INWSQFIPEL Q

Seq ID NO: 74 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 25 GGGAAGAGCC AGGCTGAGCC TTATAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTAGC CTTCCTCAGT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
 CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
 ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCAACTTCC 240
 30 TTAGTGCTGT TGACAAAAG GGCACAAAT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCCA 360
 CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCTGTTC CGGGGCGAGC CAGTGACCCA 420
 GCCCCACCAA TGGGCTTCCA GAGACCCAG GAACAATAAA ATGTCTTCTC CCACAGA

Seq ID NO: 75 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 40 MSNTQAERSI IGMIDMFHYK TRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
 KKDKNEDKKI DFSEFLSLLG DIATDYHKQS HGAAPCSGGS Q

Seq ID NO: 76 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 111-416

1 11 21 31 41 51
 50 GGGAAGAGCC AGGCTGAGCC TTATAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
 TCATCCTTCT ACTCGTAGC CTTCCTCAGT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
 CTCAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
 ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCAATTTC 240
 TCAGTGCTGT TGACAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
 55 AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTGCTGGGA GACATAGCCG 360
 CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCTGTTC TGGGGGAAGC CAGTGATCCA 420
 GCCCCACCAA GGGGCTTCCA GAGACCCAG GAACAATAAG TGTCTCTTCC CACCAGA

Seq ID NO: 77 Protein sequence:
 Protein Accession #: XP_048124.1

1 11 21 31 41 51
 60 MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
 65 KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

Seq ID NO: 78 DNA sequence
 Nucleic Acid Accession #: Z73678.1
 Coding sequence: 253-2433

1 11 21 31 41 51
 75 GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TGGCCAGTGC 60
 CAGAGAGGGA CGAACCAGGG TGAAGCGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
 CCTCGCACTC TATGGCGGTA GGGAGCGGCT GAGAGCGAGA AGAGCAGCT CCTGCCCGCC 180
 CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCGCGGCGC GCGCCACCCG 240
 CCTCCGCCCA CCATGAACCA CTGCGCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
 GACCAGGACA ACTCCAGTT GGCCTTTCG TCGGACCAA AGATGAACA AGGCACGTCT 360
 80 GGCAGGCAGC GCGTGCAGGA GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
 TCCAGTCTGT CCACCTGTAG CCACTCCAAT CGAGGTTCCT TGTATGATGG CTGGCTGAC 480
 AATTACAAT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
 GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
 TTCAGTCTCT ACAGCCAGAT GGAGAACTGG AGCCGGCACT ACCCCCGGG CAGCTGTAAC 660
 85 ACCACCGGCG CAGGCAGCGA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGAG 720
 CCGGACCTCT ACTGTGACCC ACGGGCACCC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC 780
 CAGAAGACCA CCCAGAACC CTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
 AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCTGT GTATATCCCG 900

	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TCGAGTGCAG	TGGGCTGACC	ATCCCCAAGG	CTGTGCAGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAGGC	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAGAACGT	CCAGCAGGCC	GCGGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCAGCA	CCAAACAGCT	GGAGACCCGG	AGGCAGAAATG	GGATCCGCGA	GGCAGTCTAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTGCCG	ACGCCCTGCC	TGTTCTGGCC	1380
10	GACCCGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	GCGTAACCTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTCTCTGACA	ACCTCTCCTA	CCGCCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAAAG	CCCGCAACGC	CTACACCGAG	AAGTCTCTCA	CTGGCTGCTT	CAGCAACAAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTTGTA	CCATTTCAGAT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAGAA	AAGATGTCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGCACAGC	1920
	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTG	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTG	CCCGCCTCCT	GCAATCTGGC	AACCTCTGATG	TGGTGCAGTC	CGGAGCCTCC	2040
	CTCCTGAGCA	ACATGTCCCG	CCACCCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAAGCCAC	ACTGGCAATA	CCAGCAACTC	CGAAGACATC	2160
	TTGTCTCGG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAG	2220
	CAGTACTTCT	CAGACGACAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAAG	CAGTGCCTCA	2280
25	CCCAAGGCGG	CAGAAGCTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAACCTG	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCCGATTG	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCTC	GCTGGATGGG	GTTTCTGTGC	2520
	CATCCTGTGC	AGTATTGTGG	AAAGTTCACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	GATTTTITAGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGTTTG	GGGCGGGGGG	GGCTTCTCTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTCTCCT	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GCGTGATGT	GTGTGTGTGT	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATT	TTTGTGAGCT	CATAAGGTGG	TGAAAAGGAC	TCTCCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCCGTGAA	TGTGTGGTGC	2940
	CAGGGCAAGG	GGGCCATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCCCTGAG	GCTTCTTACC	3000
	AGTGTCTTCC	AAGGGTGCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCTTTCCACG	AAGGGAGGTC	TGGTGTATCT	CATGGGAGAA	TCTGGGGTGT	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGCGCCACA	AGGACTGAGG	TTGGGTAGGT	GTGAGGTTCC	AGAGGACAGC	3180
40	AGGACACTCT	CGCATACTTT	GCCAAATGAG	GCTGTCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCTTCC	ACCCTCTTGG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAAAGGCC	3300
	TGCATTGAGA	GGTCTGTGTA	TCTACTGTGT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTT	3360
	TTAAGAAAAG	CTATTTTATT	CGAGCTCTTT	CCCAAGAGCT	GTCTCTGGGA	TGGCTGGTCT	3420
	TCATATTTCC	AGTGGAGAGG	GGAAACAAGT	GGGCTGGGCA	TATACCTATT	CCGGCTTCTA	3480
45	TTGGGATGGA	GTTGGGGTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
	AGTCAATTGA	GGGAGTGTGT	GGGTCCGAGG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
	AGGAAGAGAA	AGTGCCATAT	CAGGGTACCG	GTACCGGCAA	GCTCAGATCT	CAGCCAGGGG	3660
	CCATGCCCCA	CTTCCCTGTA	CCCCAGCTGT	CTTGTCTCCA	CTCTGTGAAA	CCCAAGGGG	3720
	ATGTGATAAA	CAGGGCTATT	AGGGGTATCA	GCCACGTCGA	GCCCCAGAC	TCTGTGCACT	3780
50	TCAGACCAGC	AGCAGCAGGA	GGGCTCCCGA	GGGCTTATG	AGAAAACCTG	TGTGGACATC	3840
	CCTTGGTGTG	CACTAAGACA	GAGCAGAGCC	CAGCGCTCCC	AAGCCTTCTC	CCTTCCAGCT	3900
	TCTACTTCCA	TGCTAGCATT	GCTGGTGTGA	GAGAGGAATT	AACCTCTCTG	TCTGTGCCCT	3960
	TCTCTAGAAG	AATATAAGAT	GCTCTCTCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCTCTCTCTG	CACACACCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCATT	CAGGCTGGAA	4080
55	AACACTGATG	TGGAATCAGT	ATGACAACTG	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCCTCCGA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTGTCT	TGGGTCTGTG	4200
	ATACCTCTCC	TGCTTCTCTG	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCTCTCT	4260
	AGGGACCCAC	GTGGAGAGCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCTCT	4320
	CTTTGTTGTC	ATCAGAACCC	AGAGGAATTC	TTCTCCTAAA	AAATACGTAT	GGCATAACCA	4380
60	TCGTGTGGGG	CGAGTGTCTT	AAGCACTTAG	ACTACATCAG	GGAAGAACAC	AGACCACATC	4440
	CCGTCCTCTA	TGCGGCTTAT	GTTTCTGTGA	GGAAAGTGGG	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCCC	GGCTGGGGGC	TGTGCAGTCC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
	CATGTGAACC	TTACCAAGCC	AGGCGGATGC	CCCTTCCCTT	TAGCACTACC	CTGGCCTCCT	4620
	GCATCCCCCT	GCCTCATGTT	CCTCCCACTT	TCAAAGAATG	AAGAGCCCCA	TGGGGCCAGC	4680
65	CCCTGCGCTG	GGAAACGAGC	AGCCTTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
	AGGGCTGACT	TGGTGTACAC	TGCCCATTC	CTCTCAGGCC	AGCTCAGGTC	ACCCGGGCCT	4800
	CTGACCCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACCTAGA	GGGGCTTTTC	CTAGAGAAAG	4860
	AGAACAAGGA	GCTTGCAGG	CTTCATGTAG	CCGACACACG	TCTCAGGATT	TTAAGTCCAC	4920
	ATTGGCCTCA	CACTAGCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAATT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCTTGGGAT	CTCCTGTGCT	AGCGGGCAAT	GACAAATCCA	5040
	GTCAATTGGC	ACCAGCCACC	TCTGCAGTGG	GGACCACTAT	AGCAGCCCTG	ACTCCACACT	5100
	CCTCCTGGGG	ACCCAAGAGG	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGGA	ATCTGGCTGA	5160
	ACTGGCTGGG	AGGACCAAGA	CTCGGCTGG	GGTGGGCAGG	GAAGGGAAGC	CGGGGGCTGC	5220
	TGTGAGGGAT	CTTGGAGCTT	CCCTGTAGCC	CACCTTCCCC	TGCTTTCATG	TTTGTAGAGG	5280
75	AACTTGTGTC	CGGCCAGGCC	CAGTTTCTCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
	GGAAATAGAG	AAAATCAATA	AATTGCTAGT	GTTTCTTTGA	AAAAAATA		

Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

80	1	11	21	31	41	51	
	MNHSPLKTL	AYECFQDQDN	STLALPSDQK	MKTGTSGRQR	VQEQVMHTVK	RQSKSSQSS	60
	TLSHSNRSGM	YDGLADNYNY	GTTSRSSYYS	KFQAGNGSWG	YPIYNGTLKR	EPDNRFRSSY	120
	SQMNWSRHY	PRGSCNTTGA	GSIDCFMQKI	KASRSEPDLY	CDPRGLTRKG	TLGSKGQKTT	180
85	QNRYSFYSTC	SGQKAIKKCP	VRPPSCASKQ	DPVYIPIISC	NKDLSPGHRS	ASSKICSEDI	240
	ECSGLTIPKA	VQYLSQDEK	YQAIGAYYIQ	HTCFQDESAK	QQVYQLGGIC	KLVDLLRSPN	300
	QNVQQAAGA	LRNLVFRSTT	NKLETRRQNG	IREAVSLLR	TGNABIQKQL	TGLLWNLSST	360

DELKEELIAD ALPVLADRV IPFSGWCDGN SNMSREVVDV EVFFNATGCL RNLSSADAGR 420
 QTMRYNSGLI DSLMAYVQNC VAASRCDDKS VENCMLVLHN LSYRLDAEVP TRYRQLEYNA 480
 RNAYTEKSSST GCFPSNKSXDM MNNNYDCPLP EETNPFGSG WLYHSDAIRT YLNLMGKSKK 540
 DATLEACAGA LQNLTASKGL MSSGMSQLIG LKERGLPQIA RLLQSGNSDV VRSGASLLSN 600
 MSRHPLLRHV MGNOVPFEVT RLLTSHTGNT SNSEDILSSA CYTVRNLMAS QPQLAKQYFS 660
 SSMLNINIINL CRSSASPKAA EAARLLLSDM WSSKELQGV L RQQGFDRNML GTLAGANSLR 720
 NFTSRF

Seq ID NO: 80 DNA sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180-1658

1 11 21 31 41 51
 TAGTCGCGGG TCCCCGAGTG AGCACGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTCCGA 60
 GTCAGAGTCG CAGTGGGAGT CCCCAGGACG GAGCACGAGC CTGAGCGGGA GAGCGCGCT 120
 CGCAGCGCCG TCGCCACCGG CGTACCCGGC GCAGCCAGAG CCACCAGCGC AGCGCTGCCA 180
 TGGAGCCCAG CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240
 TTGGCTCCCT GCAGTTTGGC TACAACACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300
 AGGAGTTCTA CAACCAAGACA TGGGTCCACC GCTATGGGGA GAGCATCCTG CCCACCAAGC 360
 TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTCTGTG TGGGGGCATG ATTGGCTCCT 420
 TCTCTGTGGG CCTTTTCGTT AACCGCTTTG CCGGGCGGAA TTCAATGCTG ATGATGAACC 480
 TGCTGGCCCT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540
 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTACTGCGG CTGACCACA GGCTTCGTGC 600
 CCATGTATGT GGGTGAAGTG TCACCACAG CCTTTCGTGG GGCCCTGGGC ACCCTGCACC 660
 AGCTGGGCAT CGTCTCGGC ATCCTCATCG CCCAGGTGTT CGGCGTGAC TCATCATGG 720
 GCAACAAGGA CTTGTGGCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGCTGCAGT 780
 GCATCGTGCT GCCCTTCTGC CCGGAGAGTC CCGCTTCCTT GCTCATCAAC CGCAACGAGG 840
 AGAACCGGCG AGAGAGTGTG CTAAAGAAGC TGCGCGGGAC AGCTGACGTG ACCATGACC 900
 TGCAGGAGAT GAAGGAAGAG AGTGGGCGA TGATGCGGGA GAAGAAGGTC ACCATCCTGG 960
 AGCTGTTCGG CTCGCCCGCC TACCGCCAGC CCATCTCAT CGCTGTGGTG CTGCAGCTGT 1020
 CCCAGCAGCT GTCGTGCATC AACGCTGTCT TCTATTACT CACGAGCATC TCGAGAAGG 1080
 CGGGGGTGCA GCAGCCTGTG TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCTTCA 1140
 CTGTCTGTGC GCTGTTTGTG GTGGAGCGAG CAGGCGGGCG GACCCTGCAC CTCATAGGCC 1200
 TCGCTGGCAT GCGGGTGTG GCCATACTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC 1260
 TACCCTGGAT GTCTATCTG AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG 1320
 TGGGTCTCGG CCCCATCCCA TGGTTCATCG TGGCTGAAC CTTCAGCCAG GGTCCACGTC 1380
 CAGCTGCCAT TGCCGTGTGA GGCTTCTCCA ACTGGACCTC AAATTTTATT GTGGGCATGT 1440
 GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGCTT CATCATCTTC ACTGTGCTCC 1500
 TGGTCTGTGT CTTCATCTTC ACCTACTTCA AAGTTCCTGA GACTAAAGGC CGGACCTTCG 1560
 ATGAGATCGC TTCGGCTTC CGGCAGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620
 AGCTGTTCCT TCCCTTGGGG GCTGATTCCC AAGTGTGAGT CGCCCCAGAT CACCAGCCCG 1680
 GCCTGCTCCC AGCAGCCCTA AGGATCTCTC AGGAGCAGAG GCAGCTGGAT GAGACTTCCA 1740
 AACCTGACAG ATGTACGCG AGCCGGGCTT GGGGCTCCTT TCTCCAGCCA GCAATGATGT 1800
 CCAGAAGAAT ATTACGAGCT TAACGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTGCTC 1860
 AAATCTATTC AGACRAAGCA CAGGTTTTAT AATTTTTTAA TTAAGTATT TGTATTATTT 1920
 ATATCAGCCT GAGTCTCCTG TGCCACATC CCAGGCTTCA CCTGAATGG TTCCATGCTT 1980
 GAGGGTGGAG ACTAAGCCCT GTCGAGACAC TTGCCTTCTT CACCAGCTA ATCTGTAGGG 2040
 CTGGACCTAT GTCTTAAGGA CACACTAATC GAACATGAA CTACAAAGCT TCTATCCAG 2100
 GAGGTGGCTA TGCCACCCG TCTGTCTGGC CTGGATCTCC CCACTTAGG GGTGAGGCTC 2160
 CATTAGGATT TGCCCTTCC CATCTCTTCC TACCAACCA CTCAATTAA TCTTCTTTA 2220
 CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAGGGGCC AGTCTGGGCT 2280
 GCCGGTCTCT AGTCTCCTT GCAGTGAAGG CCACTAATC ACCATGAGAA GAGGGCTGT 2340
 GGGAGCCTGC AAACCTACTG CTCAGAAGA CATGGAGCT CTGCGCTGT TGTGTATAGA 2400
 TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAT TACAGACACT AAGTTATAGT 2460
 ATATCTGGAG AAGCCAACT GTAAATACAC CACCTCACTC CTGTACTTAA CCTAAACAGA 2520
 TATAAATGGC TGGTTTTAG AAACATGGTT TTGAAATGCT TGTGATTGA GGGTAGGAGG 2580
 TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTGCAACC ACTGCAACGG CTTAGACTTC 2640
 GACTCAGGAT CCACTCCCTT ACACGTACCT CTCATCAGTG TCCTCTGTCT CAAAATCTG 2700
 TTTGATCCCT GTTATCCAGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTCT 2760
 ATCATATATT TGATAGTTGG TGTTCAAAA AACACTAGTT TGTGCCAGC CGTGATGCTC 2820
 AGGCTTGAAA TCGATTATT TTGAATGTGA AGGGAA

Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_006507.1

1 11 21 31 41 51
 MEPSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI BEFYNTQTVH RYGESILPTT 60
 LTTLWSLSVA IFVSGMGIGS FSVGLFVNRF GRRNSMLMMN LLAPVSAVLM GFSKLKGSFE 120
 MLILGRPIIG VYCGLTTFPV PMYVGEVSPT AFRGALGTLH QLGIVVGILI AQVFGLDSIM 180
 GNKDLWPLLL SIIPFALLQ CIVLPFCPEP PRPLLINRNE ENRAKSVLKK LRGTADVTHD 240
 LQEMKEESRQ MMREKVVITL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIFEK 300
 AGVQQPVVAT IGSIVNTAF TVVSLFVVER AGRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPWMSYLSIV AIPGFVAFPE VPGGPPIWFI VARLFSQGPR PAIAVAGFS NWTNPFIVGM 420
 CFQYVEQLCG PYVFIIFTVL LVLFFIPTYF KVPETKGRTP DEIASGFRQG GASQSDKTPE 480
 ELFEPLGADS QV

Seq ID NO: 82 DNA sequence
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541

1 11 21 31 41 51
 GGGGGCGCGG CGCGCTGACC CTCCTGGGCG ACCGCTGGGG ACAGATGGCG TGCTCGCCTT 60
 GCTGCTGTGC GTGGCCCTAC CGCGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120

Seq ID NO: 83 Protein sequence:
Protein Accession #: AAH01291

Seq ID NO: 84 DNA sequence
Nucleic Acid Accession #: NM_022893.1
Coding sequence: 229-2726

220

5
10
15
20
25
30
35
40
45
50
A

ATCTGTATGG GGC AATACTA TTGCAATTTA CGCAAACTTT GAGCCTTTCT CTTGTGCAAT 3060
AATTTCACATG TTGTGTATGT TTTT TTTTAA ACTTAGACAG CATGTATGGT ATGTTATGGC 3120
TATTTTAAAT TGTCCTTAAT TCGTTGCTGA GCAAAACATGT TGCTGTTTCC AGTTCCCGTTC 3180
TGAGAGAAAA AGAGAGAGAG AGAGAAAAAG ACCATGCTGC ATACATTCTG TAATACATAT 3240
CATGTACAGT TTTATTTTAT AACGTGAGGA GGA AAAACAG TCTTTGGATT AACCTCTAT 3300
AGACAGAATA GATAGCACTG AAAAAAATC TCTATGAGCT AAATGTCTGT CTCTAAAGGG 3360
TTAAATGTAT CAATTGGAAA GGAAGAAAAA AGGCCTTGAA TTGACAAATT AACAGAAAAA 3420
CAGAACAAAGT TTATTTCTATC ATTTGGTTT AAATATAGAG TGCCTTGGAT CTATTAAAAA 3480
CACATCGATG GTTCTTTCTA CTGTGTATAA ACTTGTAGCT TAATTCAGCA TTGGGTGAGG 3540
TAATAAACCT TAGGAAGTAG CATATAATTC TATATTGTAT TTCTCACAA AATGGCTACC 3600
TAAAAAGATG ACCCATATAG TCCTAGTTAA TCATCATTTT TCCTTTAGTT TAATTTTATA 3660
AACAAAACCTG ATTATAACAG TATAAAAGCT ACTTTGCTCC TGGTGAGAGC TTAAGAAAAA 3720
TGGGCTGTTT TGCCCAAGT TTTATTTT TTAACAATG ATTAATTTGA ATGTGTAATG 3780
TGCAAAAGCC CTGGAACGCA ATTAATACA CTAGTAAGGA GTTCATTTTA TGAAGATATT 3840
TGCTTTAATA ATGTCTTTT AAAAACTAG GCACCAAAAG AAATAGATCC AGATCTACTT 3900
GGTTGTCAAG TGACAAATCA AATGATAAAC TTTAAGACCT TGTATACCAT ATTGAAAGGA 3960
AGAGGCTGAC AATAAGGTTT GACAGAGGGG AACAGAAGAA AATAATATGA TTTATTAGCA 4020
CAACGTGTGA CTATTTGCCA TTTAAAACTA GAACAGGTAT ATAAGCTAAT ATTGATACAA 4080
TGATGATTAA CTATGAATTC TTAAGACTTG CATTAAATG TGACATTCCT AAAAAAGAA 4140
GAGAAAGAAT TTTAAGAGTA GCAGTATATA TGTCTGTGCT CCCTAAAAGT TGTACTTCAT 4200
TTCTTTTCCA TACACTGTGT GCTATTGTG TTAACATGGA AGAGGATTCA TTGTTTTTAT 4260
TTTTATTTT TTAATTTT TTTT TTTT AAGCTAGCAT CTGCCCCAGT TGGTGTTCAA 4320
ATAGCACTTG ACTCTGCTTG TGATATCTGT ATCTTTTCTC TAATCAGAGA TACAGAGGTT 4380
GAGTATAAAA TAAACCTGCT CAGATAGGAC AATTAAGTGC ACTGTACAAT TTTCCAGTT 4440
TACAGGTCTA TACCTAAGG AAAAGTTGCA AGAATGCTGA AAAAAAATG AACACAATCT 4500
CATTGAGGAG CATTTT TAA AACTAAAAA AAAAAAACT TTGCCAGCCA TTTACTTGAC 4560
TATTGAGCTT ACTTACTTGG ACGCAACATT GCAAGCGCTG TGAATGGAAA CAGAATACAC 4620
TTAACATAGA AATGAATGAT TGCTTTCGCT TCTACAGTGC AAGGATTTT TTGTACAAAA 4680
CTTTT TAA TATAATGTT AAGAAAAATT TTTT TAA AACTTTCAT TATGTTTAGG 4740
GGGGAACCTG ATTTTAGGTT TCCATTGTCT TGGTGGTGT ACAAGACTG TTATCCATT 4800
AAAAATGGTA AATGAAATTC TATGCTTGG ATACACACCG CTCTTCAGGT TGTAAAAAAA 4860
AAAAACATAC ATTGGGAAA GGT TTAAGAT TATATAGTAC TTAATATAG GAAATGCAC 4920
ACTCATGTTG ATTCCTATGC TAAAAATCAT TTATGGTCT TTTCTGTAT TTCTAGAAATG 4980
GTATTGGAAT TAAATGTCA TCTAGTGTTA GGCATATAG TATTATATAT GAAGCTTGTA 5040
TTTTTAACCT TTGCTTGTTC TCTTAAAAAG TATCAATGTA CCTTTTGG TAGTGGAAAA 5100
AAAAAGACA GGCCTGCCA GTATATTTT TTAATTGGC AGGATAATAT AGTGCAAAAT 5160
ATTTGTATGC TTCAAAAA AAAAAAGAG AGAAACAAA AAGTGTGACA TTACAGATGA 5220
GAAGCCATAT AATGGCGTTT TGGGGGAGCC TGCTAGAAATG TCACATGGAT GGCTGTCTA 5280
GGGGTGTAC ATATCTCTTT TTGTTCTCTT TTCTGCTGC CATACTGTAT GCAGTACTGC 5340
AAGCTAATAA CGTGTGTTG TTATGTAGTG TGCTTTTGT CCCTTCTCT CTATCACCT 5400
ACATTCAGC ATCTTACCT CATATGCAGT AAAAGAAAGA AAGAAAAA AAGGAAAAA 5460
AAAAAAAAC CAATGTTTTC CAGTTT TTT CATTGCCAAA AACTAAATGG TGCTTATAT 5520
TTAGATTGGA AAGAATTTCA TATGCAAGC ATATTAAAGA GAAAGCCCG TTTAGTCAAT 5580
ACTTTTGT AAATGGCAAT GCAGAAATAT TTGTTATTGG CCTTTTCTAT TCTGTAAATG 5640
AAAGCTGTT GTCTGAACCT GAAATTTTAT CTTTACTAT GGGAGTCACT ATTTATTATT 5700
GCTTATGTGC CCGTTTCAA ACAGAGGCAC TTAATTTGAT CTTTATTATT TCTTGTGTTT 5760
TATTTT TTTATTTAGA TGACCAAGG TCATTACAAC CTGGCTTTT ATTGTATTG 5820
TTCTGTGCT TCTTAAAGT CTATTGGAAA AACCACTGTC TGTGTTT TGGCAGTTGT 5880
CTGCATTAC CTGTTACAT ACCCATTTTG TCCCTTTATT GAAAAATAA AAAAAATTA 5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

55
60
65
70

1 11 21 31 41 51
MSRRKQKQKP HSKREFSPE PLEAILTDDE PDHGPLGAPE GDHDLITCQ QMNFPLGDI 60
LIFIEHKRKQ CNGSLCLEKA VDKPPSPSP EMKASNPVE VGIQVTPEDD DCLSTSSRI 120
CPKQEHIA DK LHWRLSSP RSHAGALIP PGMSAEYAP GICKDEPSSY TCTCKQPPT 180
SAWFLLOHAQ NTHGLRIYLE SEHGSPLTFR VGIPSGLGAE CPSQPPLHGI HIADNPNFNL 240
LRIPGSVSRE ASGLABGRFP PTPPLFSPPP RHHLDPHRIE RLGAEEEMALA THHPSAFDRV 300
LRLNPMAMEP PMDPFSRRLR ELAGNTSSPP LSPGRPSPMQ RLLQPFQPGS KPPFLATPPL 360
PPLQSAPPPS QPVPKSKSCE FCGKTFKFQS NLVVHRSHT GEKPYKCNLC DHACTQASKL 420
KRHMKTHMHK SSPMTVKSDD GLSTASSPEP GTSDLVGSAS SALKSVVAKF KSENDPNLIP 480
ENGDEEEED DEEEEEE EEEELTESER VDYGFGLSLE AARHHENSSR GAVVGVDDES 540
RALPDVMQGM VLSSMQHFSE AFHQVLGEKH KRGLAEAEAG HRDTCDEDSV AGESDRIDDG 600
TVNNGRCSPG ESASGGLSKK LLLGSPSSLS PFSKRIKLEK EFDLPATMP NTEENVYSQWL 660
AGYAAASRLK DPFLSFGDSR QSPFASSEH SENGSLRFS TPPGELDGGI SGRSGTSGSG 720
STPHISGPGT GRPSSKEGRR SDTCEYCGKV FKNCNLTVH RRSHTGERPY KCELCNYACA 780
QSSKLTRHMK THGQVGKDVY KCEICKMPFS VYSTLEKHMK KWHSDRVLNN DIKTE

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

75
80
85

1 11 21 31 41 51
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG 120
GGAGAAGATG CTGGCGCCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG 180
CGTGACCTGT CAGCGCAACA TCACGCTGCT CAACGCGCTG GCCATCATCG TGGGGACCAT 240
TATCGGCTCG GGCATCTTGG TGACGCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCGGG 300
GCTGGCGCTG GTGGTGTGGG CCGCGTGGCG CGTCTTCTCC ATCGTGGCG CGCTCTGCTA 360
CGCGGAGCTC GGCAGACCA TCTCCAAATC GGGCGGCGAC TACGCTACA TGCTGGAGGT 420
CTACGGCTCG CTGCGCGCTC TCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGCGCTTC 480
ATCGCAGTAC ATCGTGGCCC TGGTCTTCCG CACCTACCTG CTCAGCCCG TCTTCCCCAC 540

CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCGCG CACCCGGGTC CAGGATGCCT TTGCCGCGCG 660
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAATCGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900
 CATCGTGACG CTGGTGATCG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCTTGATC ATCCCGTCT TCGTGGGCTT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
 GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TAGCCCTTCT CCAAGGACAT CTCTCCGTTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
 CCTCTTCTG ATCGCGTCT CTCTCTGGAA GACACCGTG GAGTGTGGCA TCGGCTTCAC 1440
 CATCATCCTC AGCGGCTGC CCGTCTACTT CTTGGGGTTC TGGTGGAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
 CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCGGGA GGAGCATGC

Seq ID NO: 87 Protein sequence:
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
 LEVYGSILPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLVL 180
 LLTAVNCYSV KAATRVQDAF AAARKLLALAL IILGPFVQIG KGDVSNLDPN FSFEGTKLDV 240
 GNIVLALYSY LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSAA VAVDFGNHYL GVMSWIIPVF VGLSCFGSVN GSLPTSSRLP FVGSREGHLP 360
 SILSMIHPQL LTFVPSLVFT CVMTLLEYAFS KDIPSVINFP SFFNWLCLVAL AIGMIWLRH 420
 RKPELERPIK VNLALFVFFI LACFLIAVVS FWKTFVECGI GFTIILSLGP VYFFGVWWMKN 480
 KPKWLLQGIF STTVLCQKLM QVVPQET

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 168-989

1 11 21 31 41 51
 TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCCGCT 60
 TCTGGATATG AAATTCAGC TGCTTGCTGA GTCTATTGC CGGCTGCTGG GAGCCAGGAG 120
 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
 TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
 TGTCTCTGGT CTTCTCTTC CGCGTGTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
 GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
 TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGG CCTGCAGCTT ATCCTGGTGA 420
 CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
 ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGCG AAGAAGCGGG 540
 GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600
 TTCTCTATGT GTTCCAATCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
 TTTTCACCTT CTTCTATGGT GCCACAGCTG CCATCTGCAT CTGCTCAAC TCCTGGGAGC 780
 TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCCTGG AGCAAGGAAA GCTCAAGCCA 840
 TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTCTCTG CAAACAAGAC GACCTCCTTT 900
 CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
 GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCTCG GACTGTGCTG GCAGGTTGGG 1020
 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
 CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
 TCAACTCCAG CCACCTGCC CAGCTCGACG GCACCTGGGC AGTTCCCCCT CTGCTCTGCA 1200
 GCTCGGTTTC CTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC

Seq ID NO: 89 Protein sequence:
 Protein Accession #: NP_005259.1

1 11 21 31 41 51
 MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
 GKRRGGLWWT YVCSLVFKAS VDIAPLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DDLISGLDIF LGSDSHPPLL PDRPRDHVKK TIL

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 26-457

1 11 21 31 41 51
 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCC TCACCTCTCT 60
 CGCCCTGCTG CGCTCAACCT CCGCGGTCCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
 CCGCGGGAGC GAGTGTGCTG AGTGGGCTCG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAAGGT 240
 GCCCTGCAAC TGAAGAAGG AGTTTGAGAG CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
 TGCGTGTGAT GGGGGCAGAG GCACCAAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAAGC 420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGAAGCTAGC CCAAGCCTGG ATGCCAAGGA 480
GCCCCTGTGT TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCGT TGTCCCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAAATTC 720
ATTACTAAGA AACACATCAA ATAACTGAC TTTTCCCCC CAATAAAAGC TCTTCTTTT 780
TAATAT

Seq ID NO: 91 Protein sequence:
Protein Accession #: NP_002382.1

1 11 21 31 41 51
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
CGAQTRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGLTKKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKGK GKD

Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_005130.1
Coding sequence: 98-802

1 11 21 31 41 51
CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCCTT GCCTGGGATT GCCTGGATC 60
CGTGTGCTCA GAACAGGTG AACGCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCTT 120
GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA 180
GAATGGACTT CACAGCAAG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTG ACCAAAGACC AAGCCAACTG 300
CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCATCAATT 360
GGACCATGAA TTTTCTGTG TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
TGAGAGAGTC TATTGGAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
ATATTCCAAG ACAGCTGTGA AAACAGAGT GTGCAGAAAG GATTTCCAG AATCCAGTCT 540
TAAGCTAGTC AGCTCCACTC TATTTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
GTCCCCCAGG GAGCAGATCA AGGGCAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660
GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
GACTGCCCTG GAGTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT 780
AGTGCAAGAC ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
TGTGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCAAAAA TATGAACCTT 900
TGTGCTTAGT GAGTGCAAGC AATATTTTAA ACAAGTTTGT TATTTTGTG TTTTGTGTTT 960
TGGAAATTTG CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCTCG CAGCATGTAT 1020
TTCCATGGCC CACACAGCTA TGTGTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
GAGTGATAAT TTCAGTGCAA CGAAGTTTCT GCTGAATTAA TGTGAATAAA ACTCTGGGTG 1140
TTTTTCAAAA AAAAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
Protein Accession #: NP_005121.1

1 11 21 31 41 51
MKICSLTLLS FLLLAQVLL VEGKKKVKNG LHSKVVSEK DTLGNTQIKQ KSRPGNKGKP 60
VTKDQANCRW AATEQEGIS LKVECTQLDH EFSCVFAGNP TSLCLKDER VYWKQVARNL 120
RSQKIDICYS KTAVKTRVCR KDFPSSSLKL VSSTLFGNTK PRKEKTEMSF REHIKKGKETT 180
PSSLAVTQTM ATKAPECVED PDMAQRKTA LEFCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_012101
Coding sequence: 125-1891

1 11 21 31 41 51
CTCCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCTGCTC CCACTCCCTG CCGAGACGCC 60
TGCCAGAAAG GTCACTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
TGCGATGGA GCTGCAGATG CCTCCAGGAG CAACGGGTG AGCCAGAGG CCAAGGATGC 180
CGGAGCCCG TCGGGCCCCA GTGGCAGCCT GGAGAATGGC ACCAAGGCTG ACGGCAAGGA 240
TGCCAAGACC ACCAAGGGG ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCAGGCG 300
CCTGAAGCCA GGGGAAGGTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GGCAGCCCAT 360
CATCCAGTTT GTGAGTCCG GGGAGCAGAA GAACCTCAAC TACTTCAGCA TGGACTCTAT 420
GGAAGGCAAG AGGTCCCGGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCGT 480
TACCTTTGCC GAAAAGGGCG ACGTGCAGAA GTCCATTTC TCGAGTCCC GGAAGCCAC 540
GGTGTCATC ATGGAGCCCG GGGAGACCG GCGGAACAGC TACCCCGGG CCGACACGGG 600
CCTTTTTC CCGTCCAAGT CCGGCTCCGA GGAGGTGCTG TCGACTCCT GCATCGGCAA 660
CAAGCAGAA GCGGTCAAGT CTGCTGCTGT GTGCCAGGCC TCCTTCTGCG AGCTGCATCT 720
CAAGCCCCC CTGGAGGGCG CCGCCTTCG AGACCACAG CTGCTCGAGC CCATCCGGGA 780
CTTTGAGGCC CGCAAGTGTG CCGTGCATGG CAAGACGATG GAGCTCTCT GCCAGACCGA 840
CCAGACCTGC ATCTGTACCT TTTGCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900
AGTGAGGAG GCCAAGCGG AGAAGGAGC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGG 1080
GGACCTGGAG AACCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
TGTGACCAA GTGAAGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
GGACAGCAG ACCCGGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTTGT TTCTGCAGGA 1260
ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCACCT ATCATGTCT 1320
GCTGGAGGGG GAGGCGCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
ATGCATGGCG CACGTTGAGA AGATGTGCAA GCGGAGCCTG AGCCGTAAT TCATTGAGAG 1440
GAACACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

5
 10
 15
 20
 25

```

GGGTGAGTGG AGTGCACCGG ACACCATGAA GAGATACTCC ATGTACCTGA CACCCAAAGG 1560
TGGGGTCCGG ACATCATACC AGCCCTCGTC TCCTGGCCGC TTCACCAAGG AGACCACCCA 1620
GAAGAATTC AACATCTCT ATGCCACCAA AGGTAACATC ACCTCCCGGG TCTGGGAGTA 1680
CTCCTCCAGC ATTCAGAACT CTGACAATGA CCTGCCCGTC GTCCAAGGCA GCTCCTCCTT 1740
CTCCCTGAAA GGCTATCCCT CCCTCATGCG GAGCCAAAGC CCCAAGGCC AGCCCCAGAC 1800
TTGGAATCT GGCAAGCAGA CTATGCTGTC TCACTACCGG CCATTCTACG TCAACAAAGG 1860
CAACGGGATT GGGTCCAACG AAGCCCCATG AGCTCCTGGC GGAAGGAACG AGGCGCCACA 1920
CCCTCTGCTC TCCTCTGAC CCTGCTGCTC TTGCTTCTA AGCTACTGTG CTGTCTGGG 1980
TGGGAGGGAG CCTGGTCTG CACCTGCCCT CTGAGCCCT CTGCGAGCCT CTGCGGGGCA 2040
GTTCCGGCCT CTCGACTTC CCACTGGCC ACACTCCATT CAGACTCCTT TCCTGCTTGG 2100
TGACCTCAGA TGGTCACCAT CATTCTGTG CTCAGAGGCC AACCCATCAC AGGGGTGAGA 2160
TAGGTGAGG CCTGCCCTAA CCGCCAGACC TCCTCTCTC GGGCTGGATC TGGGGGCTAG 2220
CAGTGAGTAC CGCATGGTA TCAGCTGCG TCCTCCGCCC ACGCCCTGT GTCTCCAGCG 2280
CTATAGACGT TTCTCTCAA GGCCTTATCC CCCAATGTTG TCAGCAGATG CTGGACAGC 2340
ACAGCCACCC ATCTCCATT CACATGGCCC ACCTCTGCT TCCAGAGGGA CTGGCCCTAC 2400
GTGCTCTCTC TCGTCTTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAAGG 2460
CTGCAGATGG AAACCTCTCA GTGCTTGAC ATCACCCTAC CCAGCGCGTG GGTCTCCACC 2520
ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CCTGACTGGC AGGATGACCT 2580
TAGCCAGAT ATTCTCTGT TCCTCTGCT GAGATAAAGA ATTCCTTAA CATGATATAA 2640
TCCACCCATG CAAATAGCTA CTGGCCAGC TACCATTAC CATTGCTTA CAGAAATTC 2700
TTCAGTCTAC ACTTTGGCAT TCTCTGTGC GATGGAGTGT GGTGGGCTG ACGCAAAAG 2760
TTGCTTACA CACTGCCCC ACCCTCAGC GTTCCCAT CAGAGGCTGC CTCCTCTTC 2820
TGATTACCCC CATGTTGCA TATCAGGGT CTCAAGGAT GGAGAGGAGA CAAAACAGG 2880
AGCAGCACAG TGGGGACATC TCCCGTCTCA ACAGCCCCAG GCCTATGGG GCTCTGGAAG 2940
GATGGGCCAG CTTCAGGGG TTGGGGAGG AGACATCCAG CTTGGGCTT CCCCTTGG 3000
ATAAACCAT GGTCTGTC
  
```

Seq ID NO: 95 Protein sequence:
Protein Accession #: NP_036233.1

30

```

1 11 21 31 41 51
MEAADASRSN GSSPEARDAR SPSGPGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL 60
KPGEGRSALF AGNEWRRII QFVESGDDKN SNYFSMDSME GKRSFYAGLQ LGAARKPPVT 120
FAEKGDVYRK IFSESRKPTV SIMEFGETRR NSYPRADTGL FSRKSGSEE VLCDSCIGNK 180
QKAVKSLCVC QASFCBLHLK PHLEGAEFRD HQLLEPIRDF EARKCPVHGK TMELFCQTDQ 240
TCICYLMPFQ EHKHNSVTIV EEAKAEKETE LSLQKEQLQL KIIIEDEAE KWQKEKRIK 300
SFTTNEKAIL EQNFRDLVRD LEKQKEEVRA ALEQREQDAV DQVKVIMDAL DERAKVLHED 360
KQTREQLHSI SDSVLFLOEF GALMSNYSLP PPLETYHVL EGEGLGQSLG NFKDDLINVC 420
MRHVEMCKA DLSRNFIERN HMENGGDHRY VNNYTNFSGG EWSAPDTMKR YSMYLFKGG 480
VRTSYQSSP GRFTKETQK NFNLYGKKG NYTSRVWEYS SSIQNSDNDL PVVQSSSFS 540
LKGYPPLMRS QSPKAPQW KSGKQTMESH YRPFYVNEGN GIGSNEAP
  
```

Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

50
55
60
65
70
75
80
85

```

1 11 21 31 41 51
GGCACGAGGG CAGCAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGCGCGC GGCCTGGAG 60
GAGCTCGAGA CGAGAGCTAG TTATGTCTGG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA 120
GCGCTCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC 180
AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCGG AAGACACCCA GTGCGGCTGC 240
AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCAGCTGT 300
CCAATCACCT CGCAGGAGCC CTAGGATTCT CTTTCTTG GAGAAAGAAA ACGAGCCCCC 360
TGGCAGGGAG CTTACTAAGG AGGACCTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC 420
CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGAGC 480
CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTTCCTAC AGCCGGCTGG AGACCTGGG 540
CTCTGCCTCT ACCTCCACCC CAGGCCGCGG GTCTGCTTT GGCTCGAGG GGCTGTGGG 600
GGCAGAAGAC TTGTCCGGAG TCTCGCCAGT GGTGTGCTCC AACTCACCG AGTCCCCAG 660
GGTTTGTGCA AAGCCCTGGG CCCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCCGA 720
GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG 780
GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG 840
AGATGCAGTG GGGGGTGAC CTGGCCAGAC TCTCCCTCCT GTCCTGTACA TAGCCACCTC 900
CCTGTGGAGA GGACACTTAG GGTCCCTCC CTGGTCTTG TTACCTGTGT GTGTGCTGGT 960
GCTGCGCATG AGGACTTCTC GCCTTTGAGG GCTTGGGAG CAGCGGCAGC CATCTGGTT 1020
TTAGGAAATG GGGCCGCTG GCCCAGCCAC TCACTGGTGT CTTGTCTCTT GTCGTCTGT 1080
CCTTCTATC TCCCAAAGT ACCATAGCCA GTTCCAGAT GGGCCACAGA CTGGGGAGGA 1140
GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACTCTGCT 1200
CTTGTGGGA GGGGTGCTG CTTGGAATA GGGCCAGGGG CTCTGCCAGC CTCGGCCTCT 1260
CCCTCCTGAG TTGCTTCTG TTGGTGGCTT TCTTCTTGAA CCCACCTGTG TAAAGAGGTT 1320
TTAGTTCCG TGGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380
GAGGGCAATT CTGTCTTGGG GGAAGAAGCT GGACATTCAG CCTGTGGAGT CTGAGTTTGT 1440
AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT 1500
GTTTTCTAGT TCTGGTCTGC TGTGAGATG TTTGTAATG GCCAGGTTGA TAGGGCGCTG 1560
GCTGCTTGA GCAAGGGTG CATTTCAGGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG 1620
GCTCATGGCC TCTGGGCTGG TCCCTTGCAC AGGGCCACG CTGGAGTCTT ACCACTCTGC 1680
TGCAAGGGTG GAAGGTGGCC CCTCTTGTCA CCCATACCCA TTTCTTACAA AATAAGTTAC 1740
ACCGAGTCTA CTTGGCCCTA GAAGAGAAAG TTGAAGATC CCAGACCTAC TAGCATTTTG 1800
CAACTATGCT TGTAAAGTCC TCGGAAAGT TCCTCGGTA CCAGACAGCG GCGGGGGCTG 1860
ATAGCAATTT TAGTTTGG CCTCCCTATC CTCTCACATG AGAACCTGC CTGGATGCAT 1920
CTCATGATCT CTGAGAAAT TCCCATCTT TCTCTCTTT CCATCGTGTG GATTCAATAG 1980
TTTGATTTG AAGGCTGCC TGCCCGGAC TCTCTGCGG CACCCCTGGC CATTGTACCT 2040
TTTGATGTTT AGAAGTTCGT GGAAGTAGAC GCTGAGGTGT GCAGAGGAGC TGGTGGATAA 2100
CAGAGAATGC CAGGGAAGAT GAGTGTCTGG TCAGGCTACT TGGATGAAAC GGTGCAGGCC 2160
AGCGGGGCC TAATAAAACC CTCTGCCAG TCTGGGAGTC CCAGGCCATC TGCTCAACGC 2220
  
```


TCTGTGGTTT GTCAGACCTG CAAGCAAGCC CCTGTCTGGG GAAGCCTAGG TGTCTCTGAG 2280
 CTGAACCGCA CTGAAGAACT CTTGTCTCTCA CTGGCTGATG CAGCAGAACT CTTGGGAAAT 2340
 GTCTTAGTCC TGCAGATCA GGAGTCACCA GATGATGAG AGTTGAGATC ATCATTGCAA 2400
 AGTTCTCTGT TCCTGAGGAA CTAAATTTAA GGAATAAATG GGATTTTGT TTAGAGTTGG 2460
 AAAAAAAGCC TGATTAAAGA GTTCTGCGCT GTTAAAAAAA AAAAAA AAAA

Seq ID NO: 97 Protein sequence:
 Protein Accession #: NP_542399.1

1 11 21 31 41 51
 MSGRRTRSGG AAQRSGPRAP SPTKPLRRSQ RKSGSELPSI LPEIWPKTFS AAVRKPVL 60
 KRIVAHAVEV PAVQSPRRSP RISPFLEKEN EPPGRELTKE DLFKTHSVPA TPTSTPVNFP 120
 EAESSSKEGE LDARDLEMSK KVRRSYSRLT TLGSASTSTP GRRSCFGFEG LLGAEDLSGV 180
 SPVVCCKLTE VPRVCAKPWA PDMTLPGISP PPEKQKRKKK KMPKILKTEL DEWAAAMNAE 240
 FEAAEQFDLL VE

Seq ID NO: 98 DNA sequence
 Nucleic Acid Accession #: Ros sequence
 Coding sequence: 58-12444

1 11 21 31 41 51
 GGGGCATTTC CGGGTCCGGG CCGAGCGGGC GCACGCGCGG GAGCGGGACT CGGCGGCATG 60
 GCGGGCTCCG GAGCCGGTGT GCGTTGCTCC CTGCTGCGGC TGCAGGAGAC CTTGTCCGCT 120
 GCGGACCGCT GCGGTGCTGC CTGCGCGGCT CATCAACTGA TCCGCGGCCT GGGGCGAGAA 180
 TCGCTCCTGA GCAGCAGCCC CGCGGTGCTG GCATTACAGA CATCTTTAGT TTTTCCAGA 240
 GATTTCGGTT TGCTTGATTT TGTCCGGAAG TCACTCAACA GTATTGAATT TCGTGAATGT 300
 AGAGAAGAAA TCCTAAAGTT TTTATGTATT TTCTAGAAA AAATGGGCCA GAAGATCGCA 360
 CCTACTCTG TTGAATTTAA GAACACTTGT ACCAGTGTAT ATACAAAAGA TAGAGCTGCT 420
 AAATGTAAAA TTCAGCCCTT GGACCTTCTT ATTAAGTTAC TTCAGACTTT TAGAAGTTCT 480
 AGACTCATGG ATGAATTTAA AATTGGAGAA TTATTAGTA AATTCTATGG AGAAGTTGCA 540
 TTGAAAAAAA AAATACAGA TACAGTTTA GAAAAAGTAT ATGAGCTCCT AGGATTATTG 600
 GGTGAAGTTC ATCTAGTGA GATGATAAAT AATGCAGAAA ACCTGTTCGG CGCTTTTCTG 660
 GGTGAACCTA AGACCCAGAT GACATCAGCA GTAAGAGAGC CCAAACTACC TGTCTCGGCA 720
 GGATGCTCTGA AGGGGTTGTC CTCACCTCTG TGCAACTTCA CTAAGTCCAT GGAAGAAGAT 780
 CCCCAGACTT CAAGGGAGAT TTTTAATTTT GACTAAAGG CAATTCGTCC TCAGATTGAT 840
 CTGAAGAGAT ATGCTGTGCC CTCAGCTGGC TTGGCGCTAT TTGCCCTGCA TGCATCTCAG 900
 TTTAGCACCT GCCTTCTGGA CAACTACGTG TCTCTATTG AAGTCTTGT AAAGTGGTGT 960
 GCCCACACAA ATGTAGAATT GAAAAAGCT GCACTTTCAG CCCTGGAATC CTTTCTGAAA 1020
 CAGGTTTCTA ATATGGTGGC GAAAAATGCA GAAATGCATA AAAATAAATC GCAGTACTTT 1080
 ATGAGCAGT TTTATGGAAT CATCAGAAAT GTGGATTCTG ACACAAGGA GTTATCTATT 1140
 GCTATCCGTG GATATGGACT TTTTGCAGGA CCGTGCAGG TTATAAACGC AAAAGATGTT 1200
 GACTTCATGT ACGTTGAGCT CATTACGCGC TGCAAGCAGA TGTTCCTCAC CCAGACAGAC 1260
 ACTGGTACG ACCGTGTTTA TCAGATGCCA AGCTTCCTCC AGTCTGTGTC AAGCGTCTTG 1320
 CTGTACCTTG ACACAGTTCC TGAGGTGTAT ACTCCAGTTC TGGAGCACCT CGTGGTGATG 1380
 CAGATAGACA GTTTCACACA GTACAGTCCA AAAATGCAGC TGGTGTGTTG CAGAGCCATA 1440
 GTGAAGGTGT TCTTAGCTTT GGCAGCAAAA GGGCCAGTTC TCAGGAATTG CATTAGTACT 1500
 GTGGTGATC AGGGTTAAT CAGAAATATG TCTAAACAG TGGTCTCTCC AAAGGGCCCT 1560
 GAGTCTGAAT CTGAAGACA CCGTGCTTCA GGGGAAGTCA GAACTGGCAA ATGGAAGGTG 1620
 CCCACATACA AAGACTACGT GGATCTCTTC AGACATCTCC TGAGCTCTGA CCAGATGATG 1680
 GATTCTATT TACAGATGA AGCATTTTTC TCTGTGAATT CCTCCAGTGA AAGTCTGAAT 1740
 CATTACTTTT ATCATGAATT TGTAATAATC GTTTTGAAGA TTGTTGAGAA ATTGGATCTT 1800
 ACATTGAAA TACAGACTGT TGGGAACAA GAGAATGGAG ATGAGGCGCC TGGTGTGTTG 1860
 ATGATCCCAA CTTTCAGATCC AGCGGCTAAC TTGCATCCAG CTAAACCTAA AGATTTTTCG 1920
 GCTTCTATTA ACCTGTGTTG TTTTGCAGA GAGATTCTCC CTGAGAAACA AGCAGAAATT 1980
 TTTGAACCAT GGTGTACTC ATTTTCATAT GAATTAATTT TGCAATCTAC AAGGTTGCC 2040
 CTCATCAGTG GTTCTACAA ATTGCTTTCT ATTACAGTAA GAAATGCCAA GAAATAAATA 2100
 TATTTCGAGG GAGTTAGTCC AAAGAGTCTG AAACACTCTC CTGAAGACCC AGAAAAGTAT 2160
 TCTGTCTTGT CTTATTGTT GAAATTTGGC AAAGAGGTGG CAGTTAAAT GAAGCAGTAC 2220
 AAAGATGAAC TTTTGGCCTC TTGTTTGACC TTTCTTCTGT CCTTGCCACA CAACATCAIT 2280
 GAACCTGATG TTAGAGCCTA CGTTCTGCA CTGCAGATGG CTTTCAAACT GGGCCTGAGC 2340
 TATACCCCTT TGGCAGAGT AGGCCTGAAT GCTCTAGAAG AATGGTCAAT TTATATTGAC 2400
 AGACATGTAA TGCAGCCTTA TTACAAGAC ATTCTCCCTT GCCTGGATGG ATACCTGAAG 2460
 ACTTCAGCCT TGTTCAGATG GACCAAGAAT AACTGGGAAG TGTGAGCTCT TTCTCGGGCT 2520
 GCCCAGAAAG GATTTAATA AGTGGTGTTA AAGCATCTGA AGAAGACAAA GAACCTTTCA 2580
 TCAAACGAAG CAATATCTTT AGAAGAAATA AGAATTAGAG TAGTACAAAT GCTTGGATCT 2640
 CTAGGAGGAC AAATAACAA AAATCTCTG ACAGTCAGCT CCTCAGATGA GATGATGAAG 2700
 AGCTATGTGG CCTGGGACAG AGAGAAGCGG CTGAGCTTTG CAGTGCCTTT TAGAGAGATG 2760
 AAACCTGTCA TTTTCTGGA TGTGTTCTG CCTCGAGTCA CAGAATTAGC GCTCACAGCC 2820
 AGTGACAGAC AAACATAAGT TGCAGCCTGT GAACTTTTAC ATAGCATGGT TATGTTTATG 2880
 TTGGGCAAAAG CCACGCGATG GCCAGAAAGG GGACAGGGAG CCCCACCAT GTACCAGCTC 2940
 TATAAGCGGA CGTTTCTGT GCTGCTTGA CTGCGTGTG ATGTTGATCA GGTGACAAGG 3000
 CAACTGTATG AGCCACTAGT TATGCAGCTG ATTCAGTGGT TCACTAACAA CAAGAAATTT 3060
 GAAAGTCAGG ATACTGTGTC CTTACTAGAA GCTATATTGG ATGGAATTTG GGACCTGTT 3120
 GACAGTACTT TAAGAGATT TTGTGGTGG TGTATTGAG AATTCCTTAA ATGGTCCATT 3180
 AAGCAAATAA CACCACAGCA GCAGGAGAAG AGTCCAGTAA ACACCAAAATC GCTTTTCAAG 3240
 CGACTTTATA GCCTTGGCT TCACCCCAAT GCTTTCAAGA GGCTGGGAGC ATCACTTGCC 3300
 TTTAATAATA TCTACAGGGA ATTCAGGGAA GAAGAGTCTC TGGTGAACA GTTGTGTTT 3360
 GAAGCCTTGG TGATATACAT GGAGAGTCTG GCCTTAGCAC ATGCAGATGA GAACTCCTTA 3420
 GGTACAATTC AACAGTGTG TGATGCCATT GATCACCTAT GCCGCATCAT TGAAGAAGAG 3480
 CATGTTTCTT TAAATAAAGC AAGAAACGA CGTTTGGCGG GAGGATTTCC ACCTTCCGCA 3540
 TCAATGTGTT TATGTGATCT GGTCAAGTGG CTTTATAGCTC ATGTGGGAG GCCCAGACA 3600
 GAATGTGAGC ACAATCCAT TGAATCTTT TATAAATCG TTCCTTATT GCCAGGCAAC 3660
 AGATCCCTTA ATTTGTGGCT CTCAGGAAG AAGGTGTCTC TTTTCTCATC 3720
 AACACCTTGG AGGGGGGTGG CTGTGGCCAG CCCTCGGGCA TCCTGGCCCA GCCCACCTC 3780
 TTGTACCTTC GGGGGCCATT CAGCCTGCAG GCCAGCTAT GCTGGCTGGA CCTGCTCCTG 3840

	GCCGCGTTGG	AGTGCTACAA	CACGTTCAAT	GGCGAGAGAA	CTGTAGGAGC	GCTCCAGGTC	3900
	CTAGGTACTG	AAGCCAGTC	TTCACTTTTG	AAAGCAGTGG	CTTTCTTCTT	AGAAAGCATT	3960
	GCATGTCATG	ACATTATAGC	AGCAGAAAAG	TGCTTTGGCA	CTGGGGCAGC	AGGTAACAGA	4020
5	ACAAGCCAC	ACAGGGGAGA	AAGGTACAA	TACAGCAAAT	GCACCGTTGT	GGTCCGGATT	4080
	ATGGAGTTTA	CCACGACTCT	GCTAAACACC	TCCCCGGAAG	GATGGAAGCT	CCTGAAGAAG	4140
	GACTTGTGTA	ATACACACCT	GATGAGAGTC	CTGGTGACAG	CGCTGTGTGA	GCCCGCAAGC	4200
	ATAGGTTTCA	ACATCGGAGA	CGTCCAGGTT	ATGGCTCATC	TTCTGATGT	TTGTGTGAAT	4260
	CTGATGAAAG	CTCTAAAGAT	GTCCCATAC	AAAGATATCC	TAGAGACCCA	TCTGAGAGAG	4320
10	AAAAATAACAG	CACAGAGCAT	TGAGGAGCTT	TGTGCCGTCA	ACTTGTATGG	CCCTGACGCG	4380
	CAAGTGGACA	GGAGCGGCT	GGCTGCTGTT	GTGTCTGCCT	GTAAACAGCT	TCACAGAGCT	4440
	GGGCTTCTCG	ATAATATATT	ACCGTCTCAG	TCCACAGATT	TGCATCATTC	TGTTGGCACA	4500
	GAACTTCTTT	CCCTGGTTTA	TAAAGGCATT	GCCCTGGAG	ATGAGAGACA	GTGTCTGCCT	4560
	TCTCTAGACC	TCAGTTGTAA	GCAGCTGGCC	AGCGGACTTC	TGGAGTTAGC	CTTTGCTTTT	4620
	GGAGGACTGT	GTGAGCGCCT	TGTGAGTCTT	CTCCTGAACC	CAGCGGTGCT	GTCCACGGCG	4680
15	TCCTTGGGCA	GCTCACAGGG	CAGCGTCATC	CACCTTCTCC	ATGGGGAGTA	TTTCTATAGC	4740
	TTGTCTCTAG	AAACGATCAA	CACGGAATTA	TTGAAAAATC	TGGATCTTGC	TGTATTGGAG	4800
	CTCATGCACT	CTTCAGTGA	TAATACCAA	ATGGTGAGTG	CCGTTTTGAA	CGGCATGTTA	4860
	GACCAGAGCT	TCAGGGAGCG	AGCAAACAG	AAACACCAAG	GACTGAAACT	TGCGACTACA	4920
20	ATTCTGCAAC	ACTGGAGAG	GTGTGATTCA	TGTTGGGCCA	AAGATTCCCC	TCTCGAAACT	4980
	AAAAATGGCAG	TGCTGGCCTT	ACTGGCAAAA	ATTTTACAGA	TTGATTCATC	TGTATCTTTT	5040
	AATACAAGTC	ATGGTTCAAT	CCCTGAAGTC	TTTACAACAT	ATATTAGTCT	ACTTGTGAC	5100
	ACAAAGCTGG	ATCTACATTT	AAAGGGCCAA	GCTGTCACTC	TTCTTCCATT	CTTCACCAGC	5160
	CTCACTGGAG	GCAGTCTGGA	GGAACCTAGA	CGTGTCTGG	AGCAGCTCAT	CGTTGCTCAC	5220
25	TTCCCATGCG	AGTCCAGGGA	ATTTCTCTCA	GGAACCTCGC	GGTTCAATA	TTATGTGGAC	5280
	TGCATGAAAA	AGTTTCTAGA	TGCATTGGAA	TTATCTCAA	GCCCTATGTT	GTGGAATTG	5340
	ATGACAGAAAG	TTCTTTGTG	GGAAACAGCAG	CATGTCATGG	AAGAATTATT	TCAATCCAGT	5400
	TTACGAGAGA	TTGCCAGAAG	GGGTTCAATG	GTCAACAAG	TAGGCCTTCT	GGAAAGCGTG	5460
	TATGAAATGT	TCAGGAAGGA	TGACCCCGCG	CTAAGTTTCA	CAGGCCAGTC	CTTTGTGGAC	5520
30	CGCTCCCTCC	TCACTCTGCT	GTGGCACTGT	AGCCTGGATG	CTTTGAGAGA	ATTCTTCAGC	5580
	ACAAATTGGG	TGAGTCCCAT	TGATGTGTTG	AAGTCCAGGT	TTACAAAGCT	AAATGAATCT	5640
	ACCTTTGATA	CTCAATCAC	CAAGAAGATG	GGCTACTATA	AGATTCTAGA	CGTGATGTAT	5700
	TCTCGCCTTC	CCAAAGATGA	TGTTTCATGCT	AAGGAATCAA	AAATTAATCA	AGTTTTCCAT	5760
	GGCTCGTGT	TTACAGAAGG	AAATGAACCT	ACAAAGACAT	TGATTAAAT	GTGCTACGAT	5820
35	GCATTTACAG	AGAACATGGC	AGGAGAGAAT	CAGCTGCTGG	AGAGGAGAAG	ACTTTACCAT	5880
	TGTGAGCAT	ACAACATGCG	CATATCTGTC	ATCTGCTGTG	TCTTCAATGA	GTTAAATTTT	5940
	TACCAAGGTT	TTCTGTTTAG	TGAAAAACCA	GAAAAGAACT	TGCTTATTTT	TGAAATCTG	6000
	ATCGACCTGA	AGCGCGCTA	TAATTTCTCT	GTAGAAGTTG	AGGTTCTCTAT	GGAAAGAAAG	6060
	AAAAAGTACA	TTGAAATTAG	GAAAGAAGCC	AGAGAAGCAG	CAATGGGGA	TTGAGATGGT	6120
40	CCCTTCTATA	TGCTTCTCCCT	GTCAATTTG	GCAGACAGTA	CCCTGAGTGA	GGAAATGAGT	6180
	CAATTTGATT	TCTCAACCGG	AGTTCAGAGC	TATTTCATACA	GCTCCCAAGA	CCCTAGACCT	6240
	GCCACTGGTC	GTTTTCCGAG	ACGGGAGCAG	CGGGACCCCA	CGGTGCATGA	TGATGTGCTG	6300
	GAGCTGGAGA	TGGACGAGCT	CAATCGGCAT	GAGTGCAATG	CGCCCTGAC	GGCCCTGGTC	6360
	AAGCACATGC	ACAGAAGCCT	GGGCCCGCCT	CAAGGAGAAG	AGGATTCAGT	GCCAGAGAT	6420
45	CTTCTCTCTT	GGATGAAATT	CTTCCATGGC	AACTGGGAA	ATCCAATAGT	ACCATTAAAT	6480
	ATCCGCTCTT	TCTTAGCCAA	GCTTGTATT	AATACAGAAG	AGGTCCTTCG	CCCTTACCGG	6540
	AAGCACTGGC	TTAGCCCTCT	GCTGCAGCTG	GCTGCTCTG	AAAACAATGG	AGGAGAAGGA	6600
	ATTCACTACA	TGTTGGTTGA	GATAGTGGCC	ACTATTCTTT	CATGGACAGG	CTTGGCCACT	6660
	CCAAACAGGG	TCCCTAAAGA	TGAAGTGTTA	GCAATTCGAT	TGCTTAATTT	CCTAATGAAA	6720
50	CATGTCTTTC	ATCCAAAAG	AGCTGTGTTT	AGACACAACC	TTGAAATTTAT	AAAGACCTCT	6780
	GTGAGTGTCT	GGAGAGATTG	TTTATCCATC	CCTTATAGGT	TAATATTGGA	AAAGTTTCC	6840
	GGTAAAGATC	CTAATTTCTAA	AGACAACCTCA	GTAGGGATTC	AATTGCTAGG	CATCGTATG	6900
	GCCAATGACC	TGCTCCCTTA	TGACCCACAG	TGTGGCATCC	AGAGTAGCGA	ATACTTCCAG	6960
55	GCTTTGGTGA	ATAATGTGTC	CTTTGTAAGA	TATAAAGAAG	TGATGCCCG	TGCAGCAGAA	7020
	GTTCTAGGAC	TTATACTTCG	ATATGTTATG	GAGAGAAAA	ACATACTGGA	GGAGTCTCTG	7080
	TGTGAACCTGG	TTGCGAAACA	ATTGAAGCAA	CATCAGAATA	CTATGGAGGA	CAAGTTTATT	7140
	GTGTGCTTGA	ACAAAGTGAC	CAAGAGCTTC	CCTCCTCTTG	CAGACAGGTT	CATGAATGCT	7200
	GTGTCTTCTC	TGCTGCCAAA	ATTTCATGGA	GTGTGAAAA	CACCTCTGCT	GGAGGTGGTA	7260
60	CTTTGTGCTG	TGGAGGGAAT	GACAGAGCTG	TACTTCCAGT	TAAAGAGCAA	GGACTTCTGT	7320
	CAAGTCATGA	GACATAGAGA	TGATGAAAGA	CAAAAAGTAT	GTTTGGACAT	AATTTATAAG	7380
	ATGATGCCAA	AGTTAAACCC	AGTAGAATCT	CGAGAACTTC	TGAACCCCGT	TGTGGAATTC	7440
	GTTTCCCATC	CTTCTACAAC	AFTGAGGAA	CAATGTATA	ATATTCTCAT	GTGGATTCAAT	7500
	GATAATTACA	GAGATCCAGA	AAGTGAGACA	GATAATGACT	CCCAGGAAAT	ATTTAAGTTG	7560
65	GCAAAAGATG	TGCTGATTCA	AGGATTGATC	GATGAGAACCC	CTGGACTTCA	ATTAATTTAT	7620
	CGAAATTTCT	GGAGCCATGA	AACTAGGTTA	CCTTCAAATA	CCTTGGACCG	GTGTCTGGCA	7680
	CTAAATTTCT	TATATTCTCC	TAAGATAGAA	GTGCACTTTT	TAAGTTTAGC	AACAAATTTT	7740
	CTGCTCGAAA	TGACCAAGAT	GAGCCAGAT	TATCCAAACC	CCATGTTTGA	GCATCTCTG	7800
	TCAGAAATGCG	AAATTCAGGA	ATATACCAAT	GATTCTGATT	GGCGTTTCCG	AAGTACTGTT	7860
70	CTCACTCCGA	TGTTTGTGGA	GACCCAGGCC	TCCCAGGGCA	CTCTCCAGAC	CCGTACCCAG	7920
	GAAGGGTCCC	TCTCAGCTCG	CTGGCCAGTG	GCAGGGCAGA	TAAGGGCCAC	CCAGCAGCAG	7980
	CATGACTTCA	CACGTGACACA	GACTGCAGAT	GGAAAGAGCT	CATTGTGATT	GCTGACCGGG	8040
	AGCAGCACTG	ACCCGCTGGT	CGACCAACCC	AGTCCCTCAT	CTGACTCCTT	GCTGTTTGCC	8100
	CACAAGAGGA	GTGAAAGGTT	ACAGAGAGCA	CCCTTGAAGT	CAGTGGGGCC	TGATTTTGGG	8160
75	AAAAAAAGGC	TGGGCTTCC	AGGGGACGAG	GTGGATAACA	AAGTGAAAGG	TGCGGCCGGC	8220
	CGGACGGACC	TACTACGACT	GCGCAGACGG	TTTATGAGGG	ACCAGGAGAA	GCTCAGTTTG	8280
	ATGTATGCCA	GAAAAGGCGT	TGCTGAGCAA	AAACGAGAGA	AGGAAATCAA	GAGTGAGTTA	8340
	AAAAATGAAG	AGGATGCCCA	GGTCTGTTCT	TACAGAAAGCT	ACCGGCAOAG	AGACCTTCTC	8400
	GACATTCAGA	TCAAGCACAG	CAGCCTCATC	ACCCCGTTAC	AGGCCGTGGC	CCAGAGGGAC	8460
	CCAATAATTG	CAAAACAGCT	CTTTAGCAGC	TTGTTTTCTG	GAATTTTGAA	AGAGATGGAT	8520
80	AAATTTAAGA	CACGTCTGTA	AAAAACAAC	ATCACTCAAA	AGTTGCTTCA	AGACTTCAAT	8580
	CGTTTTCTTA	ATACCACCTT	CTCTTCTTTT	CCACCCTTTG	TCTCTGTAT	TCAGGACATT	8640
	AGCTGTGAGC	ACGACGCCCT	CTGTAGCCTC	GACCCAGCGG	CTGTTAGCGC	TGGTTGCTGT	8700
	GCCAGCCTAC	AGCAGCCCGT	GGGCATCCGC	CTGCTAGAGG	AGGCTCTGCT	CGCCCTGCTG	8760
	CTGTCTGAGC	TGCTTGCCAA	GCGAGTCCGT	GGGAAAGCCC	GCCTCCCTCC	TGATGTCTTC	8820
85	AGATGGGTGG	AGCTTGCTAA	GCTGTATAGA	TCAATTGGAG	AATACGACGT	CCTCCGTGGG	8880
	ATTTTTTACCA	GTGAGATAGG	AACAAAGCAA	ATCACTCAGA	GTGCATTATT	AGCAGAAGCC	8940
	AGAAGTGATT	ATTTCTGAAGC	TGCTAAGCAG	TATGATGAGG	CTCTCAATAA	ACAAGACTGG	9000
	GTAGATGGTG	AGCCACAGA	AGCCGAGAAG	GATTTTTGGG	AACTTGATATC	CCTTGACTGT	9060

	TACAACCAACC	TTGCTGAGTG	GAAATCACTT	GAATACGTGT	CTACAGCCAG	TATAGACAGT	9120
	GAGAACCCCC	CAGACCTAAA	TAAAATCTGG	AGTGAACCAT	TTTATCAGGA	AACATATCTA	9180
	CTTATACATGA	TCCCGAGCAA	GCTGAAGCTG	CTGCTCCAGG	GAGAGGCTGA	CCAGTCCCTG	9240
5	CTGACATTTA	TTGACAAAGC	TATGCACGGG	GAGCTCCAGA	AGGCGATTCT	AGAGCTTCAT	9300
	TACAGTCAAG	AGCTGAGTCT	GCTTTACCTC	CTGCAAGATG	ATGTTGACAG	AGCCAAATAT	9360
	TACATTCAAA	ATGGCATTCA	GAGTTTTATG	CAGAATTATT	CTAGTATTGA	TGTCCTCTTA	9420
	CACCAAGATA	GACTCAACAA	ATTGCAGTCT	GTACAGGCTT	TAAACAGAAAT	TCAGGAGTTC	9480
	ATCAGCTTTA	TAAGCAAAAC	AGGCAATTTA	TCATCTCAAG	TTCCCTTAA	GAGACTTCTG	9540
	AACACCTGGA	CAAAACAGATA	TCCAGATGCT	AAAATGGACC	CAATGAACAT	CTGGGATGAC	9600
10	ATCATCAAA	ATCGATGTTT	CTTTCTCAGC	AAAATAGAGG	AGAAGCTTAC	CCCTCTTCCA	9660
	GAAGATAATA	GTATGAATGT	GGATCAAGAT	GGAGACCCCA	GTGACAGGAT	GGAAAGTGCA	9720
	GAGCAGGAAG	AAGATATCAG	CTCCCTGATC	AGGAGTTGCA	AGTTTTCCTT	GAAAATGAAG	9780
	ATGATAGACA	GTGCCCGGAA	GCAGAACAAT	TTCTCACTTG	CTATGAAACT	ACTGAAGGAG	9840
	CTGCATAAAG	AGTCAAAAC	CAGAGACGAT	TGGCTGGTGA	GCTGGGTGCA	GAGCTACTGC	9900
15	CGCCTGAGCC	ACTGCCGAGC	CGGCTCCAG	GGCTGCTCTG	AGCAGGTGCT	CAGTGTGCTG	9960
	AAAAACAGTCT	CTTTGTGTTG	TGAGAACAA	GTGTCAAGCT	ACTTAAGCAA	AAATATTCTG	10020
	GCTTTCCGTG	ACCAGAACAT	TCTCTTGGGT	ACAACCTTACA	GGATCATAGC	GAATGCTCTC	10080
	AGCAGTGAGC	CAGCTGCCTT	TGCTGAAATC	GAGGAGGACA	AGGCTAGAAG	AATCTTAGAG	10140
	CTTTCTGGAT	CCAGTTCAGA	GGATTTCAGAG	AAGGTGATCG	CGGGTCTGTA	CCAGAGAGCA	10200
20	TTCCAGCACC	TCTCTGAGGC	TGTGCAGGCG	GCTGAGGAGG	AGGCCAGGCC	TCCCTCTCTG	10260
	AGCTGTGGGC	CTGCAGCTGG	GGTGATTGAT	GCTTACATGA	CGCTGGCAGA	TTTCTGTGAC	10320
	CAACAGCTGC	GCAAGGAGGA	AGAGAATGCA	TCAGTTATTG	ATTCTGCAGA	ACTGCAGGCG	10380
	TATCCAGCAC	TTGTGGTGGG	GAAAATGTTG	AAAGCTTTAA	AATTAATTTT	CAATGAAGCC	10440
	AGATTGAAGT	TTCTAGAGAT	ACTTCAGATT	ATAGAACGGT	ATCCAGAGGA	GACTTTGAGC	10500
25	CTCATGACAA	AAGAGATCTC	TTCCGTTCCT	TGCTGGCAGT	TCATCAGCTG	GATCAGCCAC	10560
	ATGTTGGGCT	TACTGGACAA	AGACCAAGCC	GTTGCTGTTT	AGCACTCTGT	GGAAGAAATC	10620
	ACTGATAACT	ACCOCGAGGC	TATGTTTAT	CCCTTCATCA	TAAAGCAGCA	AAGCTATTCC	10680
	TTCAAGGATA	CTTCTACTGG	TCATAAGAAAT	AAGGAGTTTG	TGGCAAGGAT	TAAAGTAAAG	10740
	TTGGATCAAG	GAGGAGTGAT	TCAAGATTTT	ATTAATGCCT	TAGATCAGCT	CTCTAATCCT	10800
30	GAACCTGCTCT	TTAAGGATGT	GAGCAATGAT	GTAAGAGCTG	AACATAGCAA	AACCCCTGTA	10860
	AATAAAAAAA	ACATTGAAAA	AATGTATGAA	AGAATGTATG	CAGCCTTGGG	TGACCCAAAG	10920
	GCTCCAGGCC	TGGGGGCCCT	TAGAAGGAAG	TTTATTGAGA	CTTTTGAAA	AGAATTTGAT	10980
	AAACATTTTG	GGAAAGGAGG	TTCTAAACTA	CTGAGAATGA	AGCTCAGTGA	CTTCAACGAC	11040
	ATTACCAACA	TGCTACTTTT	AAAAATGAAC	AAAGACTCAA	AGCCCCCTGG	GAATCTGAAA	11100
35	GAATGTTTAC	CCTGAGTATG	CGACTTCAA	GTGGAGTTCC	TGAGAAATGA	GCTGGAGATT	11160
	CCCGGTGAGT	ATGACGGTAG	GGGAAAGCCA	TTGCCAGAGT	ACCACGTGCG	AATCGCCGGG	11220
	TTGATGAGC	GGGTGACAGT	CATGCGCTCT	CTGCGAAGGC	CCAAGCGCAT	CATCATCCGT	11280
	GGCCATGAGC	AGAGGGAACA	CCCTTTCCTG	GTGAAGGGTG	GCGAGGACCT	GCGGCAGGAC	11340
	CAGCGCGTGG	AGCAGCTCTT	CCAGGTCTATG	AATGGGATCC	TGGCCCAAGA	CTCCGCTGTC	11400
40	AGCCAGAGGG	CCCTGCGAGT	GAGGACCTAT	AGCGTTGTGC	CCATGACCTC	CAGGTTAGGA	11460
	TTAATTGAGT	GGCTTGAAAA	TACTGTTACC	TTGAAGGACC	TTCTTTTGAA	CACCATGTCC	11520
	CAAGAGGAGA	AGGCGGCTTA	CCTGAGTGAT	CCCAGGGCAC	CGCCGTGTGA	ATATAAAGAT	11580
	TGGCTGACAA	AAATGTCAAG	AAAACATGAT	GTTGGAGCTT	ACATGTCTAAT	GTATAAGGGC	11640
	GCTAATCGTA	CTGAAGACTT	CAGCTCTTTT	AGAAAACGAG	AAAGTAAAGT	GCCTGCTGAT	11700
45	CTCTTAAAGC	GGGCTTCGT	GAGGATGAGT	ACAAGCCCTG	AGGCTTTCCT	GGCGCTCCGC	11760
	TCCCACTTCG	CCAGCTCTCA	CGCTCTGATA	TGCATCAGCC	ACTGGATCTT	CGGGATTGGA	11820
	GACAGACATC	TGAACACTT	TATGTTGGCC	ATGAGAGCTG	GCGGCGTGAT	CGGGATGAC	11880
	TTTGGGCTATG	CGTTTGGATC	CGCTACACAG	TTTCTGCCAG	TCCCTGAGTT	GATGCTTTT	11940
	CGGCTAATCT	GCCAGTTTAT	CAATCTGATG	TTACCAATGA	AAGAAACGGG	CCTTATGTAC	12000
50	AGCATCATGG	TACACGCACT	CCGGGCGCTC	CGCTCAGACC	CTGGCCTGCT	CACCAACACC	12060
	ATGGATGTGT	TTGTCAAGGA	GCCTCCTTT	GATTGGAATA	ATTTTGAAAC	GAAAATGCTG	12120
	AAAAAAGGAG	GGTCATGGAT	TCAAGAAATA	AATGTTGCTG	AAAAAATTG	GTACCCCGGA	12180
	CAGAAAATAT	GTTACGCTAA	GAGAAAGTTA	GCAGGTGCCA	ATCCAGCAGT	CATTACTTGT	12240
	GATGAGCTAC	TCCTGGGTCA	TGAGAAGGCC	CCTGCCTTCA	GAGACTATGT	GGCTGTGGCA	12300
55	CGAGGAAGCA	AAGATCAAA	CATTCTGTGC	CAAGAACCCAG	AGAGTGGGCT	TTCAAGAGAG	12360
	ACTCAAGTGA	AGTGCCCTGAT	GGACCAAGCA	ACAGACCCCA	ACATCCTTGG	CAGAACCTGG	12420
	GAAGGATGGG	AGCCCTGGAT	GTGAGGTCTG	TGGGAGTCTG	CAGATAGAAA	GCATTACATT	12480
	GTTTAAAGAA	TCTACTATTG	TTTGGTTGGC	AGCATTCCAT	GAGCTGATT	TCCTGAAACA	12540
60	CTAAAGAGAA	ATGCTTTTGG	TGCTACAGTT	TCGTAGCATG	AGTTTAAATC	AAGATTATGA	12600
	TGAGTAAATG	TGATTTGGTT	AAATCAAAGA	TAAGGTTATA	GTAACATCAA	AGATTAGGTG	12660
	AGGTTTATAG	AAAGATGAT	ATCCAGGCTT	ACCAAAGTAT	TAAGTCAAGA	ATATAATATG	12720
	TGATCAGCTT	TCAAAGCATT	TACAAGTGCT	GCAAGTTAGT	GAAACAGCTG	TCTCCGTAAA	12780
	TGGAGGAAAT	GTGGGGAGGC	CTTGAATGTC	CCTTCTGGTT	CTGGCACATT	GGAAAGCACA	12840
	CTCAGAAGGC	TTCAATCACA	AGATTTTGGG	AGAGTAAAGC	TAAGTATAGT	TGATGTAACA	12900
65	TTGTAGAAGC	AGCATAGGAA	CAATAAGAAC	AATAGGTAAA	GCTATAATTA	TGGCTTATAT	12960
	TTAGAAATGA	CTGCATTGGA	TATTTTAGGA	TATTTTCTTA	GGTTTTTCTC	TTTCATTTTA	13020
	TTCTCTTCTA	GTTTGGATAT	TTTATGATAG	ATTTGCTCTC	TAGAAGGAAA	CGTCTTTATT	13080
	TAGGAGGGCA	AAAATTTTGG	TCATAGCATT	CACTTTTGCT	ATTCCAATCT	ACAACCTGGAA	13140
	GATACATAAA	AGTGCTTTGC	ATTGAATTTG	GGATAACTTC	AAAAATCCCA	TGGTTGTTGT	13200
70	TAGGGATAGT	ACTAAGCATT	TCAGTTCCAG	GAGAATAAAA	GAAATTCCTA	TTTGAATATGA	13260
	ATTCCTCAT	TGGAGGAAAA	AAAGCATGCA	TTCTAGCACA	ACAAGATGAA	ATTATGGAAT	13320
	ACAAAAGTGG	CTCCTTCCCA	TGTGCAGTCC	CTGTCCCCCC	CCGCCAGTCC	TCCACACCCA	13380
	AACTGTTTCT	GATTGGCTTT	TAGCTTTTTT	TTTCTTTTCT	TTTCTTTTCT	AACACTTGTA	13440
75	TTTGAGGCT	CTTCTGTGAT	TTTGAGAAGT	ATACTCTTGA	GTGTTTAAAT	AAGTTTTTTT	13500
	CCAAAAGTA						

Seq ID NO: 99 Protein sequence:
Protein Accession #: NP_008835.5

80	1	11	21	31	41	51	
	MAGSGAGVRC	SLRLRLQETLS	AADRCGAALA	GHQLIRGLGQ	ECVLSSSPAV	LALQTSLVFS	60
	RDFGLLVFVR	KSLNSIEFRE	CREEILKFLC	IFLEKMGQKI	APYSVEIKNT	CTSVMYTKDRA	120
	AKKIPALDL	LKLLQTFRS	SRLMDEFKIG	ELFSKFYGBL	ALKKKIPDVT	LEKVYELLGL	180
85	LGEVHPSEMI	NNAENLPRAF	LGLKLTQMTS	AVREPFLFVL	AGCLKGLSSL	LCNFKSMEE	240
	DPQTSREIFN	FVLKAIKRFI	DLKRYAVPSA	GLRLPALHAS	QFSTCLLDNY	VSLFEVLLKX	300
	CAHTNVELKX	AALSALSFQL	KQVSNMVAKN	AEMHKNKLQY	FMEQFYGIIR	NVDSNNKELS	360

IAIRGYGLFA GPCRVINAKD VDFMYVELIQ RCKQMFLTQT DTGDDRVYQM PSFLQSVASV 420
 LLYLDTPPEV YTPVLEHLVV MQIDSFPQYS PKMQLVCCRA IVKVFLALAA KGPVLRNCIS 480
 TVVHGLIRI CSKEVVLPGK PESEEDHRA SGEVTRGKWK VPTYKDYVDL FRHLLSSDQM 540
 MDSILADEAF FSVNSSSESL NHLLYDEFVK SVLKIVEKLD LTLEIQTVGE QENGDEAPGV 600
 WMIPTSDPAA NLHPAKPKDF SAFINLVEFC REILPEKQAE FFEPPWVYSPS YELILQSTRL 660
 PLISGFYKLL SITVNRANKI KYFEGVSPKS LKHSPEDEPK YSCFALFVKF GREVAVKMKQ 720
 YKDELLASCL TFLLSLPHNI IELDVRAYVP ALQMAFKLGL SYTFLAEVGL NALEWSYIYI 780
 DRHVMQPYK DILPCLDGYL KTSALSDETK NNNEVSALSR AAQKGFNKVV LKHLKCTKNL 840
 SSNEAISLEE IRRVVMQLG SLGGQINKNL LTVTSSDEMM KSYVANDREK RLSFAVPFRE 900
 MKPVIFLDVF LPRVTELALT ASDRQTKVAA CELLSHMMVF MLGKATQMPG GGQGAPPMYQ 960
 LYKRTFPVLL RLACDQDQVT RQLYSEPLVMQ LIHWFTNNKK FESQDTVALL EAILDGIQVDP 1020
 VDSTLRDFCG RCIREPLKWS IKQITPQQQE KSPVNTKSLF KRLYSALHLP NAFKRLGASL 1080
 AFNNIYREFR EEESLVEQFV FEALVIYMES LALAHADEKS LGTIQQCCDA IDHLCRIIEK 1140
 KHVSINKAKK RRLPRGFPSP ASLCLDLVK WLLAHCGRPQ TECRHKSIEL FYKFVPLLP 1200
 NRSNPLWLDK VLKEEGVSFL INTFEGGCGC QPSGILAQPT LLYLRGPFSL QATLCWLDLL 1260
 LAALCEYNTL IGERTVGLAQ VLGTEAQSSL LKAVAPFLES IAMHDI IAAE KCFGTGAAGN 1320
 RTSPOGEGRY NYSKCTVVVR IMEFTTLLN TSPGKWLK KDLNTHLMR VLVQTLCEPA 1380
 SIGFNIGDVQ VMAHLPDVCV NLMKALKMSP YKDILETHLR EKITAQSIEE LCAVNLYGPD 1440
 AQVDRSRLAA VVSACQQLHR AGLLHNILPS QSTDLLHVSQ TELLSLVYK IAPGDERQCL 1500
 PSLLSLCQQL ASGLLELAF FGLCERLVS LLLNPAVLST ASLGSSQGSV IHSFSGEYFY 1560
 SLFSETINTE LLKNLDLAVL ELMQSSVDNT KMSAVLNGM LDQSPRERAN QKHQGLKAT 1620
 TILQHWKCD SWAKDSPL ETLQIDSSVS TKMAVLALLA KILQIDSSVS FNTSHGSPFE VFTTYISLLA 1680
 DTKLDLHLKQ QAVTLFFFT SLTGGSEEL RRVLEQLIVA HFMQSPREPP PGTPRFNNYV 1740
 DCMKKFLDAL ELSQSPMLLE LMTVLCREQ QHVMEEFLQS SFRIARRGS CVTQVGLLES 1800
 VYEMFRKDDP RLSFTTRQSFV DRSLTLWLH CSLDALREFF STIVVDAIDV LKSRTFKINE 1860
 STFTDQITKK MGYYKILDMV YSRLPKDDVH AKESKINQVF HGSCITEGNE LTKTLIKLCY 1920
 DAFNTMAGE NQLELRRRLY HCAAYNCAIS VICCVFNLK FYQGLFSEK PEKNLLIFEN 1980
 LIDLKRRYNF PVEVEVPMER KKKYIEIRKE AREAANGSD GPSYMSLSY LADSTLSEEM 2040
 SQQDFSTGVQ SYSSSQDPR PATGRFRRE QRDPTVHDDV LELEMDLNR HECHAPITAL 2100
 VKHMRSLGP PQGEEDSVPR DLPSWKKFLH GKLGNIPLV NLRFLAKLV INTEEVFRPY 2160
 AKHWLSPQLL LAASENNGGE GIHYMVVEIV ATILSWTGLA TPTGVPKDEV LANRLLNFM 2220
 KHVFHPKRAV FRNLEIITK LVECKDKCLS IPYRLIFEKF SGKDPSKDN SVGIQLLGV 2280
 MANDLPPYDQ CCGIQSSSEY QALVNNMSFV RYKEVYAAA EVGLILRLV MERKNILEES 2340
 LCELVAQLK QHQTMDKDF IVCLNKVTKS FPPLADRFMN AVFLLPKFH GVLKTLCEV 2400
 VLCRVEGME LYQLKSKDF VQVMRRHDE RQKVCLDIY KMPKLPVE LRELLNPVE 2460
 FVSHPTTCCR EQMYNLMWI HONYRDEPE TDNDSSQEIF LAKDVLIGL IDENPGQLI 2520
 IRNFWSHETR LPSNTLDRLL ALNSLYSPKI EVHFLSLATN FLEMTSMSP DYPNMFEPH 2580
 LSECEFEYET IDSDFRFRST VLTPMFVETQ ASQGTQLQRT QEGSLSARWP VAGQIRATQ 2640
 QHDTLTQTA DGRSSFDWLT GSTDPLVDH TSPSSDLSLF AHKRSERLQ APLKSVGPDF 2700
 GKRLGLPGD EVDNKVGAA GRTDLRLR RFMRDQEKLS LMYARKGVAE QKREKEIKSE 2760
 LKMKQDAQV LYRSYRHGDL PDIQIKHSL ITPQAVAR DPLIAKQLFS SLFSGILKEM 2820
 DKFTLSEKN NITQKLQDF NRFLNTTSPF PPPFVSCIQD ISQHAALLS LDPAAVSAGC 2880
 LASLQPPVGI RLLEALLRL LPAELPAKRV RGKARLPFDV LRWVELAKLY RSIGEDVLR 2940
 GIFTSEIGTK QITQSALLAE ARSDYSEAK QYDEALNKQD WVDGEPTAE KDFWELASLD 3000
 CYNHLAEWKS LEYCSTASID SENPPDLNKI WSEPPYQETY LPMIRSKLK LLLQGEADQS 3060
 LLTFIDKAMH GELOKALIEL HYSQELSLLY LLQDDVDRAK YYIQNGIQSF MQNYSSIDVL 3120
 LHQSRLTKLQ SVQALTEIQE FTSFISKQGN LSSQVPLKRL LNTWTRYPD AKMDPMNIWD 3180
 DIITNRCFFL SKIEEKLTP PEDNSMNVQ DGDPSDRMEV QEEDISSL IRSCKFSMKM 3240
 KNIDSARKQN NPSLAKMLK ELHKEKSTRD DWLVSWVQSY CRLSHCRSRG QGCSEQLTV 3300
 LKTVSLDEN NVSSYLSENI LAFRDQNLIL GTTYRIANA LSSEPACLAB IEEDKARRIL 3360
 ELSSGSSSEDS EKVIAGLYR AFQHLSEAVQ AAEBAQPPS WSCGPAAGVI DAYMTLADFC 3420
 DQDLRKEEN ASVIDSAEL AYPALVVEKM LKALKLNSNE ARLKFPRLQ IIERYPEETL 3480
 SLMTKEISS PCWQFISWIS HNVALLDKDQ AVAVQHSVEE ITDNYPOAIV YPFIISSEY 3540
 SPKDTSTGHK NKEFVARIKS KLDQGGVIQD FINALDQSLN PELLFKDWSN DVRAELAKTP 3600
 VNKKNIKMY ERMAYALGDP KAPGLGAFRR KFIQTFGKEF DKHFGKGSK LLMKLSDFN 3660
 DITNMLLLK NKDSKPPGNL KECSWMSDF KVEFLRNELE IPQYDGRGK PLPEYHVRIA 3720
 GDERVTYMA SLRRPKRII RGHDEREHF LVKGGEDLRQ DQVEQLFQV MNGILAQDSA 3780
 CSQALQLRT YSVVPMTSRL GLIEWLENTV TLKDLLLNTM SQEKAAYLS DPRAPPCEYK 3840
 DWLTKMSGKH DVGAYMLMYK GANRTETVTS FRKRESKVA DDLKRAFVRM STSPEALAL 3900
 RSHFASSHAL ICISHWILGI GDRHLNFMV AMETGGVIGI DFGHAFGSAT QFLVPPELMP 3960
 FLRTQFINL MLPMKETGLM YSIMVHALRA FRSDPGLLTN TMDVFPVKEPS FDWKNFEQKM 4020
 LKGGGSWQE INVAENWYP RQKICYAKRK LAGANPAVIT CDELLGHEK APAFRDYAV 4080
 ARGSDHNR AQEESGLSE ETQVKCLMDQ ATDENILGRT WEKWEPM

Seq ID NO: 100 DNA sequence
 Nucleic Acid Accession #: NM_000673
 Coding sequence: 101-1225

	1	11	21	31	41	51	
70	ATGTGAAGGC	ACAAGCTGCT	GTTATATACA	ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCTATGTTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACTG	CTGGAAGAGT	120
	TATTAAATGC	AAAGCAGCTG	TGCTTTGGGA	GCAGAAGCAA	CCCTTCTCCA	TTGAGGAAAT	180
75	AGAAGTTGCC	CCACCAAGA	CTAAAGAAGT	TCGCATTAAG	ATTTTGCCA	CAGGAATCTG	240
	TGCGACAGAT	GACCATGTGA	TAAAAGGAAC	AATGGTGTC	AAGTTTCCAG	TGATTGTGGG	300
	ACATGAGGCA	ACTGAGGATG	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAACACAGG	360
	TGACAAAGTC	ATCCCTCTCT	TTCTGCCACA	ATGTAGAGAA	TGCAATGCTT	GTCGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GGAGCGATAT	TACTGGTCGT	GGAGTACTGG	CTGATGGCAC	480
80	CACCAAGATT	ACATGCAAGG	GCAACACAGT	ACACCACTTC	ATGAACACCA	GTACATTTAC	540
	CGAGTACACA	GTGGTGGATG	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	CTCCTCCTGA	600
	GAAAGTCTGT	TTAATTGGCT	GTGGGTTTTC	CACTGGATAT	GGCGCTGCTG	TTAAACCTGG	660
	CAAGGTCAAA	CCTGGTTCCA	CTTGGCTCGT	CTTTGGCCTG	GGAGGAGTTG	GCCTGTCACT	720
	CATCATGGGC	TGTAAGTCAG	CTGGTGATC	TAGGATCATT	GGGATTGACC	TCAACAAAGA	780
85	CAAAATTGAG	AAGGCCATGG	CTGTAGGTGC	CACTGAGTGT	ATCAGTCCCA	AGGACTCTAC	840
	CAAAACCATC	AGTGAGGTGC	TGTGAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	CATCTTGAAA	CCATGATTGA	TGCCCTGGCA	TCCTGCCACA	TGAACATATG	960
	GACCAGCGTG	GTTGTAGGAG	TTCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCCGATGTT	1020

GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
 TGTCCCAAAA CTAGTGAAGT AGTTCCTGGC AAAGAAATTT GACCTGGACC AGTTGATAAC 1140
 TCATGTTTTA CCATTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAAG 1200
 CATTCGAACG GTCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTCATGGT 1260
 5 GAACTGGAGT TTCCTCTGTG AGAGTCCCT CATCTGAAAT CATGTATCTG TCTCACAAT 1320
 ACAAGCATAA GTAGAAGATT TGTGTAAGAC ATAGAACCCT TATAAAGAAT TATTAACCTT 1380
 TATAAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATT 1440
 TTGATTTACA TTTGTGAAG CTATAATTGT ATCTTTTAAG AAAACATACA CTGGGATTTC 1500
 10 TATGTTGAAA TGGAGATTTT TAAGAGTTTT AACCGAGTGC TGCAGATATA TAACTCAAAA 1560
 CAGATATAGC GTATAAAGAT ATAGTAAATG CATCTCCAG AGTAATATTC ACTTAACACA 1620
 TTGAACTAT TATTTTTTAG ATTTGAATAT AAATGTATT TTTAAACACT TGTATGAGT 1680
 TAACCTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
 AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAG CGATTAAAGAA TCATCATTAC 1800
 15 ATAACTTGGT GAACTGAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
 TATTAATATT TTAGAAAATA TTCCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
 ATATTATCAT ACTTATCAT ATGTTCAATT TGATACAGTA GAATTGCAAG TCCCTAAGTC 1980
 CCTATTCACT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTAAACAA 2040
 CTAACCCG

Seq ID NO: 101 Protein sequence:
 Protein Accession #: NP_000664

1 11 21 31 41 51
 25 MGTAGKVIK KAAVLWEQK PFSIEEIEVA PPKTKEVRIK ILATGICRTD DHVIKTMVS 60
 KFPVIVGHEA TGIVESIGEG VTTVKPGDKV IPLFLPQCRE CNACRNP DGN LCIRSDITGR 120
 GVLADGTTTF TCKGKPVHFF MNTSTFTEYT VVDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
 GAAVKTGKVK PGSTCVVFLG GVGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC 240
 30 ISPKDSTKPI SEVLSEMTGN NVGYTFEIVG HLETMIDALA SCHMNYGTSV VVGVPSPAKM 300
 LTYDPMLETF GRTWKGCVFG GLKSRDDVPK LVTEFLAKKF DLDQLITHVL PFKKISEGFE 360
 LLNSGQSIRT VLTP

Seq ID NO: 102 DNA sequence
 Nucleic Acid Accession #: NM_006783.1
 Coding sequence: 1..786

1 11 21 31 41 51
 40 ATGGATTGGG GSACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
 GGGGAAGGTGT GGATCAGAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
 CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
 AAAAAATGTG GCTATGACCA CTTTTTCCCG GTGTCCACCA TCCGGCTGTG GGCCTCCAG 240
 CTGATCTTGG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
 45 GAAACCACTC GCAAGTTTCA GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
 ATTAAGAAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
 TTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
 TACCACCTGC CTTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGTACTGC 540
 TTTATTCTTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
 50 ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
 AGATCAAGAA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
 CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
 AGCTAA

Seq ID NO: 103 Protein sequence:
 Protein Accession #: NP_006774.1

1 11 21 31 41 51
 60 MDWGLTHTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
 KNVCYDHFEP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED 120
 IKKHVKRIEG SLWWYTTSSI FFRIIFEAAF MYVVFYLYNG YHLPWVLKCG IDPCPNLVDC 180
 FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
 QNEMNELISD SQQNAITGFP S

Seq ID NO: 104 DNA sequence
 Nucleic Acid Accession #: NM_020411
 Coding sequence: 86-526

1 11 21 31 41 51
 70 GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
 AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTT 120
 ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC 180
 75 GCGGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
 ACAACACACG AACACACAG CCACTCCAG GAGCCAGTA ATGGAGAGCC CCAAAAAGAA 300
 GAACACGACG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
 ACAGCTGAGA TCCAGTGGC CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
 ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAGAGGGA 480
 80 ACACGTGAAA ATGCCAGAAG CAGGTGAAGA GCAACCAAA GTTTAAATGA AGACAAGCTG 540
 AAACAAGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
 CAGCTTTCAC CAAAAA AAAA

Seq ID NO: 105 Protein sequence:
 Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLWCPPQCA CSLGVFPSPAP SPVWGTTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHSTAS 60
PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120
SGVKVKIIPK EEHCKMPEAG EEQPVQV

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1 11 21 31 41 51
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCCTGGG CGTGCCCTCG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCCT CTCTGAGGGT CCACATCACC TCACTGTGTC 240
CCACCCCGCA GGACAACTCT GAGATCGTTC TGACACAGAT GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAAGCA GGCCAACGCT CTCGATACTG ACTACGACAA TTTCCTGTTT CTCTGCCTAC 420
AGGACACCCAC CACCCCTATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGAGG GGATTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTCTAGCTC ACCTCCGCCT 600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC 660
TTTCAAAGAA TAACACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAAC CTTGGAGCAT G

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1 11 21 31 41 51
MDIPQTKQDL ELPLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLETP EDNLEIVLHR 60
WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLD TDYD NFLFLCLQDT TTPIQSM MQ 120
YLARVLVEDD EIMQGFIRAP RPLPRHLWYL LDLQMEEPC RF

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 48-794

1 11 21 31 41 51
TCCAGGCAG CAGTTAGCCC GCCGCCCGCC TGTGTGTCCC CAGAGCCATG GAGAGAGCCA 60
GTCTGATCCA GAAGGCCAAG CTGGCAGAGC AGGCCGAACG CTATGAGGAC ATGGCAGCCT 120
TCATGAAGAG CGCCCTGGAG AAGGGCGAGG AGCTCTCCTG CGAAGAGCGA AACCTGCTCT 180
CAGTAGCCTA TAAGAACGTG GTGGGCGGCC AGAGGGCTGC CTGGAGGGTG CTGTCCAGTA 240
TTGAGCAGAA AAGCAACAGG GAGGGCTCGG AGGAGAAGGG GCCCGAGGTG CGTGAGTACC 300
GGGAGAGGT GGAGACTGAG CTCAGGGCGC TGTGCGACAC CGTGCTGGGC CTGCTGGACA 360
GCCACCTCAT CAAGGAGGCC GGGGACGCCG AGAGCCGGGT CTTCTACCTG AAGATGAAGG 420
GTGACTACTA CGCTACCTG GCCGAGGTGG CCACCGTGTA CGACAAGAAG CGCATCATTG 480
ACTCAGCCCG GTCAGCCTAC CAGGAGGCCA TGGACATCAG CAAGAAGGAG ATGCCGCCCA 540
CCAACCCCAT CCGCTGGGCG CTGGCCCTGA ACTTTCCGT CTTCCACTAC GAGATCGCCA 600
ACAGCCCGCA GGAGGCCATC TCTCTGGCCA AGACCACTTT CGACGAGGCC ATGGCTGATC 660
TGACACCCCT CAGCGAGGAC TCCTACAAAG ACAGCACCTT CATCATGCAG CTGCTGCGAG 720
ACAACTGAC ACTGTGGACG GCCGCAACG CCGGGGAAGA GGGGGCGGAG GCTCCCCAGG 780
AGCCCCAGAG CTGAGTGTG CCCGCCACCG CCCCGCCTG CCCCTCCAG TCCCCACCC 840
TGCCGAGAG ACTAGTATGG GGTGGGAGGC CCCACCTTC TCCCTAGGC GCTGTTCTTG 900
CTCAAAGGG CTCCTGGAG AGGACTGGC AGAGCTGAGG CCACCTGGGG CTGGGGATCC 960
CACTCTTCTT GCAGCTGTTG AGCGCACCTA ACCACTGGTC ATGCCCCAC CCCTGCTCTC 1020
CGCACCCGCT TCCTCCGAC CCCAGGACCA GGCTACTTCT CCCCTCTCT TGCTCCCTC 1080
CTGCCCTGCT TGCTCTGAT CGTAGGAATT GAGGAGTGTG CCGCTTGTG GCTGAGAACT 1140
GGACAGTGGC AGGGCTGGA GATGGGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 1200
CGCGCGCGCC AGTGCAAGAC CGAGATTGAG GGAAAGCATG TCTGCTGGGT GTGACCATGT 1260
TTCTCTCAA TAAAGTTCCC CTGTGACACT C

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

1 11 21 31 41 51
MERASLIQKA KLAEEQAERYE DMAAFMKGAV EKGEELSCEE RNLLSVAYKN VVGQRAAWR 60
VLSSIEQKSN EBGSEKQPE VREYREKVT ELQGVCDTVL GLLDSHLIKE AGDAESRVFY 120
LKMKGDIYRY LAEVATGDDK KRIIDSARSA YQEAMDISKK EMPPTNPIRL GLAINFSVPFH 180
YEIANSFEEA ISLAKTTFDE AMADLHTLSE DSYKOSTLIM QLLRDNLTW TADNAGEEGG 240
EAPQEPQS

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1 11 21 31 41 51
CAGAGTTGG TTTGGGAGCT GCCAGTCTCC TGGGAGGATC GCAGTCAGCA GAGCAGGGCT 60
GAGGCCTGGG GGTAGGAGCA GAGCCTGCGC ATCTGGAGGC AGCATGTCCA AGAAAGGGAG 120
TGGAGGTGCA GCGAAGGACC CAGGGGACGA GCCACGCTG GGGATGGACC CCTTCGAGGA 180
CACACTGCGG CGGCTGCGTG AGGCCTTCAA CTGAGGGCGC ACGCGGCCG CCGAGTTCGG 240
GGCTGCGCAG TCCAGGGGCC TGGGCCACTT CCTTCAAGAA AACAGCAGC TTCTGCGCGA 300

5	CGTGTGCGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTTGACT	ACGCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCAGC	AACCTGTCTA	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AACCCCTTGG	480
	CCTGGTCCCT	ATCATCGCAC	CCTGGAACCT	CCATTGAAAC	CTGACCCCTG	TGCTCTGGT	540
	GGGCACCCCT	CCCGCAGGGA	ATTGCGTGGT	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAAGTC	CTGGCTGAGG	TGCTGCCCCA	GTACCTGGAC	CAGAGCTGCT	TTGCCGTGGT	660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGGAGC	CCTCGTGTGG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACCTGACGCC	780
	TGTACCCCTG	GAGCTGGGGG	GCAAGAACCC	CTGCTACGTG	GACGACAACT	GCGACCCCCA	840
10	GACCGTGGCC	AACCGCGTGG	CCTGGTTCTG	CTACTTCAAT	GCGGGCCAGA	CCTGCGTGGC	900
	CCCTGACTAC	GTCTGTGTGA	GCCCGAGAT	GCAGGAGAGG	CTGCTGCCCG	CCCTGCAGAG	960
	CACCATCACC	CGTTTCTATG	GCGAOGACCC	CCAGAGCTCC	CCAAACCTGG	GCCGCATCAT	1020
	CAACAGAAA	CAGTTCACAC	GGCTGCGGGC	ATTGCTGGGC	TGCGGCGCGG	TGGCCATTGG	1080
	GGGCCAGAGC	AACGAGAGCG	ATCGCTACAT	CGCCCCCAGC	GTGCTGGTGG	ACGTGCAGGA	1140
15	GACGAGCCT	GTGATGCAGG	AGGAGATCTT	CGGGCCCATC	CTGCCCATCG	TGAACGTGCA	1200
	GAGCGTGGAC	GAGGCCATCA	AGTTCATCAA	CCGGCAGGAG	AAGCCCCCTG	CCCTGTACGC	1260
	CTTCTCCAAC	AGCAGACAGG	TTGTGAACCA	GATGCTGGAG	CGGACCAGCA	GCGGCAGCTT	1320
	TGGAGGCAAT	GAGGGCTTCA	CCTACATATC	TCTGCTGTCC	GTGCCATTGG	GGGGAGTCGG	1380
20	CCACAGTGGG	ATGGGCGGGT	ACCACGGCAA	GTTCACCTTC	GACACCTTCT	CCCACCAACG	1440
	CACCTGCTCG	CTCGCCCTCT	CCGGCCTGGA	GAAATTAAGG	GAGATCCGCT	ACCCACCTTA	1500
	TACCGACTGG	AACCAAGCAG	TGTTACGCTG	GGGCATGGGC	TCCAGAGCT	GCACCTCTCT	1560
	GTGAGCGTCC	CACCGCGCTC	CAACGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGTCT	CCAATCTACA	TTGTTCTCTC	AGACCGCAGG	CTCCCCCAGC	CTCAGGTTGC	1680
25	TGGAGCTGTC	ACATGATGTC	ATCTGCTCTG	CCAGGGCTGC	AAAGCAAGGT	CTTGCTTCTA	1740
	TCTGGGGGAC	GCTGCTCGAG	AGAGGCCGAG	AGGCCGCGAG	ACATGCCAGG	TGTCCTCACT	1800
	CACCCACCCC	TCCCAATATC	CAGCCCTTTG	CCCTCTCGGT	CAGGGTTGGC	CAGGCCCACT	1860
	CACAGGGGCA	GTGTACCCCT	GAGAAATACA	GTGCCCTGCC	TTCTTAGGGG	CATCAGCCCT	1920
	GAACGGTTGA	GAGCGTGGAG	CCCTCCAGGC	CTTGCTCTCT	CCCTCTAGGC	ACACGCGCAC	1980
30	TTCCACCTCT	CGCCCATCCC	AACTGCACCA	GCACTGCCTC	CCCCAGGGAT	CCTCTCACAT	2040
	CCACACTGCG	TCTCTGCAAC	ACCCCTCTGG	TTCAACCCGC	ACCCTGCACT	CACCCACAGC	2100
	AGCTCCATCC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTGTCTGGAA	2220
	CCAAATGGA	GTCACTATG	CCAACTCTA	ATAAAATGGA	GTCCGGGGGG	CACATAGAAG	2280
35	CCCTCACACA	CACATGCCCG	TAACAGGATT	TATCACCAG	ACACGCCCTG	ATGTAAGACC	2340
	AGACACAGGG	CGTATGGAAA	AGCAGCTCCT	CAAAGACTGT	AGTATTCAG	ATGAGCTGCA	2400
	GATGCTTACC	TACCAAGGCC	GTCTCCACCA	GAAAAACATC	GCCAACTCCT	GCGATCAGCT	2460
	TGTGACTTAC	AAACCTTGTT	TAAAGCTGCG	TTACATGGAC	TTCTGTCTCT	TAAACGTTTC	2520
40	CCCTTGGCTG	TGGCCCTCTG	TGTATGCCTG	GGATCCTTCC	AAGCACTCAT	AGCCAGATA	2580
	GGAATCCTCT	GCTCCTCCCA	AATAAATTCA	TCTGTTTC			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MKDEPRSTNL	FMKLDVSFIW	KEPFLVLII	APWNYPLNLT	LVLLVGLTLP	GNCVVLKPS	60
	ISQTEKVL	EVLPLQYLDQ	CPAVVLGGPQ	ETGQLLEHKL	DYIFFTGSPR	VGRIVMTAAT	120
	KHLTPVLEL	GKGNPCYVDD	NCDPQTVANR	VAWFYCFNAG	QTCVAPDYVL	CSPEMQRERL	180
50	PALQSTITRF	YGDDPCSSFN	LGRIINQKQF	QRLRALLGCG	RVAIGGQSNE	SDRYIAPTUL	240
	VDVQETEPVM	QEEIFGPILP	IVNVQSVDEA	IKFINRQKEP	LALYAFNSNR	QVNVQMLERT	300
	SSGSFGNNEG	FTYISLLSVP	FGGVGHSGMG	RYHGKFTPDT	FSHRTCLLA	PSGLEKLKEI	360
	RYPPYTDWNQ	QLLRNMGSGQ	SCILL				

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

60	1	11	21	31	41	51	
	GAATTCGGGG	CGACGCGCGG	GAACAACGCG	AGTCGGCGCG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAAGAAATC	TGAGAAGGGA	CCAGTTTGT	GGCGGAAGCG	TGTAATATCA	120
	GAGTACATGC	GACTGAGACA	GCTCAAGAGG	TTCAAGCAGG	CTGATGAAGT	AAAGAGTATG	180
65	TTTAGTTCCA	ATCGTCAAGAA	AATTTTGAA	AGAAACGAAA	TCTTAAACCA	AGAATGGAAA	240
	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATTGGC	CGGGACTAGG	300
	GAGTGTTCGG	TGACCAAGTA	CTTGATTTT	CCAACACAAG	TCATCCCAT	AAAGACTCTG	360
	AATGCAGTTG	CTTCAGTACC	CATAATGTAT	TCTTGGTCTC	CCCTACAGCA	GAATTTTATG	420
	GTGGAAGATG	AAACTGTTTT	ACATAACATT	CCTTATATGG	GAGATGAAGT	TTTAGATCAG	480
	GATGGTACTT	TCATTGAAGA	ACTAATAAAA	AATTATGATG	GGAAAGTACA	CGGGGATAGA	540
70	GAATGTGGGT	TTATAAATGA	TGAAATTTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCGAGA	TGATAAAGAA	AGCCGCCAC	CTCGGAAATT	TCCTTCTGAT	720
	AAAAATTTTG	AGGCCATTTC	CTCAATGTTT	CCAGATAAGG	GCACAGCAGA	AGAACTAAAG	780
	GAAAAATATA	AAGAACTCAC	CGAACAGCAG	CTCCAGGCG	CACCTCTCTC	TGAATGTACC	840
75	CCCAACATAG	ATGGACCAAA	TGCTAAATCT	GTTCAGAGAG	AGCAAGCTT	ACACTCTTT	900
	CATACGCTTT	TCTGTAGGCG	ATGTTTAA	TATGACTGCT	TCCTACATCC	TTTTCATGCA	960
	ACACCCACCA	CTTATAAGCG	GAAAGAACACA	GAAACAGCTC	TAGACAACAA	ACCTTGTGGA	1020
	CCACAGTGT	ACCAGCATTT	GGAGGGAGCA	AAGGAGTTTG	CTGCTGCTCT	CACGCTGAG	1080
80	CGGATAAAGA	CCCCACCAAA	ACGTCCAGGA	GGCCGCGAG	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGGC	CCAGCAGCCC	CACCATTAAT	GTGCTGGAAT	CAAAGGATAC	AGACAGTGAT	1200
	AGGGAAGCAG	GGACTGAAC	GAAGGAGAG	AACAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAAACTT	CGAGCTCTCT	TGAAGCAAAT	TCTCGGTGTC	AAACACCAAT	AAAGATGAAG	1320
	CCAAATATTG	AACCTCTCTA	GAATGTGGAG	TGGAGTGGTG	CTGAAGCCTC	AATGTTTAGA	1380
85	GTCTCTATTG	GCACTTACTA	TGACAAATTC	TGTGCCATTG	CTAGGTAAAT	TGGGACCAAA	1440
	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	GCTGAGGATG	TGGATACTCC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	GTGGCTGCA	1560
	CACATGCAGAA	AGATACAGCT	GAAAAGGAC	GGCTCCTCTA	ACCATGTTTA	CAACTATCAA	1620

CCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTGTGTGTAT AGCACAAAAT 1680
 TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
 TGCAAGACAC AGTGCACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
 CCTGACCTCT GTCTTACTTG TGAGCCGCT GACCATTTGG ACAGTAAAAA TGTGTCTGTC 1860
 AAGAACTGCA GTATTACAGC GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
 GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
 TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAGTGTG TGATAAATAC 2040
 ATGTGCAGCT TTCTGTTCAA CTGAAACAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
 AACAAAATTC GTTTTGCAAA TCATTGCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
 GTTAAACGGT ATCACAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
 CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCCG CATCGAAAGA 2280
 GAAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCTTAG 2340
 CTTACAGAAC CTCAGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
 AATTTGCAAA GTACTGTAG AATAATTTAT AGTAATGAGT TAAAAATCA ACTTTTATT 2460
 GCCTTCTCAC CAGCTGCAAA GTGTTTGTG CCACTGAATT TTTGCAATA TGCAGTATGG 2520
 TACATTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAAAA AAAAAA

Seq ID NO: 113 Protein sequence:
Protein Accession #: NP_004447

1 11 21 31 41 51
 MGQTGKKSEK GPVCRWRKRVK SEYMLRLQRLK RFRRRADEVKS MFSSNRQKIL ERTEILNQEW 60
 KQRRIQPVHI LTSVSSLRGT RECSVTSDDL FPTQVIPLKT LNAVASVPIM YSWSPLOQNF 120
 MVEDETVLHN IPYMGDEVLD QDGTFFIELI KNYDGKVHGD RECGFINDEI FVELVNALGQ 180
 YNDDDDDDG DDPEREERKQ KLEDEHRDDK ESRPPRKFPF DKILEAISSM FPDKGTAEBL 240
 KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFLHFFH 300
 ATPNTYKRNK TETALDNKPC GQCYQHLEG AKFPAALTA ERIKTPPKRP GRRRRGRLPN 360
 NSSRSPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEBEK KDETSSSSEA NSRCQTPKIM 420
 KPNIEFPENV EWSGAEASMF RVLIGTYDYN FCAIARLIGT KTCRQVYEFV VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ 540
 NPCEKFCQCS SEQNRFPPG RCKAQCNTEQ CPCYLAVREC DPLCLCTCGA ADHWDKSNVS 600
 CKNCSTQRGS KKHLLAPSD VAGWGIFIKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660
 YMCSTFLNIN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKYVGIE REMEIP

Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: NM_001827
Coding sequence: 96-335

1 11 21 31 41 51
 AGTCTCCGGC GAGTGTGTGC CTGGGCTGGA CGTGGTTTGG TCTGCTGCGC CGCTCTTCG 60
 CGCTCTCGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120
 CGGACAAGTA CTTGCGAGAA CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT 180
 CCAACAAGT ACCTAAAGT CATCTGATGT CTGAAGAGGA TGGAGGAGA CTTGGTGCC 240
 AACAGAGTCT AGGCTGGGTT CATTACATGA TTCATGAGCC AGAACCATAT ATTCTTCTCT 300
 TTAGAGGACC TCTTCCAAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT 360
 TTTTCAAAAT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
 ACAATCTTTT CATCCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
 AAATGCAACT GCAAGTAGGT TACTGTAAGA TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT 540
 TTTCTCTTAA GTCCTGTTT GAGTTTACTG AAACAGTTTA CTTTGTGTCA ATAAAGTTTG 600
 TATGTTGCAT TAAAAAAA AAAAAA

Seq ID NO: 115 Protein sequence:
Protein Accession #: NP_001818

1 11 21 31 41 51
 MAHKQIYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE EEWRLGVQQ SLGWVHYMIH 60
 EPEPHILLPR RPLPKDQK

Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCCTG 60
 GCATCTGGAC CCTTGGTGCT ATCGACGAAG CTTGGGTGGG GCTCTTAGCT GCTATGTGCA 120
 AGAGGTGTGT TCCAGGGAAA GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
 GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG 240
 AAGGACTGAT CCACATTCCT ACCAGGAAGT TTAGCAGAAC CCCGCGTGC CAACTGGACC 300
 CCTTGAAGG ACCTGGCTCA GGCTGGACCA CCTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
 TCAAGAAATC TTTGCTGAGC ATGGTGCCTC ATGCCTATAA TACCAACACT TTGGGAGGCC 420
 AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
 CCCATCTCTA AAATAATAAT AATAATAAAA TAAAAAATA GCAGGGCATG GTGGCATGTG 540
 CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG 600
 AGGCTGCAAT GAACTGTGAT TACCCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
 CCTGTCTCAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAGA GACCTCTGGA 720
 TTTGAGGTGC CATTGTGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
 CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
 GACAGACCTT GTCCTTCTC CTTGTGGAAA GTGTTTCTCT TGCTGCTACT GCTCATGAGA 900
 CTCCTCCCCC TCCCTGTCCC AGGGAACCAA AGGGCTTTCT ACCACACCTT TTCTTCCCCC 960
 CCGCCTCCCA TGTCTGCTGT GCCTTTGTAC TCAGCAATTC TTGTTGCTC CATTATCTTC 1020
 CAGCCGGATA CAGAGTGAAT AGTTAACCAC ACTTAGGTCA AATAGGATCT AAATTTTGTG 1080
 TCCTGCTCCG TGTAAGAGG CCACTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAAC 1140

CTTCTCATTT GTTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
AGTTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGGAGAAGG CTTCAGCAGC AGAACTGATG 1260
GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
TTGGAAGGGC AAAAAATGAA CACTGTCTGT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380
ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCAATTGGG AGTCCATGCC AGATCATGTT 1440
GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCCTCCCC 1500
CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT 1560
ACTCTGTAGC CAACATACAC ATGATTTAAA ACCCTTTCTA AATATCTATC ATGGTTTCATC 1620
CTTGTCCAAA TGCAGAGTCA GAGCTATTG TACTTCATTA TTATTTCCAA GCGAATAGT 1680
TGGCTTTCTT TTTGCAAAAA TAATTAAGT TTTTGTATGT TGCAAAAAAA AAAAAAATA 1740
AACAATAAAA

Seq ID NO: 117 DNA sequence

Nucleic Acid Accession #: BC012178.1

Coding sequence: 204-2285

1 11 21 31 41 51
CTTCTCTCCC GCGGCGCTGG GCGCCGCGCT CCGCTGCTGT TGCTCCATTC GGCGCTTTTC 60
TGGCGGCTGG CTCCTCTCCG CTGCGGCGCTG CTCCTCGACC AGGCCTCCTT CTCAACCTCA 120
GCGCGCGGCG CCGACCCCTC CGGCACCCCTC TCGTACTGTC GCGCTCACCG 180
CCGCGGCTCC GCGCCTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAAATG 240
CTGGAGGAGA CCTTAAGGAT GCGCACCACT ACTATGAAGG AGCTGTGTG ATCTGGATG 300
CTGGTGTCTA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAAGTGTTC GTGCAGTCTG 360
AAATTTTCCC CTGTGAAACA CCGACATTG CTATAAAGGA ACAAGGATTC CGTGCTATTA 420
TCATCTCTGG AGGACCTAAT TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA 480
TATTCACTAT TGGCAAGCCT GTTCTTGGAA TTTGCTATGG TATGCAGATG ATGAATAAGG 540
TATTTGGAGG TACTGTGACG AAAAAAAGTG TCAGAGAAGA TGGAGTTTTC AACATTAGTG 600
TGGATAATAC ATGTTTCAAT TTCAGGGGCC TTCAGAAGGA AGAAGTTGTT TTGCTTACAC 660
ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAACA 720
TAGTAGCAGG CATAGCAAAAT GAATCTAAAA AGTTATATGG AGCAGAGTTC CACCTGAAG 780
TTGGCCTTAC AGAAAATGGA AAGTAATAC TGAAGAATTT CCTTTATGAT ATAGCTGGAT 840
GCAGTGAAC CTTACCCGTG CAGAACAGAG AACTTGAGTG TATTGAGAG ATCAAAGAGA 900
GAGTAGGCAC GTCAAAAAGTT TTGGTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTG 960
CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAAGTCA TGCTGTGCAC ATTGATAATG 1020
GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTGGAATTC 1080
AGGTCAAAGT GATAAATGCT GCTCATTCTT TCTACAATGG AACAAACAAC CTACCAATAT 1140
CAGATGAAGA TAGAACCCCA CGGAAAAGAA GTTAAATATG ACCCAAGTC 1200
CTGAAGAGAA AAGAAAATC ATTGGGGATA CTTTGTGTTA GATTGCCAAT GAAGTAATG 1260
GAGAAATGAA CTTGAAACCA GAGGAGGTTT TCCTTGCCCA AGGTACTTTA CGGCTGATC 1320
TAATTGAAGG TGATCCCTCT GTTGCAAGTG GCAAAAGCTGA ACTCATCAA ACCCATCACA 1380
ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG 1440
ATTTTCATA AGATGAAGTG AGAATTTTGG GCAGAGAACT TGGACTTCCA GAAGAGTTAG 1500
TTTCCAGGCA TCCATTTCCT GGTCTTGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560
CTTATATTGG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTT 1620
CTGCAAGTGT TAAAAGGCCA CATACCCCTAT TACAGAGAGT CAAAGCCTG ACAACAGAA 1680
AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1740
CAATTAAGG TGTAGGTGTC CAGGGTGACT GTCGTTCCTA CAGTTACGTG TGTGGAATCT 1800
CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTCTT GGCTAGGCTT ATACCTCGCA 1860
TGTGTACAA CGTTAACAGA GTTGTTTATA TATTTGGCCC ACCAGTTAAA GAACCTCCTA 1920
CAGATGTTAC TCCCACTTTC TTGCAACAG GGGTGCTCAG TACTTTACGC CAAGCTGATT 1980
TTGAGGCCCA TAACATCTC AGGGAGTCTG GGTATGCTGG GAAAATCAGC CAGATGCCGG 2040
TGATTTTGAC ACCATTACAT TTTGATCGGG ACCCACTTCA AAAGCAGCCT TCATGCCAGA 2100
GATCTGTGGT TATTCGAACC TTTATTACTA GTGACTTCAT GACTGGTATA CCGTCAACAC 2160
CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATT 2220
CTGGTATTTT TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAAT ACTGAGTGGG 2280
AGTAATAAAC TTCTGTCTCT ATTAATAA

Seq ID NO: 118 Protein sequence:

Protein Accession #: AAH12178.1

1 11 21 31 41 51
MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGVK IDRRVRELFV QSEIFPLETP 60
APAIKEQGFRI AIISGGPNS VYAEAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
KSVREDGVFN ISVDNTCSLF RGLQKEBVVL LTHGDSVDKV ADGFKVVARV GNIVAGIANE 180
SKKLYGAQFH PEVGLTENGK VILKNFLYDI AGCSGTFVTQ NRELECIREI KERVGTSKVL 240
VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
HSFYNGTTTL PISDEDTRPR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
EVFLAQGTLLR PDIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR 420
ILGRELGLEPE ELVSRHPFPF PGLAIRVICA EEPYICKDFP ETNNILKIVA DPFASVKKPH 480
TLLQVRKACT TEEDQEKLMQ ITSLHSLNAP LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
ESLIPLARLI PRMCHNVNRV VYIFGPPVKE PPTDVPTFL TTGVLSTLRQ ADPEAHNLR 600
ESGYAGKISQ MPVILTPLHF DRDPLQKQPS QORSVVIRTF ITSDFMGTGP ATPGNEIPVE 660
VVLKMWTEIK KIPGISIRIMY DLTSKPPGTT EWE

Seq ID NO: 119 DNA sequence

Nucleic Acid Accession #: NM_006500.1

Coding sequence: 27..1967

1 11 21 31 41 51
ACTTGGGTCT GCCTCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TGCCCGCTCT CTGCTGCTGT CCTCGCGTGG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240

5	TCATCTTCCG	TGTGGGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGCTCCGCG	420
	TCACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCTAAG	540
	TCATCTGGTA	CAAGAATGSC	CGGCCTCTGA	AGSAGGAGAA	GAACCGGGTC	CACATTCACT	600
	CGTCCACAGC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAGATC	GCCAGTTTTT	ACTGTGAGCT	CAACTACCCG	CTGCCAGTGC	720
10	GGAACCATAT	GAGGAGTCTC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAAATCAGGT	840
	GTGTTGGCTGA	TGCAACCCCT	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCACCA	900
	GGGAGGCAGA	GGAAAGAGCA	ACCAACGACA	ACGGGGTCTT	GGTGCTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAGG	CCTGGAACCT	GGACACCATG	ATATCGCTGC	1020
	TGAGTGAACC	ACAGGAACCTA	CTGGTGAACT	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
15	CCCTTGAGAG	AGCGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCAGTGGCTG	AGAGAAGAGA	CAGACCAGGT	GCTGGAAAGG	GGGCTCTGTC	1200
	TTCAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TCGCTCGCTG	CGCTCTGTGC	1260
	CCAGCATACC	CGGCTTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTCTT	GGCCCCCTT	1320
20	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTGT	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCACCCTC	CGGCCACCA	TCTCTGGAA	CGTCAACCGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTCTGA	GCACCCCTGAA	TGTCCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCCTTCTGGA	GCTGGTCAAT	TTAACCAACC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
25	TACGCACTTC	CAGTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
	TGCCCGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCTCTGGTC	1740
	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CCGTGACGGC	1800
	GCTCAGGGAA	CGAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAAGCT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAGCTCCCA	GAGAGAGTGG	GCCTCCTGCA	GGGCAGCAGC	GGTGACAAAG	1920
30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCTGG	ACCATTCCTCA	GCTCCCTGCT	CACCTCTCTC	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCGCTTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCCTCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGCT	AGGAGAGTTT	CTTGACAGAA	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCCTGCGG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
	CAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
	GGCTGCTCAT	GTTGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCTAGTGTGC	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCCTGTG	2520
40	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGACAGAGC	CATCCTGGCT	AACACGGTGA	AACCCGTGCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GGGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
45	CAGTGCATC	CAGCTGGGGC	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAA	2880
	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTGAG	TTCAAGGTGAA	TTAGGCTCAA	2940
	TCCCGTGTGT	CAGTGTCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAACT	GAAAGGCAGC	3000
	GGGAGACAGA	CAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGTTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAATAGAG	3120
50	AGAATGGTAC	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA		3240
	TTGTTTCTCT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCACGAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGGTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCTTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATATG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

65	1	11	21	31	41	51	
	MGLPRLVCAF	LLAACCCCPR	VAGVPGAEQ	PAPELVEVEV	GSTALLKCGL	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRRQQ	GQSEPGEYEQ	RLSLQDRGAT	LALTVQTPQD	ERIFLCQGR	120
	PRSQEYRIQL	RVYKAPBEPN	IQVNPILGIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVSSSG	LYTLQSLKKA	QLVKEDKDAQ	FYCELNYRLP	SGNHMKESRE	240
70	VTVVPVFPTE	KVWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNPB	TREAEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPQELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEAESS	QDLFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKKLAFGP	PWMAFKERKV	WVKENMVLNL	SCEASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNLVLT	ELLTGVECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTGTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLP	RRSGKQETIL	600
	PFSRKTELTV	EVKSDKLPFE	MGLLQSSSD	KRAPGDQGEK	YIDLRL		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

80	1	11	21	31	41	51	
	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAGCCA	60
	TGGAGACTTC	AGCATCCTCC	TCCAGCCTC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAACA	ATATGAGAGA	AACAAGTCTT	CTTCTCTCTC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTCATCCTCC	TCTCTCTCAG	GTCCCTGGCA	TGGGGAGCCT	GACGTTTTGA	300

5
10
15
20

```

AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCCTCT GGGGAATCAG 360
GACTCCGAGG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTTT TCCATTTCGT CCTCCTGTGC TTGCCATCG 480
GGGCCTTGCT GGTGTGTAT CACTATTACG CAGACTGGTT CATGTCTCTT GGGGTCGGCC 540
TGCTCACCTT CGCCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCTT CCAAGGCTTC ATCCCCCTCT TCCAGAAAGT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCCAGTGT GACCACCACT 720
GGGACCCCTG AGCCACAGAG GGCAGAGCAG CATCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAACACT TTTCTTCCA TGTGGTCTGA ATGTTGGCAC CAGCCCGGGC 840
AGGGGCATCT CATTGGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCCTGAGG CTTCACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGGACCCTG AGCTCTGCAA GCTGTGATCT GTCTGGTTTC 1020
ATGTTTTTTC TCAATCCCA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGTTCCAC TGCTTTGAGG CAGGGAGCCA TCGGGCTGGG GCCCCTTGGT 1140
GAACCTGATG CAGGTAAGAT GCTGAGGACT AAAACCAATT TTTTTCACC CAAAAAATAA 1200
GGCAGGAAAA TGATCATCAG AAACATAATG GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGCAG CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCCAGC TACTCAAGAG GCTGAGGAGG GAGGACTGCT 1440
TGAGCCCAAG AGTTCAGGGC TGCAGTGAGG TACGATCAAG CCATGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAAAAT

```

Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30

```

1 11 21 31 41 51
| | | | |
METSASSSQP QDNSQVHRET EDVDYGETDF HKQDGLKGLF SQEQVERNKS SSSSFSSSSS 60
SSSSSSSSSS GPGHGEPLVL KDELQLYGDA PGEVVPSEGS GLRRRGSDPA SGEVEASQLR 120
RLNIKKDDEF FHFVLLCPAI GALLVCYHY ADWFMSLVG LLTFASLETV GIYFGLVYRI 180
HSLVQGFPL FQKRLTGFR KTD

```

Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

40
45
50
55
60
65
70

```

1 11 21 31 41 51
| | | | |
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCTGCTG TCCGACCTCG GCCCGCGCGG CCCCTCTCGG GCGTCCGGG TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGCGG GTTCGGGCGG CGCCCTGGCT GCTCCTCGGG GCGGCGACGG 180
GGCTCACGCG CGGGCCCGCC ACGGCCCTCA CCGCCGCGCG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTT TGAATTTATT TTGAGGCAAG AAGTTTTGAA AGATGGTTTC CACAGAGACC 300
TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAAATT TGATATAGAG GCCCCTAACT 480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGAG AGATTACAG TGCAATTGACT 540
GTTTCAAGC CTTTTGGCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTGTATGTT TTGTGACCAA GAGTTCCTGA 660
TTTTGAATG CTGGGCTCAC TCAGAAAGTG CAGCCCTTGG TGCTTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
TTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAATATGCG CCATTTTTC CTATAAGTTT 900
TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGCTACAA ATTGAGAAAA 1260
CCGTATATAA TAAGATATAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCCAGCAC 1320
TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCCTGTCTC TACTAAAAAT ACAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
GAGCCAAGAT CGCACCACCT CACTACAGCC TGGGCGACAG AACGAGACCC TGCTCCCAA 1560
GAGAAAAACA AAAAGAAGAA TAAATAATT TGGATGAAAA TCATGTTTAT TTAAATAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAACAGTGA CTAAGATTTG GTACAGAGTA TGTCAAGGAG ACAACTCAGA 1860
TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA

```

Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

80

```

1 11 21 31 41 51
| | | | |
MCSEIILRQE VLKDGPHRDL LIKVKGESI EDLHTRLLI KQDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARRDSCIDC FOAFLPVHCR YHRPHSEDEG 120
ASIVVNPDL LMFCDQAGR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNKMKYSVY KNVILQVPVG LTVHTSLVCS VTLLITLCS KKKKK

```

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

1 11 21 31 41 51
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTCG GTCTCTGGTG TCCTGGTGCT 60
 GGGCTGTGTC TTGTGCTGCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA 120
 5 CTTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
 CACTCGGGTG GCAGAGATGC GTGGAGATC GAAATCTCTG GGGCCTGGCG TGCTGCTTCT 240
 CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGGCCACGCG TGAAGGCCAT 300
 GCGAACCACA CGGTGCGGGG TCCCAGACCT GGCAGATTC CAAACCTTTG AGGGCGACCT 360
 CAAGTGGCAC CACCAACA CAACCTATTG GATCCAAAC TACTCGGAAG ACTTGCCTCG 420
 10 GGCGGTGATT GACGACGCTT TTGCCCGCGC CTTGCACTG TGGAGCGCGG TGACGCGCGT 480
 CACCTTCACT CGCGTGTACA GCGGGAGCGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
 GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC 600
 TGGCCCCGGC ATTCAAGGAG ACGCCCATTT CAGCATGAC GAGTTGTGGT CCCTGGGCAA 660
 GGGCGTCTGT GTTCCAATCT GGTTTGGAAA CCGAGATGGC GCGGCTGCGC ACTTCCCTTT 720
 15 CACTTCTGAG GGCCTGCTCT ACTCTGCTCG CACCACGAC GGTGCTCGG ACGGCTTGCC 780
 CTGGTGCTAGT ACCACGGCCA ACTACGACAC CAGACGACCG TTTGGCTTCT GCCCCAGCGA 840
 GAGACTCTAC ACCCGGGAGC GCAATGTCTG TGGGAAACCC TGCCAGTTTC CATTTCATCTT 900
 CCAAGGCCAA TCCCTACTCG CTTGCACCA GACCGGTGCG TCCGACGGCT ACCGCTGGTG 960
 CGCCACCACT GCCAATACG ACCGGGACAA GCTCTTGGC TTTCTGCGCA CCCGAGCTGA 1020
 20 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCTT TCACTTTCTT 1080
 GGGTAAGGAG TACTCGACCT GTACCAAGCA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC 1140
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
 TTTGTCTCTC GTGGCGGCGC ATGAGTTGCG CCACGCGCTG GGCTTAGATC ATTCCTCAGT 1260
 25 GCGGAGGCGC CTCTATACCG CTTCACTGAG GGGCCCCCTT TGCATAAGGA 1320
 CGACGTGAAT GGCATCCGCG ACCTCTATGG TCTTCGCGCT GAACCTGAGC CACGGCCTCC 1380
 AACCACCACT ACACCGCAGC CCACGGCTCC CCGACGGTTC TGCCCCACCG GACCCCCCAC 1440
 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGCCCCCAC 1500
 AGGTCCCCCC ACTGTGCGGC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560
 30 TGCCCTCAAC GTGAACATCT TCGACGCCAT GCGGAGATT GGGAAACGAG TGTATTGTGT 1620
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGCGCGC AGGGCCCCCTT 1680
 CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
 GCTCTCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800
 GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC 1860
 35 CGGGGCCCTC CCGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGCGCGC GCCTCTGGAG 1920
 GTTTCGAGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
 CCCCAGGGTG CCTTTGACA CCGACGAGCT CTTCCAGTAC CGAGAGAAAG CCTATTCTCTG 2040
 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT 2100
 GGGCTACGTG ACCTATGACA TCGTGCAGTG CCTGAGGAC TAGGGCTCCC GTCTCTGCTT 2160
 40 GCAGTGCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCGGATA 2220
 CAAACTGGTA TTCTGTCTCT GAGGAAAGGG AGGAGTGAGG GTGGGCTGGG CCCTCTCTTC 2280
 TCACCTTGT TTTTGTGG AGTGTCTTA ATAACTTG ATTCTTAAC CTTT

Seq ID NO: 126 Protein sequence:
 Protein Accession #: NP_004985.1

45 1 11 21 31 41 51
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRLNLT DRQLAEYLY RYGYTRVAM 60
 RGEKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLLKWHHN 120
 50 ITYWIQYSE DLPRVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIOF GVAEHGDGYP 180
 FDGKDGLLAH AFFFFPGIQQ DAHPDDELW SLKGVVVPT RFGNADGAAC HFFPIFEGRS 240
 YSACTTDRSR DGLPWCSTTA NYDTRDRFGF CPSERLYTRD GNADGKPCQF PFIFQGGSYS 300
 ACTTDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FFLGKEYST 360
 CTSEGRGDGR LWCAATSNFD SDKKNWFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420
 55 PMYRFTGEPF LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER 480
 PTAGPTGPPS AGPTCPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLPKDGKYW 540
 RFSEGRGSRP QGFPLIADKW PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR RGMMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFGVPLD 660
 THDVQYREK AYFCQDRFYW RVSSRSELNQ VDQGVYTYD ILQCPED

Seq ID NO: 127 DNA sequence
 Nucleic Acid Accession #: NM_004181
 Coding sequence: 32-670

65 1 11 21 31 41 51
 GCAGAAATAG CCTAGGGAGA TCAACCCCGA GATGCTGAAC AAAGTGCTGT CCCGGCTGGG 60
 GGTGCGCGCG CAGTGGCGCT TCGTGGACGT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC 120
 GGTGCCAGCG CCGCTGCTGG CCGTCTGCTG GCTGTTTCCC CTCACGGCCC AGCATGAGAA 180
 70 CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCTTA AAGTGACTT 240
 CATGAAGCAG ACCATTGGGA ATTCTGTGG CACAATCGGA CTTATTACAG CAGTGGCCAA 300
 TAATCAAGAC AAATCGGGAT TTGAGGATGG ATCAGTTCTG AACAGTTTC TTTCTGAAAC 360
 AGAGAAAATG TCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC 420
 AGCCCATGAT GCGCTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA 480
 75 TTTTATTCTG TTTAAACAAG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCTTT 540
 TCCGGTGAAC CATGGCGCCA GTTCAGAGGA CACCCTGCTG AAGGACGCTG CCAAGGTGTG 600
 CAGAGAATTC ACCGAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA 660
 GGCAGCCTAA TGTCTGTGG GAGGGAATTT GCTGATTTC CCTCTTCCCT TCAACATGAA 720
 80 AATATATACC CCCCATGCAG TCTAAATGC TTCAGTACTT GTGAAACACA GCTGTTCTTC 780
 TGTCTCTGAC ACACGCTTTC CCTCAGCCA CACCCAGGCA CTTAAGCACA AGCAGAGTGC 840
 ACAGCTGTCC AACTGGGCCAT TGTGTGTGA GCTTCAGATG GTGAAGCATT CTCCCAGTG 900
 TATGTCTTGT ATCCGATATC TAACGCTTAA AATGGCTACT TTGGTTCTG TCTGTAAGTT 960
 AAGACCTTGG ATGTGTTTAT GTTGTCTTAA AGAATAAATT TTGCTGATAG TAGC

Seq ID NO: 128 Protein sequence:
 Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKVLSRLG	VAGQWRFDV	LGLEESLGS	VPAPACALLL	LFPLTAQHEN	FRKKQIEELK	60
GQEVSPKVYP	MKQITIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKKQFLSET	EKMSPEDRAX	120
CFEKNEAIQA	AHDAVAQEGQ	CRVDDKVNPH	FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
TLLKDAARKVC	REPTERBQGE	VRFSVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

1	11	21	31	41	51	
CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCAG	GCGCGGAGGG	AGCGAGTCCG	60
CCCCGAGGTA	GGTCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCGG	GAGAGGGAGG	120
AAGAGGATGG	CAGGCGCCAG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAAC	CGTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTCAGGGAC	300
CGGCGCTGCA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
GTATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCCAC	CCTGCGGGCG	420
AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTT	480
GAGCTGGAGG	TGTTTGAGCC	ACTGGAGAGC	CCCGTGACC	TGTACATCCT	CATGGACTTC	540
TCCAACTCCA	TGTCCTGATG	TCTGGACAAC	CTCAAGAAGA	TGGGGCAGAA	CCTGGCTCGG	600
GTCTGAGGCG	AGCTCAGCAG	CGACTACACT	ATTGGATTGT	GCAAGTTTGT	GGACAAAGTC	660
AGCGTCCCGC	AGACGGACAT	GAGGCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
CCCCCTTCT	CCCTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAT	780
AAACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTCGATGCC	840
ATCTCTGAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCCACCTG	900
CTGGCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTGTCTGGT	960
GGCATCATGA	CGCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGCAC	CTACACCCAG	1020
TACAGGACAC	AGGACTAGCC	GTCCGTGCCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAAAC	1080
ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
TATTTCCCTG	TCTCCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAAACAT	CGTGGAGCTG	1200
CTGGAGGAGG	CCCTCAATCG	ATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
CGAGGCCTTC	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTCTT	1320
CACATCCGGC	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
GATGGGACGC	ACGTGTGCCA	GCTGCCGGAG	GACCAGAAGG	GCAACATCCA	TCTGAAACCT	1440
TCCCTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
CTGCAAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
GACATTACGC	CCTGCTCGCG	GAGGCGCGAG	GACAAGCCGT	GCTCCGGCCG	TGGGGAGTGC	1680
CAGTGCGGGC	ACTGTGTGTG	TAACGGCGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
GACAACTTCC	AGTGTCCCGG	CACTTCCGGG	TTCCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
ATGGGCCAGT	GTGTGTGTGA	GCCTGTGTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTCAGC	1860
AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
TGCGCGATCC	ACCGGGCCCT	CTGCGAGGAC	CTACGCTCCT	GCTGTCAGTG	CCAGGCGTGG	2040
GGCACCGGCG	AGAGAAAGGG	GGCACGCTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
CTGGTGACCA	AGAAAGAGGA	GGTCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
CTCCTCCTCC	TGCCGCTCCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCTGTC	2340
TGCAAGGCCCT	GCCTGGCACT	TCTCCCGTGC	TGCAACCGAG	GTCCATGTGT	GGGCTTTAAG	2400
GAAGACCACT	ACATGCTGGG	GGAGAACCCTG	ATGGCCTCTG	ACCACCTTGA	CACGCCCATG	2460
CTGCCGACGC	GGAACTCAA	GGGCCGTGAC	GTGGTCCGCT	GGAAAGTAC	CAACAACATG	2520
CAGCGGCCCTG	GCTTTGCCAC	TCATGCCGCG	AGCATCAACC	CCACAGAGCT	GGTGCCTTAC	2580
GGGCTGTCTT	TGCGCTTGGC	CCGCTTTTGC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
GAGTGGCGCC	AGCTGCGCCA	GGAGGTGGAG	GAGAACTTGA	ACGAGGTCTA	CAGGCAGATC	2700
TCCGGTGTAC	ACAAGCTCCA	GCAGACCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAAAAAG	2760
CAAGACCAAC	CCATTGTGGA	CACAGTGTG	ATGGGCGCCC	GCTCGGCCAA	GCGGCCCTTG	2820
CTGAAGCTTA	CAGAGAAGCA	GGTGAACAG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
GGCTACTACA	CCCTCACTGC	AGACAGGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
GTGGAGCTGG	TGGACGTACG	GGTGCCCTTC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
CAGCTGTGCG	TGGAGGCCAT	CGACGTGCCC	GCAGGCACTG	CCACCTCTCG	CGCGCGCTG	3060
GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCTTTTGA	GCAGCCTGAG	3120
TTCTCGGTCA	CGCCCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTTGGAC	3180
GGCGGGAAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
TACATCCCGG	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCGT	3360
TTCCAGCTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
ACCATCATCA	TCAGGGACCC	AGATGAACCTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
TCACAGCCAC	CCCTCAGCG	CGACCTGGGC	GCCCCGCGAG	ACCCCAATGC	TAAGGCCGCT	3540
GGGTCCAGGA	AGATCCATTT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
GTAAAGTACT	GGATTCAAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGTCTGA	CAGCAAGGTG	3660
CCCTCAGTGG	AGCTCAGCAA	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACCAGGAA	3780
GTGCCAGCGG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCAGGGT	GACCCAGCTG	3840
AGCTGGGCTG	AGCGGGCTGA	GACCAACGGT	GAGATCAAG	CCTACGAGGT	CTGCTATGGC	3900
CTGGTCAAGG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGTGTTG	TGACAACCTT	3960
AAGAACCGGA	TGCTGTCTTAT	TGAGAACCCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
AAGGCGCGCA	ACGGGGCCGG	CTGGGGCCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
CAGCCCAAGA	GGCCCATGTC	CATCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCACG	4140
AGCGGGGAGG	ACTACGACAG	CTTCCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
GGCAGCCAGA	GGGCCAGCGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
TTTGCTCTCC	CGGCGAGCAC	CNACTCCCTG	CACAGGATGA	CCAAGACCAG	TGCTGCTGCC	4320
TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

ACACGGGACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCGGAGG 4440
 GACTACTCCA CCCTCACTCT CGTCTCTCC CACGACTCTC GCCTGACTGC TGGTGTGCC 4500
 GACAGCCCA CCCGCTTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG 4560
 CAGGAGCCGC GGTGCGAGCG GCGCTGCGAG GCGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620
 GCGGCTGAGC TGATCTGGCT CAACATCCCC AACCTGCCCC AGACCTCGGT GGTGGTGGAA 4680
 GACCTCTGCG CCAACCACTC CTACGTGTTT CCGGTGCGGG CCCAGAGCCA GGAAGGCTGG 4740
 GGCGGAGAGC GTGAGGGTGT CATCACCAAT GAATCCCAGG TGCACCCGCA GAGCCCACTG 4800
 TGTCCCTGCG CAGGCTCGCG CTTCACCTTG AGCACTCCCA GTGCCCCAGG CCCGCTGGTG 4860
 TTCACTGCCC TGAGCCAGA CTGCTGCGAG CTGAGCTGGG AGGGGCCACG GAGGCCCAAT 4920
 GGGGATATCG TCGGCTACCT GGTGACCTGT GAGATGGCCC AAGGAGGAGG GCCAGCCACC 4980
 GCATTTCGGG TGATGGAGAG CAGCCCGGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG 5040
 AACGTGCCCT ACAGTTTCAA GGTGCAAGCC AGGACCACTG AGGGCTTCGG GCCAGAGCGC 5100
 GAGGGCATCA TCACCATAGA GTCCCAAGAT GGAGGACCCT TCCCGCAGCT GGGCAGCCGT 5160
 GCGGGCTCT TCCAGCACCC GCTGCAAAAG GAGTACAGCA GCATCACCA CACCACACCC 5220
 AGCGCCACCG AGCCCTTCCT AGTGGATGGG CCGACCCCTGG GGGCCAGCA CCTGGAGGCA 5280
 GCGGCTCTCC TCACCCGSCA TGTGACCCAG GAGTTTGTGA GCGGACACT GACCACAGC 5340
 GGAACCTTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTGACCCGCA CCCTGCCCCA 5400
 CCCCAGCAT GTCCCTCTCC GCGTCTCTCC GACTCTCTC CCGAGCCCTC CTCAGCTACT 5460
 CCATCTTTCG ACCCTGGGG GCCCAGCCCA CCCGATGCA CAGAGCAGGG GCTAGGTGTC 5520
 TCCTGGGAGG CATGAAGGG GCAAGGTCG TCCTCTGTGG GCCCAAACCT ATTTGTAAAC 5580
 AAAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTCTG CACTTAATAA ATGGTTTTCG 5640
 ACTG

Seq ID NO: 130 Protein sequence:
 Protein Accession #: NP_000204

1 11 21 31 41 51
 MAGPRPSPWA RLLLAALISV SLSGTLANRC KKAAPVKSCTE CVRVDKDCAY CTDEMFRDRR 60
 CNTQAEELAA GCGRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL 120
 EVFEPLSEPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SGLTSDYTIG FGKFDVKVSV 180
 PQTDMRPEKL KEPWPNSDPP FSFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240
 QTAVCTRDIG WRPDSTHLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR 300
 TDYFVSFVTL VRLLAHNIPI PIPAVTNYSY SYYEKLHTYF PVSSGLVQLG DSSNIVELLE 360
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGIYQV QLRALHVDG 420
 THVQQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540
 FQCPRTSGLF CNDGRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCHQQLSYT DTICEINYSY IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVD 660
 LKRAEEVVRV CSFRDEDDDC TSYTYMEGDG APGPNSTVLV HKKXDCPPGS FWLIPILLL 720
 LLPLALALLL LCKWYCAACK ACLALLPCCN RGHMVGFED HYMLRENMA SDHLDTPLMR 780
 SGNLKGDRDV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840
 AQLRQVEEEN LNEVYRQISG VHKLQQTFR QPNAGKKQD HTIVDTVLM PRSAKPALLK 900
 LTEKQVEQRA FHDLVKAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSQVSYRTQD GTAQGNRDYI PVEGELLFPQ GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLQGPSTTII IIRDPDELDR SFTSQMLSSQ PPHGDLGAP QPNNAKAAGS 1140
 RKIHFNLPPF SGKPMGYRKY YIQGDSESE AHLDSKVPV VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQEV SEPGRLAFNV VSSTVTQLSW AEPAETNGEI TAYEVCYGLV 1260
 NDDNRPFGPM KKVLVNPNKN RMLLIENLRE SQPYRYTVKA RAGAGWGPER EAIINLATQP 1320
 KRPMSPILIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDDETH LNVNRMDF 1380
 FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSSLTTR DYNLSLTRSEH SHSTTLPRDY 1440
 STLTSSVSSD SRLTAGVPDT PTRLVFSALG PTLRLVSWQE PRCEPLQGY SVEYQLLNGG 1500
 ELHRLNINPN AQTSVVVEDL LFNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSLPCP 1560
 LFGSAFTLST PSAPGLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM AQGGGPATAP 1620
 RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1680
 LFQHLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSGT 1740
 LSTHMDQQFF QT

Seq ID NO: 131 DNA sequence
 Nucleic Acid Accession #: BC004372
 Coding sequence: 132..2231

1 11 21 31 41 51
 CCTCGTGCGG CGGACCCCGG CCTCTGCCAG GTTGGGTCGG CCATCCTCGT CCCGTCCTCC 60
 GCCCGCCCTT GCCCGCGGCC CAGGGATCCT CCAGCTCCTT TCGCCCGCGC CCTCCGTTCC 120
 CTCGGGACAC CATGGACAAG TTTTGGTGGC ACGCAGCCTG GGGACTCTGC CTGCTGCGCG 180
 TGAGCCTGGC GCAGATCGAT TTGAATATAA CCTGCCGCTT TGCAGGTGTA TTCCACGTGG 240
 AGAAAAATGG TCGCTACAGC ATCTCTCGGA CGGAGGCGCG TGACCTCTGC AAGGCTTTCA 300
 ATAGCACCTT GCCACAATG GCCCAGATGG AGAAAGCTCT GAGCATCGGA TTTGAGACCT 360
 GCAGGTATGG GTTCATAGAA GGGCATGTGG TGATTCCCGG GATCCACCCC AACTCCATCT 420
 GTGCAGCAAA CAACACAGGG GTGTACATCC TCACATCCAA CACCTCCAG TATGACACAT 480
 ATTGCTTCAA TGCTCTAGCT CCACCTGAAG AAGATTGTAC ATCAGTCACA GACCTGCCCA 540
 ATGCTTTTGA TGGACCAATT ACCATAACTA TTGTAAACCG TGATGGCACC CGCTATGTCC 600
 AGAAAGGAGA ATACAGAAAG AATCTGAAG ACATCTACCC CAGCAACCTT ACTGATGATG 660
 ACGTGAGCAG CGGTCTCTCC AGTGAAAGGA GCAGCACTTC AGGAGGTTAC ATCTTTTACA 720
 CCTTTTCTAC TGTACACCCC ATCCAGACG AAGACAGTCC CTGGATCACC GACAGCACAG 780
 ACAGAAATCC TGCTACCACT AGTCTTCAA ATACCATCTC AGCAGGCTGG GAGCCAAATG 840
 AGAAAAATGA AGATGAAAGA GACAGACACC TCAGTTTTTC TGGATCAGGC ATTGATGATG 900
 ATGAAGATTT TATCTCCAGC ACCATTCAA CCACACCAAG GGCTTTTGAC CACACAAAC 960
 AGAACCAAGA CTGGACCCAG TGGAAACCAA GCCATTCAA TCCGGAAGTG CTAATTTCAGA 1020
 CAACACAGAG GACTGCTGAT GTAGACAGAA ATGGCACACC TGCTTTATGA GGAACCTGGA 1080
 ACCCAGAAAG ACACCTCTCC CTCAATCACC ATGAGCATCA TGAGGAAGAA GAGACCCAC 1140
 ATTCTACAAG CACAATCCAG GCAACTCTTA GTAGTACAAC GGAAGAAACA GCTACCCAGA 1200
 AGGAACAGTG GTTTGGCAAC AGATGGCATG AGGGATATCG CCAACACACC AGAGAAGACT 1260

5
10
15
20

```
CCCATTCGAC AACAGGGGAC GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
GGACAACACC AAGCCCAGAG GACAGTTCTT GGACTGATTT CTTCAACCCA ATCTCACACC 1380
CCATGGGACG AGGTCATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
CGCTTCAGCC TACTGCAAAAT CCAAAACACAG GTTTGGTGGG AGATTTGGAC AGGACAGGAC 1500
CTCTTTCAAT GACAAAGCAG CAGAGTAATT CTCAGAGCCT CTCACATCA CATGAAGGCT 1560
TGGAAGAAGA TAAAGACCAT CCAACAACCT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
TCACAGGTGG AAGAAGAGAC CCAAATCATT CTGAAGGCTC AACTACTTTA CTGGAAGGTT 1680
ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCCACTG ACCTCAGCTA 1740
AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTTGGAGA TTCCAACTCT AATGTCAATC 1800
GTTCCCTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCAT ACCACTCATG 1860
GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAAC ACAACCTCTG 1920
GTCTTAAGAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTGGGCATCC CTCTTGGCCT 1980
TGGCTTTGAT TCTTGCAGTT TGCAATGCAG TCAACAGTCG AAGAAGGTGT GGGCAGAAGA 2040
AAAAGCTAGT GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
ACGAGAGAGC CAGCAAGTCT CAGGAAATGG TGCATTGGT GAACAAGGAG TCCTCAGAAA 2160
CTCCAGACCA GTTTATGACA GCTGATGAGA CAAGGAACCT GCAGATGTG GACATGAAGA 2220
TTGGGGTGTA ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTGGGAA ACATAACCAT 2280
TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT 2340
TTTTTAGCAT AAAATTTTCT ACTCTTAAAA AAAAAA AAAAAA
```

Seq ID NO: 132 Protein sequence:
Protein Accession #: AAH04372

25
30
35
40

```
1 11 21 31 41 51
MDKFWHAAW GLCLVPLSLA QIDLNITCRF AGVFHVEKNG RYSISRTEAA DLCKAFNSTL 60
PTMAQMEKAL SIGFETCRYG FIEGHVVIPIR IHPNSICAAH NTGVYILTSN TSOYDITYCFN 120
ASAPPEEDCT SVTDLNPAFD GPITITIVNR DGTRYVQKGE YRTNPEDIYP SNPTDDDVSS 180
GSSSSRSSTS GGYIFYTFFST VHPIDEDSP WITDSTDRIP ATSTSSNTIS AGWEPNEENE 240
DERDRHLSPS GSGIDDDDEF ISSTISTTFR AFDHTKQND WTQWNPESHN PEVLQQTTR 300
MTDVRNRGTT AYEGRWNPEA HPPLIHHEHH EEEETPHSTS TIQATPSSTT BETATQKEQW 360
FGNRWHEGYR QTPREDSSHST TGTAASAAHT SHPMQGRTP SPEDSSWTFD FNPISHPMGR 420
GHQAGRRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSSNSQSF STSHEGLEED 480
KDHPTTSTLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTSY YPHTKESRTF LPVTSKTSKS 540
FGVTAVTVGD SNSNVNRSLS GDQDTFHPSG GSHHTHGES DGHSHGSQEG GANTTSGPIR 600
TPQIPWLIIL LALLLALALI LAVCIAVNSR RRCGQKKLV INSGNGAVED RKPGLNGEA 660
SKSQEMVHLV NKESSETPDQ FMTADETRNL QNVDMKIGV
```

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_002882
Coding sequence: 150-755

45
50
55
60

```
1 11 21 31 41 51
CGAGGTTCCG GTGTGGGGC GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GGCAGCAGAC 60
GCGGAGGGAA GGAGCTACGA GTAGCCGCGC AGAGGCGCGC GAGCCAGCGA CGACCGACCC 120
AGCCGAGCGC CGCCGCGCGC CGCGCCCCCA TGGCGGCCGC CAAGGACACT CATGAGGACC 180
ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCTCAGTTT GAGCCAATAG 240
TTTCTCTTCC TGAGCAAGAA ATTAACAAC TGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
TGCGGGCAAA ACTGTCCGA TTTGCCTCTG AGAACGATCT CCCAGAATGG AAGGAGCGAG 360
GCACTGGTGA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGCATCCGC CTCCTCATGC 420
GGAGGGACAA GACCCGTAGG ATCTGTGCCA ACCACTACAT CACGCGGATG ATGGAGCTGA 480
AGCCCAACGC AGGTAGCGAC CGTGCCTGGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
AGTGCCCAAA GCCAGAGCTG CTGGCCATCC GCTTCCTGAA TGCTGAGAAT GCACAGAAAT 600
TCAAAACAAA GTTTGAAGAA TGCAGGAAAG AGATCGAAGA GAGAGAAAAG AAAGCAGGAT 660
CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
TCTCTTTCTT TTCTTTT TAAAAAATTT TACCCTGCCC CTCTTTTTCG GTTTGTTTTT 840
ATTCTTTTAT TTTTACAAGG GACGTTATAT AAAGAACTGA ACTC
```

Seq ID NO: 134 Protein sequence:
Protein Accession #: NP_002873

65
70

```
1 11 21 31 41 51
MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELFK MRKLFRFAS 60
ENDLPEWKER GTGDVKKLKH KEKGAIKLLM RRDKTLKICA NHYITPMEL KPNAGSDRAW 120
VWNTHADPAD ECPKPELLAI RFLNAENAQK FKTKFEECRK EIEEREKAG SGKNDHAEKV 180
AEKLEALSVK EETKEDAEK Q
```

Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 277-742

75
80
85

```
1 11 21 31 41 51
CCCAACCTGG GGGGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC 60
TCCTCGAGC ACTCGCTCAC GCGCTCCCTT TGCCCTGAAA GATACCGCGG TCCCTCCAGA 120
GGATTGTAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGAGGAGG GAAAGAGGAG 180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGGC CTCGGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CGGGAGCAG CATGGAGCCG CGGCGGGGGA GCAGCATGGA 300
GCCTTCGGCT GACTGGCTGG CCACGGCCGC GGCCCGGGGT CGGGTAGAGG AGGTGCGGGC 360
GCTGCTGGAG GCGGGGCGCG TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA 420
GGTCATGATG ATGGGCGCGC CCGGAGTGGC GGAGCTGCTG CTGCTCCAGC GCGCGGAGCC 480
```

CAACTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGAC GACGCTGCC GGGAGGGCTT 540
CCTGGACACG CTGCTGTGTC TGACACGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCCTG 600
GGGCGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGGTAOCT 660
GGCGCGGCT GCGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
TCCCTCAGAC ATCCCGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACGTCC CCGCCACAA CCCACCCGCG 840
TTTCGTAGTT TTCAATTTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCACTG TGTGGAGTT TTCTGGAGTG 1020
AGCACTCAGC CCCTAAGCGC ACATTCATGT GGGCATTCTT TGCGAGCCTC GCAGCCTCCG 1080
GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAC TAGGG AAGCTCAGGG GGGTTACTGG 1140
CTTCTCTGA GTCACTGTC TAGCAATGG CAGAACCAA GCTCAATAA AAATAAATA 1200
ATTTTCATTC ATTCACTC

Seq ID NO: 136 Protein sequence:
Protein Accession #: NP_000068.1

1 11 21 31 41 51
MEPAAGSSME PSADWLATAA ARGRVEEVRA LLEAGALPNA PNSYGRRIPIQ VMMGSGARVA 60
ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAE 120
LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: NM_058196.1
Coding sequence: 104-421

1 11 21 31 41 51
TGTGTGGGG TCTGCTTGGC GTTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG 60
GCCCCACCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
CGAGTGGCG GAGCTGTGTC TGCTCCACGG CGCGGAGCCC AACTGCGCGG ACCCGGCCAC 180
TCTACCCGA CCGGTGCAAG AGCTGCCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCTGG GGCCTCTGCG CCGTGGACCT 300
GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CCGGGGGCAC 360
CAGAGGCAGT AACCATGCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCGATTG 420
AAGAACCAG AGAGGCTCTG AGAAACCTCG GGAACCTTAG ATCATCAGTC ACCGAAGGTC 480
CTACAGGGCC ACAACTGCC CCGCCACAAC CCACCCCGCT TTGTAGTTT TCATTTAGAA 540
AATAGAGCTT TTAATAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
TAAATGTCCA TTATATCAT TTTTATATA TTCCTATAAA AATGTAAAA AGAAAAACAC 660
CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CCTAAGCGCA 720
CATTATGTC GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTCATGACA 780
AGCATTTTGT GAAC TAGGG AGCTCAGGG GGTACTGGC TTCTCTTGA TCACTACTGT 840
AGCAATGGC AGAACCAAG CTCAAATAAA AATAAATAA TTTTCATTCA TTCCTC

Seq ID NO: 138 Protein sequence:
Protein Accession #: NP_478103.1

1 11 21 31 41 51
MMGSGARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAH ARLDVRDAWG 60
RBPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAEGP SDIPD

Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272-684

1 11 21 31 41 51
CCCAACCTGG GCGGACTTCA GTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCAC 60
TCCTCCGAGC ACTCGCTCAC GCGCTCCCT TGCTGGAAA GATACCGCGG TCCCTCCAGA 120
GGATTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGAGGAGG GAAAGAGGAG 180
GGGCTGCGTG GTACACAGAG GTTGGGGCGG ACCGCTGCG CTGCGCGGCT GCGGAGAGGG 240
GGAGAGCAGG CAGCGGGCGG CCGGGAGCAG CATGGAGCCG CGCGCGGGGA GCAGCATGGA 300
GCCGCGCGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG 360
GGGTGCGGTA GAGGAGTGC GGGCGCTGCT GGAGGCGGGG CGCTGCCCA ACGCACCGAA 420
TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCAGCGGGAG CAGGGGATGG 480
CGGGCGACTC TGGAGGACGA AGTTTGACAG GGAATTGGAA TCAGGTAGCG CTTGATTCT 540
CCGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAGGG GTTTGTAATC ACAGACCTCC 600
TOCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCAACGCGCT 660
ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
TCATGATGAT GGGCAGCGCC OGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA 780
ACTGCGCGCA CCCGCCACT CTCACCGSAC CCGTGACGCA CGCTGCCCGG GAGGGCTTCC 840
TGGACACGCT GGTGGTGTCT CACCGGGCCG GGGCGCGGCT GGAOGTGGC GATGCCTGGG 900
GCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCGA CGGTACCTGC 960
GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
CCTCAGACAT CCCCGATTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
CATCAGTCA CAGAGGTCTC ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCTTTTAA CGTAGATATA 1200
TGCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
TGTAATAAAG AAAAACACCG CTCTGCTTTC TGCATGTGT TGGAGTTTTC TGGAGTGAGC 1320
ACTCAGCCCC TAAGCGCACA TTATGTGGG CATTCTTTC GAGCCTCGCA GCCTCCGGAA 1380
GCTGTGAGT TCATGACAAG CATTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGGCTT 1440
CTCTGAGTC ACACGTCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAAAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

1 11 21 31 41 51
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL EAGALPNAPN SYGRRPIQVG 60
RRSAAGAGDG GRLWRKTFAG ELESSESASIL RKGRLPGEF SEGVCNHRPP PGDALGAWET 120
KEEE

Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

1 11 21 31 41 51
CCTCCTACG GCGCCTCCG GCAGCCCTTC CCGCTGCGC AGGGCTCAGA GCGTTCOGA 60
GATCTTGAG GTCGGGTGG GAGTGGGGGT GGGGTGGGG TGGGGTGAA GGTGGGGGGC 120
GGGCGGCTC AGGAAGGCG GGTGCGGCC TCGGGGGGG AGATGGGCAG GGGCGGTGC 180
GTGGGTCCCA GTCTGCAGT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAG 240
GGGCGGCAG CGGTGCCGA GCTCGGCCCT GGAGGCGGCG AGAACATGGT GCGCAGGTTC 300
TTGGTGACCC TCCGATTTC GCGCGCGTG GCGCGCGCG GAGTGAGGT TTTCTGTGT 360
CACATCCGCG GGTCAAGGG GAGTGGGCA GCGCCAGGG GCGCGCGCG TGTGGCCCTC 420
GTGCTGATG TACTGAGGAG CCAGCGTCTA GGGCAGCAG CGCTTCTAG AAGACCAGT 480
CATGATGAT GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCACGGCG CGGAGCCCAA 540
CTGCGCGGAC CCGCCACTC TCACCGGACC CGTGACGAC GCTGCCGGG AGGGCTTCCT 600
GGACACGCTG GTGTGTCTG ACCGGGCGCG GCGCGGCTG GACGTGCGCG ATGCTGGGG 660
CCGTCTGCCC GTGACCTGG CTGAGGAGCT GGGCCATGCG GATGTGCGAC GGTACCTGCG 720
CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCGGATTGAA AGAACAGAG AGGCTCTGAG AACCTCGGG AAACCTTAGAT 840
CATCAGTCAC CGAAGTCTCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 900
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAATGTCC TGCCTTTTAA CGTAGATATA 960
TGCTTCCCC CACTACCGTA AATGTCCAT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAAACACCG CTCTGCGCTT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTCTTGC GAGCCTCGCA GCCTCGGAA 1140
GCTGTGACT TCATGACAG CATTTTGTA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCTT 1200
CTCTGAGTC ACCTGCTAG CAAATGGCAG AACCAAGCT CAAATAAAAA TAAATAATT 1260
TTCATTCAIT CACTC

Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

1 11 21 31 41 51
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AAELGPGGGE NMVRRFLVTL RIRACGPPR 60
VRVFFVHPR LTGEWAAPGA PAAVALVLM LRSQRLGQP LPRRPGHDDG QRPSSGAAAA 120
PRRGAQLRRP RSHSPTARR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

1 11 21 31 41 51
GAAATGTCAC ACTTAAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT 60
GATAAGAGA GACAGAGACT TTTGGAGAAA ATTCGAGTCC TTGAGGCTGA GAAGGAGAAG 120
AATGCTTATC AACTCACAGA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG 180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA 240
AGGAGGGAGC AGGTGTGAA AGCCTTATCT GAAGAGAAAG ACCTATTGAA ACAACAGTTG 300
TCTGCTGCAA CCTCAGCAAT TGCTGAACTT GAAAGCAAAA CCAATACACT CCGTTTATCA 360
CAGACTGTGG CTCGAACTG CTTCACCTCA TCAATAAATA ATATTGATGA AATGGAAATA 420
CAGCTGAAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA 480
GTCTATGTAA AAGGACTTTT AGCAAGATC TTTGAGTTGG AAAAGAAAAC GGAAACAGCT 540
GCTCATTCAC TCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTTATCT TCAAGAAGAG 600
AAGCAGAAAT GTTCAACGCA TCTCTTGCCA AGTGCAAAAA AAGATCTTGA GGTGAAACGA 660
CAAACATAA CTGAGCTGAG TTTTGAACCT AGTGAATTTC GAAGAAAATA TGAAGAAACC 720
CAAAAGAAAG TTCACAATTT AAATCAGCTG TTGTATTCAC AAAGAAGGGC AGATGTGCAA 780
CATCTGGAAG ATGATAGGCA TAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT 840
ATTGCTAGGG GAAACTTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC 900
CAGTCTCTTT ACACATCTCT GCTAAAGCAG CAAGAAGAAC AAACAAGGCT AGCTCTGTTG 960
GAACAACAGA TGCAGGCATG TACTTTAGAC TTTGAAAATG AAAAAGCTCGA CCGTCAACAT 1020
GTGAGCATC AATTGATGT AATTCTTAAG GAGCTCCGAA AAGCAAGAAA AAATAACACA 1080
GTTGGAATCC TTGAACAGC TTCATGAGTT TGCCATCACA GAGCCATTAG TCACTTTCCA 1140
AGGAGAGACT GAAACAGAG AAAAAGTTGC CCGCTCACC AAAAGTCCCA CTGCTGCACT 1200
CAATGGAAAC CTGCTGGAAT GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG 1260
CGATCTGCTT GTCCATGTGG AATCTGTTC AAAGTAGCAA AATAAGTATT TGTTTTGATA 1320
TTAAAGGATT CAATACTGTA TTTTCTGTTA GCTTGTGGGC ATTTTGAATT ATATATTCCA 1380
CATTTTGCAT AAAACTGCTT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT 1440
CTTTTAGGCT GCTGTGCATT TCTCTTGCCA GTGATACCTC CCTGACATGG TTCATCATCA 1500
GGCTGCAATG ACAGAAATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGCACTGTC 1560
AAAATACTTG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGGTTAAT GCACCAGCAA 1620
GCAAAATATT TTATGTTTCG GGGGTTTGA AAAATCAAAG ATAATTAACC AAGGATCTTA 1680
ACTGTGTTCC CATTTTAT CCAAGCACTT AGAAACCTA CAATCCTAAT TTTGATGTCC 1740
ATTGTTAAGA GGTGGTGATA GATACTATTT TTTTTCATA TTGTATAGCG GTTATTAGAA 1800

AAGTTGGGGA TTTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
 TCCCCAATCT TGTTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
 CACACAATGT TTTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
 TCTGCTTAG CTAATAATGT TAAATAAATC TTTAATAAAC CCATGTAGCC CTCTCATTGT 2040
 ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCATGTAA TGATCAGATC 2100
 TTTGTTTGTG TGAACAGGTA TTTTATACA TGCCTTTTGT AAACCAAAA CTTTAAATTT 2160
 TCTCAGGTT TTCTAACATG CTTACCCTG GGCTACTGTA AATGAGAAAA GAATAAAATTT 2220
 ATTTAATGTT TT

Seq ID NO: 144 Protein sequence:
 Protein Accession #: NP_060601

1 11 21 31 41 51
 MEIQLKDALE KNQQLVVDQ QREVVYKGLL AKIFELEKKT ETAHSLPQQ TKKPESEGYL 60
 QEEKQKCYND LLASAKKDL VERQTITQLS FELSEFRKY EETQKEVHNL NQLLYSQRRRA 120
 DVQHLEDDRH KTEKIQLKRE ENDIARGKLE EEKKRSEELL SQVQSLYTSL LKQEEQTRV 180
 ALLEQQMQAC TLDPENKELD RQHVQHQLHV ILKELRKARK NNTVGILETA S

Seq ID NO: 145 DNA sequence
 Nucleic Acid Accession #: NM_001168
 Coding sequence: 50..478

1 11 21 31 41 51
 CCGCCAGATT TGAATCGCGG GACCCGTTGG CAGAGGTGGC GGCGGCGGCA TGGGTGCCCC 60
 GACGTTGCCC CCTGCTTGGC AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
 CTGGCCCTTC TTGAGGGGCT GCGCTGCGAC CCGGAGCGG ATGGCCGAGG CTGGCTTCAT 180
 CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCCACTGT TTCTTCTGCT TCAAGGAGCT 240
 GGAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
 CGCTTCTCTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTTGGTGAAT TTTTGAAACT 360
 GGACAGAGAA AGAGCCAAGA ACAAAATTGC AAAGGAAACC AACAATAAGA AGAAAGAATT 420
 TGAGGAAACT GCGAAGAAAG TCGCCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
 CCTCTGGCGG GAGCTGCGCT GTCCAGAGT GGCTGCACCA CTTCCAGGGT TTATTCCCTG 540
 GTGCCACACG CCTTCTGTG GGCCCTTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
 CAAATTAGAT GTTTCAACTG TGTCTCTGTT TTGTCTTGAA AGTGGCACC AAGGTGCTTC 660
 TGCTGTGCA GCGGCTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTT 720
 GGGGCTCAT TTTTGTGTT TTGATTCCCG GGCTTACCAG GTGAGAAGT AGGGAGGAAG 780
 AAGGCAGTGT CCTTTTGTCT AGAGCTGACA GCTTTGTTCG CGTGGGCGA GCCTTCCACA 840
 GTGAATGTGT CTGGACCTCA TGTGTGTGAG GCTGTACAG TCCTGAGTGT GGAATTGGCA 900
 GGTGCTGTT GAATCTGAGC TGCAAGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
 ACAGTTTTTT TGTGTGTGTG TTTTGTGTT TTTTGTGTT GGTAGATGCA TGACTTGTGT 1020
 GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCCTCTACT GTTTAAACA ATGGCTTTCT 1080
 TATTTGTGTT GAATTGTTAA TTCACAGAA AGCACAACCT ACAATTAAAA CTAAGCACAA 1140
 AGCCATTCTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAATAG 1200
 AGTGATAGGA AGCGTCTGGC AGATACTCCT TTGCGCACTG CTGTGTGATT AGACAGGCC 1260
 AGTGAGCCGC GGGGCACATG CTGGCCGCTC CTCCCTCAGA AAAAGGCAGT GGCCTAAATC 1320
 CTTTTTAAT GACTTGCTC GATGCTGTGG GGGACTGGCT GGGCTGTGTC AGGCCGTGTG 1380
 TCTGTACGCC CAACCTTCAC ATCTGTACAG TTCTCCACAC GGGGAGAGGA CGCAGTCCGC 1440
 CCAGGTCCCC GCTTCTTTTG GAGGCAGCAG CTCCGCGCAG GCTGAAGTCT GGCCTAAGAT 1500
 GATGGATTGT ATTGCGCCTC CTCCTGTGCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
 GCTGGAACC TCTGGAGGTC ATCTCGGCTG TTCCTGAGAA ATAAAAAGCC TGTCTATTC

Seq ID NO: 146 Protein sequence:
 Protein Accession #: NP_001159

1 11 21 31 41 51
 MGAPTLPPAW QPFLKDHRS TFKNWPFLG CACTPERMAE AGPIHCPTEN EPDLAQCFPC 60
 FKELEGWEPD DDPIEHKKH SSGCAFLSVK KQFBEELTGE FLKLDREKAK NKIAKETNNK 120
 KKEFEETAKK VRRALBQLAA MD

Seq ID NO: 147 DNA sequence
 Nucleic Acid Accession #: NM_014176.1
 Coding sequence: 127-720

1 11 21 31 41 51
 GCGCGCAGCG CTGTACCCC GTTGGTCCGC GCGTGTGCTG GTTGTGAGGG GTGTAGCTC 60
 AGTGCATCCC AGGCAGCTCT TAGTGTGGAG CAGTGAACCT TGTGTGGTTC CTCTACTTGT 120
 GGGATCATGC AGAGAGCTTC ACCTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
 CCCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATAGG ATGACCTGCG AGCTCAAATA 240
 TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
 GAGAGGTACC CATTGTAACC TCCTCAGATC CGATTCTTCA CTCCAATTTA TCATCAAAAC 360
 ATTGATTCTG CTGGAAGGAT TTGTCTGGAT GTTCTCAAAT TGCCACCAAA AGGTGCTTGG 420
 AGACCATCCC TCAACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTCAGAACCC 480
 AACCCGTATG ACCCGTCTAT GGCTGACATA TCCTCAGAA TTAATATATA TAAGCCAGCC 540
 TTCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
 GAGGAAGAGA TGCTTGATAA TCTACCAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
 CAGAAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTTTCATC TGATGTTTAG 720
 GGGACTTGTC CTGGTTTATC TTAGTTAATG TGTCTTTTGC CAAGGTGATC TAAGTTGCCT 780
 ACCTTGAAT TTTTTTTAAA TATATTGAT GACATAATTT TTGTGTAGTT TATTTATCTT 840
 GTACATATGT ATTTTGAAT CTTTAAACC TGAAAAATA ATAGTCATTT AATGTTGAAA 900

Seq ID NO: 148 Protein sequence:
 Protein Accession #: NP_054895.1

1 11 21 31 41 51
 | | | | |
 MQRASRLKRE LMLATEPPPP GITCWQDKDQ MDDLRAQILG GANTPYEKGV FKLEVIIPER 60
 YPFEPPIQIRF LTPIYHPNID SAGRICLDVL KLPPKGAWRP SLNIATVLTS IQLLMSEPNP 120
 DDPLMDISS EFKNKPAFL KNARQWTEKH ARQKQRADEE EMLDNLPEAG DSRVHNSTQK 180
 RKASQLVGIE KKFHPDV

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_003812
 Coding sequence: 224-2722

1 11 21 31 41 51
 | | | | |
 TCCTCTGCGT CCCGCCCGCG GAGTGGCTGC GAGGCTAGGC GAGCCGGGAA AGGGGGCGCC 60
 GCCCAGCCCC GAGCCCCGCG CCCCGTGCCT CGAGCCCGGA GCCCCTTGCC CGCGGCGGCA 120
 CCATGCGCGC CGAGCCCGCG TGACCGGCTC CGCCCGCGGC CGCCCGCGAG CTAGCCCGGC 180
 GCTCTGCGCG GCCACACGGA GCGCGCGCCG GGAGCTATGA GCCATGAAGC CGCCCGGCGAG 240
 CAGCTGCGCG CAGCCGCCCC TGGCGGGCTG CAGCCTTGCC GCGCTTCTCT GCGGCCCCCA 300
 ACGCGGCCCG GCCCGCTCGG TGCTTGCCAG CGCCCGCGGC CGCAOGCCGC CCTGCGCGCT 360
 GCTTCTCGTC CTTCTCCTGC TGCTCCGCT CGCCCGCTCG TCCCGGCCCC GCGCTGGGG 420
 GGCTGCTGCG CCCAGCGCTC CGCATTGGAA TGAAGTGA GAAAAAATT TGGGAGTCTT 480
 GGCAGATGAA GACAATACAT TGCAACAGAA TAGCAGCAGT AATATCAGTT ACAGCAATGC 540
 AATGCAGAAA GAAATCACAC TGCTTCAAG ACTCATATAT TACATCAACC AAGACTCGGA 600
 AAGCCCTTAT CAGCTTCTTG ACACAAAGGC AAGACACCAG CAAAAACATA ATAAGGCTGT 660
 CCATCTGGCC CAGGCAAGCT TCAGATTGA AGCCTTCGGC TCCAAATTCA TTCTTGACCT 720
 CATACTGAAC AATGGTTGTG TGTCTTCTGA TTATGTGGAG ATTCACTACG AAAATGGGAA 780
 ACCACAGTAC TCTAAGGGTG GAGAGCACTG TTAATACCAT GGAAGCATCA GAGGCGTCAA 840
 AGACTCAAAG GTGGCTCTGT CAACCTGCAA TGGACTTCAT GGCATGTTTG AAGATGATAC 900
 CTTCGTGATAT ATGATAGAGC CACTAGAGCT GGTTCATGAT GAGAAAAGCA CAGGTGCGAC 960
 ACATATAATC CAGAAAACCT TGGCAGGACA GTATTCTAAG CAAATGAAGA ATCTCACTAT 1020
 GGAAAGAGGT GACCAAGTGC CCTTTCTCTC TGAATTACAG TGGTTGAAAA GAAGGAAGAG 1080
 AGCAGTGAAT CCATCAGCTG GTATATTGTA AGAAATGAAA TATTTGGAAC TTATGATTGT 1140
 TAATGATCAC AAAACGTATA AGAAGCATCG CTCTTCTCAT GCACATACCA ACAACTTTGC 1200
 AAAGTCCGTG GTCAACCTTG TGGATTCTAT TTACAAGGAG CAGCTCAACA CCAGGGTTGT 1260
 CCTGTGGCTG GTAGAGACCT GGACTGAGAA GGATCAGATT GACATCACCA CCAACCTGT 1320
 GCAGATGCTC CATGAGTTCT CAAAATACCG GCAGCGCATT AAGCAGCATG CTGATGCTGT 1380
 GCACCTCATC TCGCGGGTGA CATTTCATA TAAGAGAAGC AGTCTGAGTT ACTTTGGAGG 1440
 TGTCTGTTCT CGCACAGAGG GAGTTGGTGT GAATGAGTAT GGTCTTCCAA TGGCAGTGGC 1500
 ACAAGTATTA TCGCAGAGCG TGGCTCAAAA CCTTGGAAATC CAATGGGAAC CTTCTAGCAG 1560
 AAAGCCAAA TGTGACTGCA CAGAATCCTG GGGTGGCTGC ATCATGGAGG AAACAGGGGT 1620
 GTCCCATCTT CGAAATTTT CAAAGTGCAG CATTTTGGAG TATAGAGACT TTTTACAGAG 1680
 AGGAGGTGGA GCCTGCGCTT TCACAGGGCC AACAAAGCTA TTTGAGCCCA CGGAATGTGG 1740
 AAATGGATAC GTGGAAGCTG GGGAGGAGTG TGATTGTGGT TTTTATGTGG AATGCTATGG 1800
 ATTATGCTGT AAGAAATGTT CCCTCTCCAA CGGGGCTCAC TGCAGCGACG GGCCCTGCTG 1860
 TAACAATACC TCGTGTCTTT TTCAAGCCAG AGGGTATGAA TGCCGGGATG CTGTGAACGA 1920
 GTGTGATATT ACTGAATATT GTACTGGAGA CTCTGGTCAG TGCCCAACAA ATCTTCATAA 1980
 GCAAGACGGA TATGCATGCA ATCAAAATCA GGGCGCTGTC TACAATGGCG AGTGCAAGAC 2040
 CAGAGACAA CAGTGTGAGT ACATCTGGGG AACAAAGGCT GCAGGGTCTG ACAAGTTCTG 2100
 CTATGAAAAA CTGAATACAG AAGGCACTGA GAAGGGAAGC TGCGGGAAGG ATGGAGACCG 2160
 GTGGATTCTG TCGAGCAATC ATGATGTGTT CTGTGGATTG TTAATCTGTA CCAATCTTAC 2220
 TCGAGCTCCA CGTATTGGTC AACTTCAGGG TGAGATCATT CCAACTTCCT TCTACCATCA 2280
 AGGCCGGGGT ATTGACTGCA GTGGTGCCCA TGTAGTTTGA GATGATGATA CGGATGTGGG 2340
 CTATGTAGAA GATGGAAGCG CATGTGGCCC GTCTATGATG TGTATTGATC GGAAGTGCCT 2400
 ACAAATTCAG GCCCTAAATA TGAGCAGCTG TCCACTCGAT TCCAAGGTA AAGTCTGTTC 2460
 GGGCCATGGG GTGTGTAGTA ATGAAGCCAC CTGCAATTTG GATTTCACCT GGGCAGGGAC 2520
 AGATTGCGAGT ATCCGGGATC CAGTTAGGAA CCTTCACCCC CCAAGGATG AAGGACCCAA 2580
 GGGTCTAGT GCCACCAATC TCATAATAGG CTCCATCGCT GGTGCCATCC TGGTAGCAGC 2640
 TATTGTCTTT GGGGGCAGAG GCTGGGGATT TAAAAATGTC AAGAAGAGAA GGTTCGATCC 2700
 TACTCAGCAA GCGCCCATCT GAATCAGCTG CGCTGGATGG ACACCGCCTT GCACTGTTGG 2760
 ATTCTGGGTA TGACATACTC GCAGCAGTGT TACTGGAATC ATTAAGTTTG TAAACAAAAC 2820
 CTTTGGGTGG TAATGACTAC GGAGCTAAAG TTGGGGTGAC AAGGATGGGG TAAAGAAAAA 2880
 CTGTCTCTTT TGGAAATAAT GTCAAAGAAC ACCTTTCACC ACCTGTGAGT AAACGGGGGA 2940
 GGGGGCAAAA GACCATGCTA TAAAAAGAAC TGTTCAGAAA TCTTTTTTTT TCCCTAATGG 3000
 ACGAAGGAAC AACACACACA CAAAAATTAA ATGCAATAAA GGAATCATTAAAA

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_003803

1 11 21 31 41 51
 | | | | |
 MKPPGSSSRQ PPLAGCSLAG ASCGPQRGPA GSVPASAPAR TPPCRLLLV LLLPPLAASS 60
 RPRAWGAAAP SAPHWNETA EKNLGVLADEE NTLQONSSSN ISYSNAMQKE ITPSLRIIYY 120
 INQDSESPYH VLDTKARHQK KHNKAVHLAQ ASFQIEAFGS KPILDLLINN GLLSSDYVEI 180
 HYENGKPKQYS KGGHECHYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLELVHDE 240
 KSTGRPHIQ KTLAQYYSKQ MNKLTMERGD QWPLSELQW LKRRKRAVNP SRGIFEEMKY 300
 LELMIWVNDHK TYKKHRS SHA HTNNAFASV NLVDSIYKEQ LNTRVVLVAV ETWTEKDQID 360
 ITTNFVQMLH EFSKYRQRIK QHADAVHLIS RVTFFHYKRSS LSYFGGVCSR TRGVGVNEYG 420
 LPMAVAQVLS QSLAQNLG IQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR RFSKCSILEY 480
 RDLFQRGGGA CLFNPRITKLF BPTCEGNGYV EAGEECDCGF HVECYGLCCK KCSLSNGAHC 540
 SDGPCCNNTS CLFPQRGYEC RDAVNEDCIT EYCTGDSGQC PPNLHKQDGY ACNQNGRCY 600
 NGECKTRDNQ CQYIWTGTRAA GSKDFCYEKL NTEGTEKGNC GKDGDRNIQC SKHDVFCGFL 660

LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGARHVLD DTDVGVYVED GTPCGPSMMC 720
 LDRKCLQIQ A LNMSSCLPDS KGRVCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPF 780
 KDEGPKGPSA TNLIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI

5

Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: NM_023915
 Coding sequence: 250-1326

10 1 11 21 31 41 51
 | | | | |
 GGCAAGAGGG TTTCTGTTTC ATGCTTTACC AGAAAATCCA CTTCCTGACC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 CCAACGCTC ATCGTGTCCC AAGTGTGTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240
 15 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360
 AATGAATTTG ACACAATTTG CTGCGCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTGCA 540
 20 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATCTCTG CAGATACACT 600
 TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCAAT 660
 GATCGCTATC TGAAGGTGGT CAAGCCATTG GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGSTTT TATCTGTTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
 25 ATCCTGACAA ATGGTCAGGC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT 840
 CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGTGTA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGTTTGT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 30 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCTTGGATC CAATAATTTA CTTTTCATG 1200
 TGTAGGTGAT TTTCAAGAG GCTGTTCAAA AAATCAAATA TCAGAACCCAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
 GTGTAGGCTT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
 35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
 Protein Accession #: NP_076404

40 1 11 21 31 41 51
 | | | | |
 MGENLTAKL PNNEHMQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFFHI RNKTSFIYFL KNIVVADLIM TLTFFFRIVH DAGFGPWYFK FILCRYTSVL 120
 45 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTFTKV LSVCVWVIMA VLSLPIIILT 180
 NQOPTEDNIH DCSKLKSPGL VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSSRQF 240
 ISQSSRKRRH NQSIIRVVAV PFTCFPLPYHL CRIPFTFPHL DRLLDESAQK ILVYCKEITL 300
 FLSACNVCLD PIIFYFMCRS FSRRLFKKSN IRTRESIERS LQSVRRSEVR IYYDYTDV

50

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: D80008.1
 Coding sequence: 149-739

55 1 11 21 31 41 51
 | | | | |
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCGCGCG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
 60 AGTTCGTGAG GAGATGAAGG CTTGTATGA ACAAACCCAG TCTGATGTGA ATGAAGCAAA 300
 GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAATTT CGACACTGTT CTCTGTTAAG 360
 AAATCGACGC TGCACCTGTA CATACCTGTA TGACCGCTTG CTTGCGATCA GAGCATCAG 420
 ATGGGAATAT GGTAGCTGCT TGCCAAATGC ATTACGATT CACATGGCTG CTGAAGAAAT 480
 GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA 540
 65 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG 600
 GTGTCTAAAA GACTATGGAG AATTGGAAGT TGATGATGGC ACTTCAGTCC TATTAATAAA 660
 AAATAGCCAG CACTTTTATC CTGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCCT 720
 GGAGCACATC CTGTCATGAC CATGCGCCGA GGCACCTCCA GGCCTCACTC AACTCATGGA 780
 CTCCTCTGTA CTCACCTCTC CCACCACTCC CTTACCTCC CTCTTTGATT TTAGAAGCTA 840
 70 TAGACATTGT TTAAGATAAC TAAGAATACT TGGCTAAGAA GTATAATTG CTAACATATA 900
 AGGACTTTCT TTTTAAATG TGTACACTA TTCTTCTTAC TCTTTTGTG TTTTGGTTT 960
 GTTTTGTAGA GACTGTCTCA CTATGTTGCC CAAGCTGGTC TCAAACCTCT GGCCTCAAGC 1020
 AGTCTCCCA CTTAGCTTC TCAAAGTGTG GAGATCACAG GCGTGAGCCA CTGACCCCG 1080
 CCCCTACTCC TTTTCTAAT AAGCTGTATC TGTAATCACA GCATTCTTAC AGTTGTTACA 1140
 75 GTGTGTTTTT TAAATGAAAG TAAACATGGT TACATTGAA TCTCTTAAAT AAGCAGTCAC 1200
 TTGGCTGGAC AGGAAGAGG TAGATCCTGT GTGTCTTGT TCTGGTCAAT GTGATTGTA 1260
 CAAGCTAGAG AGCTGAATTT CTGAGATACA CATTTCAAA TCACATGCAA GTGAAGATGA 1320
 TGGTCTGTAG AAATTTTCAG TATATATAAT GTTAAATGAC ATACTAATTT ATCATCTGGC 1380
 TATTTGGGAA GCAAGGACAC ACATGGATTT TGACATTTC CACCATGGTG GCTGGTGTGG 1440
 80 CTTGTGGCTA TGGGGTGATC ACCAGTATCA CCACITTGGA AGGGGACAGT GAAATTTGGG 1500
 CTAGAGAAGG AACTTTGTAC AGTTTTCCTT GAGATTGAGA TTGACTGAAA AGTCACATGA 1560
 AGAGTTGATT GTCCTTTAAT GGTATGTTT AAACAGCTGA CATTTTAAAT TTTGATGAAA 1620
 TCCAGTTTAT TCGTTTGTTC TTTTATGCTT TGGGTGTGAC ATCCGAGAAA TCTTTTCCCA 1680
 85 TCCCAAGATC ACAATTTTTT TTCCTTTTTC CTCTAGAAG TGTATAATT TTAAGCTTTA 1740
 TACTTTGGTC TATGACCGGT TTTTGTGTTT GTTTTGTGTT GTTTTTCGT TTTTCTTTT 1800
 GTTTGAGAT GGAGTCTTGT TCTGTCAACC AGGCTGGGGT GCAGTGGCGT GATCTTGGCT 1860
 CACTGCAATC TCTATCCCTT GGTTCAGT GAITCTCTG TCTCAGCTC CCAAGTAGCT 1920
 GGGATTACAG GCACAGGCCG CCACGCCCTG CTAATTTTTG TATTTTGTAGT AGAGACAGAG 1980

TTTTACCATG TTGGCCAGGC TGGTTTCAAA CTCCTGACCT CAAGTGACCC ACCTTGGCCT 2040
 CCCAAGTTT TGGGATTACA AGTGTGGGCC ACCGCGGCCA GCCTATGATC CATTTTGAAT 2100
 GAATTTTATA TATGGTGCAA GGTGTCAATC CACCTTCACT TTTTCTTGGG AATATAGATA 2160
 TCCAGCTGTT TCACTACCAT TTTTGAAG GACTGCCCTT TGCTCTATCA CTTTTCATT 2220
 TTTGTTAAAA AGTAGTTGTC AATGTATATG TGGGTTTATT TCAGGACTCT GTTTTGTTC 2280
 ATTGACCTGT TTTTCTCTCC TGAATGCCAA TACCATAATT GTATGTAGTG TATGTAATTT 2340
 TCTAATAATT CTGAAACAG ATAGTATTAA TGTGTATAT TTTTGTCTGT GTTTGTATTT 2400
 TTTGTAGAGA TGGGGTTTCA CCGTGTGGC CAGGCTGTGT TGAACCTCTG AGCTAAAGCA 2460
 ATACACTTGC CTGCTCTCC CCAATGTGCTG GGATTACAGG CGTGAGCCTT GGTGCTGGCC 2520
 CAGGTGTACCA CATTTCTTTT TGAGATTGTT TTTGGCTATG TTAAGTCTCT TGCTTTTGAT 2580
 GTGAAATTTG GGAACAGGCA GGGTGTGGTG GCTTATGCCT GTAATCCTAG AACTTTGGGA 2640
 GGCCTAGATG GGTGGATCAC TTGAGCTCAG GAGTTCCAGA CCAGCCCGGG CCTATGGCAA 2700
 AACTCCGTCT CTACAAAAA TAGAAAAAT TAGCCAGGTG TGGTGGTGCA TGCCTGTAGT 2760
 CACAGTTACA CGGCAGGCTG AGGTGGGAGG ATCACTTGAA CCCAGAGGT CAAGACTGCA 2820
 GTGAGCTGAG ATCACACCAC TGTACTCCAG CCTGGGTGAC AAAGTGAGAC TCTATCTCAA 2880
 AAAGAAATTA GGATCAATTT GTCAATTTCT ACAACAACAA CAACAAAAAC CCCTGTTGGG 2940
 CACCTTGATT GAGATTGCAT TGAATTTATA TAAACTGTT GGGAGAATTG ACATCTTAAT 3000
 AATATTGAGT CTCTCGCCT ATAAACAAGG TCTGTCTTCC TAGGTATTAA TGTTTTGTCT 3060
 TCTATTCTCT TTAATAATCT TTTGTAGTTT TCAGTGTACA GGTCTACCAT GTGAGCATTT 3120
 CATAGTTTGT ATGCTAAATG GTATTTTAAA ATTTCAAATT CTAACCACTT GTTGCTAGTA 3180
 AATAGAAATA CAATTGATGT TGAACCTTGA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC 3240
 ATGGTGTGTT TGTAATATAC ATCAACAGTC ATGTGTTCTA TGAATAAAGA GTTTTACTCC 3300
 TTC

Seq ID NO: 154 Protein sequence:
 Protein Accession #: BAA11503.1

1	11	21	31	41	51	
MFCEKAMELI	RELHRAPEQG	LPAFNEGLR	QVLEEMKALY	EQNQSDVNEA	KSGGRSDLIP	60
TIKFRKSHLL	RNRRTVAYL	YDRLLRIRAL	RWEYGSVLPN	ALRFHMAAEE	MEWFNNYKRS	120
LATYMRSLGG	DEGLDITQDM	KPPKSLYIEV	RCLKDYGEFE	VDDGTSVLLK	KNSQHFLPRW	180
KCEQLIRQGV	LEHILS					

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-709

1	11	21	31	41	51	
GTTCGCGGCC	AAAGCGCGGA	GCGGAGGCCG	AGGCGAGAGC	CTGGCGCTGT	AGGACTAGAA	60
CGAAAGGAGT	GAGGCGCCGA	GAGCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
AAGGCGCGCG	GAGTGGGAAG	CGTCCGCCAT	GTTCTGCGAA	AAAGCCATGG	AACTGATCCG	180
CGAGCTGCAAT	CGCGCGCCCG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
AGTTCTGGAG	GAGATGAAAG	CTTTGTATGA	ACAAAACAG	TCTGATGTGA	ATGAAGCAAA	300
GTCAGGTGGA	CGAAGTGATT	TGATACCAAC	TATCAAATTT	CGACACTGTT	CTCTGTTAAG	360
AAATCGAGCG	TGCACTGTAG	CATACCTGTA	TGACCGCTTG	CTTCGGATCA	GAGCACTCAG	420
ATGGGAATAT	GGTAGCCTCT	TGCCAAATGC	ATTACGATTT	CACATGGCTG	CTGAAGAAAT	480
GGAGTGGTTT	AATAATTATA	AAAGATCTCT	TGCTACTTAT	ATGAGGTCAC	TGGGAGGAGA	540
TGAAGGTTTG	GACATTACAC	AGGATATGAA	ACCACCAAAA	AGCCTATATA	TGGAAGCTGG	600
ATGCAGTGGC	GCAGTCTCGG	CTCAACCTGC	AACCTCCACC	TCCAGGTTTC	ACCTCAACTG	660
CAACCTCCAC	CTCCCGGCTC	AGAGCTATGG	AGAATTGAA	GTGATGATG	720	
GCACCTTCAGT	CCTATTAAAA	AAAAATAGCC	AGCACTTTT	ACCTCGATGG	AAATGTGAGC	780
AGCTGATCAG	ACAAGGAGTC	CTGGAGCACA	TCCTGTCATG	ACCATGCGCC	GAGGCACCTC	840
CAGGCTTCAC	TCAACTACATG	GACTCCTCTG	TACTCACTCT	CTCCACCAC	CCCTTCACCT	900
CCCTCTTTGA	TTTTAGAAGC	TATAGACATT	GTTTAAGATA	ACTAAGAATA	CTTGCTTAAG	960
AAGTATAATT	TGCTAACTAT	TAAGGACTTT	CTTTTATTAA	TGTTGTACAC	TATTCTTCTC	1020
ACTCTTTTTT	GGTTTGGTT	TTGTTTGTGA	GAGACTGTCT	CACATGTTG	CCCAAGCTGG	1080
TCTCAAACCTC	CTGGCCTCAA	GCACTCCTCC	CACCTTAGCT	TCTCAAAGTG	TTGAGATCAC	1140
AGGCGTGAGC	CAGTGCACCC	GGCCCCACT	CCTTTTCTA	ATAAGCTGTA	TCTGTAATCA	1200
CAGCATTCCT	ACAGTTGTTA	CAGTGTGTT	TTTAAATGAA	AGTAAACATG	GTTACATTGG	1260
AACTCTCTTAA	ATAAGCAGTC	ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GTGTGTCTTG	1320
TTTTCTGGTC	ATGTGTATTG	TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	1380
AATCAGATGC	AAGTGAAGAT	GATGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAATG	1440
ACATACTAAT	TTATCATCTG	GCTATTGGG	AAGGAAGGAC	ACACATGGAT	TTTGACATT	1500
TCCACCATGG	TGGCTGGTGT	GGCTTGTGGC	TATGGGGTGA	TCACCATGAT	CACCACTTTG	1560
GAAGGGGACA	GTGAAATTTG	GGCTAGAGAA	GGAACCTTGT	ACAGTTTTC	CTGAGATTCA	1620
GATTGACTGA	AAAGTCACAT	GAAGAGTTGA	TTGTCTTTTA	ATGGTATGTT	TTAAACAGCT	1680
GACATTTTAA	ATTTTGATGA	AATCCAGTTT	ATTCTGTTGT	TCTTTTATGC	TTTGGGTGTT	1740
GCATCCGAGA	AATCTTTTCC	CATCCCAAGA	TCACAATTTT	TTTTCTTTT	TACTTCTAGA	1800
AGTGTTATAA	TTTTAAGCTT	TATACCTTGG	TCTATGACCC	GTTTTTTTTT	TTGTTTGTGT	1860
TTGTTTTTTC	GTGTTTCTCT	TTGTTTGTAG	ATGGAGTCTT	GTTCTGTAC	CCAGGCTGGG	1920
GTGCACTGGC	GTGATCTTGG	CTCACTGCAA	TCTCTATCCC	CTGGGTCAA	GTGATCTCT	1980
TGTCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACAGGC	CGCCACGCCT	GGCTAATTTT	2040
TGATATTTTA	GTAGAGACAG	AGTTTACCA	TGTTGGCCAG	GCTGGTTTCA	AACTCCTGAC	2100
CTCAAGTGAC	CCACCTTGGC	CTCCCAAAGT	TTTGGGATTA	CAAGTGTGGG	CCACCGCGGC	2160
CAGCCTATGA	TCCATTTTGA	ATGAATTTT	TATATGGTGC	AAGGTGTCAA	TCCACCTTCA	2220
CTTTTTCTTG	GGAAATATAGA	TATCCAGCTG	TTTCACTACC	ATTTTTTGAA	AGGACTGCC	2280
TTTGCTCTAT	CACCTTGTGA	TTTTTGTAA	AAAGTAGTTG	TCAATGTATA	TGTGGGTTTA	2340
TTTCAGGACT	CTGTTTGTGT	CCATTGACCT	GTTTTCTCT	CCTGAATGCC	AATACCATAT	2400
TTGTATGTAG	TGTATGTAAT	TTTCTAATAA	TTCTTGAAC	AGATAGTATT	AATGTGTCT	2460
ATTTTGTCTG	TGTTTGTAT	TTTTTGTAGA	GATGGGGTTT	CACCGTGTG	GCCAGGCTGT	2520
TTTGAACCTC	TGAGCTAAAG	CAATACACTT	GCCTCGTCT	CCCATGTGTC	TGGGATTACA	2580
GGCGTGAGCC	TTGGTGTGG	CCCAGTGTAC	CACATTTCTT	TTTGAGATTT	GTTTTGGCTA	2640
TGTTAAGTCC	TTTGTCTTGG	ATGTGAAATT	TGGGAACAGG	CAGGGTGTGG	TGGCTTATGC	2700
CTGTAATCCT	AGAATCTTGG	GAGGCTTAGA	TGGGTGGATC	ACTTGAGCTC	AGGAGTTCCA	2760
GACCAGCCCG	GGCCTATGGC	AAAACCTCCG	CTCTACAAAA	AATAGAAAAA	ATTAGCCAGG	2820

TGTGGTGGTG CATGCTGTGA GTCACAGTTA CACGGCAGGC TGAGGTGGGA GGATCACTTG 2880
 AACCCAGAG GTCAGAGCTG CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG 2940
 ACAAGTGAG ACTCTATCTC AAAAGAAAT TAGGATCAAT TTGTCAATT CTACAACAAC 3000
 AACACAAA ACCCTGTG GGCACCTGA TTGAGATTGC ATTGAATTTA TATAAACTG 3060
 TTGGGAGAA TGACATCTTA ATAATATTGA GTCTTCTGGC CTATAACAA GGTCTGTCTT 3120
 CCTAGGTATT AATGTTTGT CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCAGTGA 3180
 CAGGTCTACC ATGTCAGCAT TTCTAGTTT TGATGCTAAA TGGTATTTTA AAATTTCAAA 3240
 TTCTAACCACT TTGTGCTAG TAAATAGAAA TACAATTGAT GTTGAAGCTG TATCCTTCAG 3300
 CCTTGCTAAA CTGTGAGTTC TCATGTGTT TTTGTAAATT ACATCAACAG TCATGTGTTC 3360
 TATGAATAAA GAGTTTACT CCTTC

Seq ID NO: 156 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEGO LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TTKFRHCSLL RNRRTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEA GCSGAISAQP ATSTSQVHLN CNLHLPGPVS 180
 KRLWRI

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-621

1 11 21 31 41 51
 TTCCGGCCCA AAGCGCGGAG CGGAGGCCGA GCGGAGAGCC TGGCGCTGTA GGACTAGAAC 60
 GAAAGGAGTG AGGCGCCGAG AGCCAGATA CCATTTTGGC GTGAGAGCTG GTGGTTGGCA 120
 AGGCGCGGG AGTGGGAAGC GTCGCCATG TTCTGCGAAA AAGCCATGGA ACTGATCCGC 180
 GAGCTGCATC GCGCGCCGGA AGGGCAACTG CCTGCCTTCA ACGAGGATGG ACTCAGACAA 240
 GTTCTGGAGG AGATGAAAGC TTTGTATGAA CAAAACCAAGT CTGATGTGAA TGAAGCAAGC 300
 TCAGGTGGAC GAAGTGATTT GATACCAACT ATCAAATTTC GACACTGTTC TCTGTAAAGA 360
 AATCGACGCT GCACCTGTAGC ATACCTGTAT GACCGCTTGC TTCGGATCAG AGCACTCAGA 420
 TGGGAATATG GTAGCGTCTT GCCAAATGCA TTACGATTTC ACATGGCTGC TGAAGAAAGTC 480
 CGGTGTCTAA AAGACTATGG AGAATTGAA GTTGATGATG GCACCTCAGT CCTATTAAAA 540
 AAAAATAGCC AGCACTTTT ACCTCGATGG AAATGTGAGC AGCTGATCAG ACAAGGAGTC 600
 CTGAGACACA TCCTGTATG ACCATGCGCC GAGGCACCTC CAGGCTTCAC TCAACTCATG 660
 GACTCCTCTG TACTCACTCT CTCCACCACT CCCTTCACCT CCCTCTTGA TTTTGAAGC 720
 TATAGACATT GTTTAAGATA ACTAAGAATA CTGGCTAAG AAGTATAATT TGCTAACTAT 780
 TAAGGACTTT CTTTTAAAGC TATTCTTCTT ACTCTTTT GGTTTTGGTT 840
 TTGTTTGTGA GAGACTGTCT CACTATGTTC CCCAAGCTGG TCTCAAATC CTGGCCTCAA 900
 GCAGTCTCC CACCTTAGCT TCTCAAAGTG TTGAGATCAC AGGCGTGAGC CACTGCACCC 960
 GGCCCTACT CCTTTTCTA ATAAAGCTGA TCTGTAATCA CAGCACTTCT ACAGTTGTGA 1020
 CAGTGTGTTT TTTAAATGAA AGTAAACATG GTTACATTG AATCTCTTAA ATAAGCAGTC 1080
 ACTTGGCTGG ACAGGAAGAA GTGAGATCCT GTGTGTCTTG TTTCTGGTC ATGTGTATTG 1140
 TACAAGCTAG AGAGCTGAAT TTCTGAGATA CACATTTTCA AATCACATGC AAGTGAAGAT 1200
 GATGTGTGT AGAAATTTTC AGTATATATA ATGTTTAAAT ACATACATAT TTATCATCTG 1260
 GCTATTGGG AAGGAAGGAC ACACATGGAT TTGACATTT TCCACCATGG TGGCTGGTGT 1320
 GGCTTGTGGC TATGGGGTGA TCACCAGTAT CACCCTTTG GAAGGGGACA GTGAAATTGG 1380
 GGCTAGAGAA GGAACCTTGT ACAGTTTCC CTGAGATTCA GATTGACTGA AAAGTCACAT 1440
 GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TAAACAGCT GACATTTTAA ATTTTGATGA 1500
 AATCCAGTTT ATTGTTTGT TCTTTTATGC TTTGGGTGTT GCATCCGAGA AATCTTTTCC 1560
 CATCCCAAGA TCACAAATTT TTTTCTTTT TACTTCTAGA AGTGTATATA TTTTAAAGCT 1620
 TATACTTTGG TCTATGACCC GTTTTCTTT TTGTTTGTG TTGTTTCTT GTTTGTTTCT 1680
 TTGTTTGTAG ATGAGTCTT GTTCTGTAC CCAGGCTGGG GTGCAGTGGC GTGATCTTGG 1740
 CTCACGTCAA TCTCTATCCC CTGGGTTCAA GTGATTCTCT TGCTCAGCC TCCCAAGTAG 1800
 CTGGGATTAC AGGCACAGGC GGCACGCTT GGTAAATTT TGTATTTTGA GTAGAGACAG 1860
 AGTTTACCA TGTGGGCAG GCTGGTTTCA AACTCCTGAC CTCAGTGAC CCACCTTGGC 1920
 CTCCCAAGT TTTGGGATTA CAAGTGTGG CCACGCGGCG CAGCCTATGA TCCATTTTGA 1980
 ATGAATTTT TATATGTTGC AAGGTGTCAA TCCACCTTCA CTTTTCTG GGAATATAGA 2040
 TATCCAGCTG TTTCACTACC ATTTTGTGA AGGACTGCCC TTTGCTCTAT CACCTTTGCA 2100
 TTTTGTAA AAAGTAGTTG TCAATGTATA TGTGGTTTGA TTTCAGGACT CTGTTTGTG 2160
 CCATTGACCT GTTTTCTCT CTGAATGCC AATACCATAT TTGTATGTAG TGTATGTAAT 2220
 TTTCTAATAA TTCTGAAAC AGATAGTATT AATGTGTGAT ATTTTGTCTG TTGTTGTAT 2280
 TTTTGTAGA GATGGGTTT CACCGTGTG GCCAGGCTGT GTTGAACCTC TGAGCTAAAG 2340
 CAATACACTT GCCTCGTCT CCCCATGTGC TGGGATTACA GGCCTGAGCC TTGGTGCTGG 2400
 CCCAGTGTAC CACATTTCT TTTGAGATT GTTTTGGCTA TGTAAAGTCC TTGCTTTTGG 2460
 ATGTGAAATT TGGGAACAGG CAGGTTGTG TGGCTTATGC CTGTAATCCT AGAACTTTGG 2520
 GAGGCTAGA TGGGTGATC ACTTGAGCTC AGGAGTTCCA GACCAGCCC GGCCTATGGC 2580
 AAAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG TGTGGTGGTG CATGCCTGTA 2640
 GTCACAGTTA CACGCGAGG TGAGGTGGGA GGATCACTTG AACCCAGAG GTCAAGACTG 2700
 CAGTGAGCTG AGATCACACC ACTGTACTCC AGCCTGGGTG ACAAAGTGAG ACTCTATCTC 2760
 AAAAAGAAAT TAGGATCAAT TTGTCAATT CTACAACAAC AACACAAA ACCCTGTG 2820
 GGCACCTGA TTGAGTTG ATGAATTTA TATAAACTG TGGGAGAAT TGACATCTTA 2880
 ATAATATTGA GTCTTCTGGC CTATAACAA GGTCTGTCTT CCTAGGTATT AATGTTTGT 2940
 CTCTATTTC TCTTAATAAT CTTTGTAGT TTTCACTGTA CAGGTCTACC ATGTGAGCAT 3000
 TTCTAGTTT TGATGCTAAA TGTATTTA AAATTTCAAA TTCTAACCA CTGTTGCTAG 3060
 TAAATAGAAA TACAATTGAT GTTGAACCTG TATCCTTCAG CCTTGCTAAA CTGTGAGTTC 3120
 TCATGTGTT TTTGTAAATT ACATCAACAG TCATGTGTTC TATGAATAAA GAGTTTACT 3180
 CCTTC

Seq ID NO: 158 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |

MFCEKAMELI RELHRAPEGQ LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
TIKPRHCSLL RNRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRPHMAAEE VRCLKDYGEF 120
EVDGTSVLL KNSQHFLLR WRCEQLIRQ VLEHILS

5

Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 149-229

10 1 11 21 31 41 51
| | | | | |
GTTCCGCGCC AAAGCGCGGA GCGGAGGCGG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
CGAAAGAGGT GAGGCGCGGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
AAGGCGCGGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
CGAGCTGCAT CGCGCGCGCG AAGGGCAACT GCCTGCCTTC AACAAATTAGC TGGGTGTGGT 240
15 GGCACACACC TGTAAGTCCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA 300
GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
TGAATCCCTG TCTCAAAAAG GAAAAGGAGG ATGGAAGTCA ACAAGTTCTG GAGGAGATGA 420
AAGCTTTGTA TGAACAAAAC CAGTCTGATG TGTCTCTCTG TAAGAAATCG ACGCTGCACT 480
GTAGCATACC TGATATGACC CTGTCTCGG ATCAGAGCAC TCAGATGG

20

Seq ID NO: 160 Protein sequence:
Protein Accession #: Eos sequence

25 1 11 21 31 41 51
| | | | | |
ATGTTCTGCG AAAAAGCCAT GGAAGTATC CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
CTGCCCTGCC TCAACAATTA G

30

Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: U10694
Coding sequence: 1333-2280

35 1 11 21 31 41 51
| | | | | |
GGATCCGGCC GGATCTCAGG GAGGTGAGGA CTTTGTCTC AGAGGGTGTG TGTGGACAAA 60
ACAGGGAGGC CCTGTGTTCT ACAGACACAG TGGTCCCAGG ATTGGAGAGC AGTCCAGGTG 120
AGGAACCTAA GGGAGGATCG AGGTACCTC CAGGCCAGAG AAAGCTCTCAG ATCAAGAGAG 180
TTTGCCCTGC CCCTACTGTC ACCCCAGAGA GCCCGGGCAG GGCTGTCTGC TGAGGTCCCT 240
40 CTTTATCTCT GGGATCACTG GTGTGGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCCT 300
CAGCTCAGCA GAGGGAGGGT CCCAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC 360
CCCACTCACC AAACACAGAG GACCTAGCCC CACCCTGCCC CTTGTGTGAG CTGAGGGGAG 420
CGCTGGGTG GATGGAATCC CCTCACTTCC TCTTCAGTGT TCTCTGAGG ATAGGGCCTC 480
AGGTCAACAG AGGGAGGGTT CCAAGCCCTG CAGGCATCAA GATGAGGACC AGGCAGTATC 540
45 CTCACCCAG GACACATGGA CCCCATGAA TTTAGACATC TCTTACTGTA CTTCCGAGGA 600
AACCTTGGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTT CATATCAGGG 660
ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
CAGGAGAAAG CTCAGGGCCC TCAGGTGAGC CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
AGAAGTCAAG AGTGTCCAGC CCGCCCTCTT GACAGCACTG AGGGACCGGG GCTCTGCCTG 840
50 CAGTCTGAGC CCTAAGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
CTTGTCTGTA GACAGTGTCC TCAGTTCGCA GAGCAGAGGA GACCCAGGCA GTGTGAGCAG 960
TGAAGGTGAA GTGTTCAACC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG 1020
GGACCCCATTA GCACCTGGCC CCATTCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
AGGCTAGCTG CACGCTGAGT AGCCCTCTCA CTTCTCTCCT CAGGTTCTCG GGACAGGCTA 1140
55 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
GCCTTTGTTA GAACTCCCAA GGTTCGGTTC TCAGTGAAG TCTCTCACAC ACTCCCTCTC 1260
TCCCAAGGCC TGTGGGTCTC CATCGCCAGC CTCCTGCCCA CGTCTCTGAC TGCTGCCCTG 1320
ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
GAAGCCCAAG GAGAGGACTT GGGCCTGATG GGTGCACAGG AACCACAGG CGAGGAGGAG 1440
GAGACTACCT CCTCTCTGTA CAGCAAGGAG GAGGAGGTGT CTGCTGCTGG GTCATCAAGT 1500
60 CCTCCCCAGA GTCCTCAGGG AGGCGCTTCC TCCTCCATT CCGTCTACTA CACTTTATGG 1560
AGCCAATTCT ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAGCTC CTCGGTCGAC 1620
CCAGCTCAGC TGGAGTTCAT GTTCCAAGAA GCACTGAAAT TGAAGGTGGC TGAGTTGGTT 1680
CATTTCTCTG TCCACAAATA TCAGTCAAG GAGCCGCTCA CAAAGGCAGA AATGCTGGAG 1740
AGCGTCATCA AAAATTACAA GCGCTACTTT CCGTGTATCT TCGGCAAGGC CTCGAGTTTC 1800
65 ATGCAGGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGCGCA CTCCTACATC 1860
CTTGTCACTG CTCTTGGCCT CTGCTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC 1920
AAGGCGCCCC TCCTGATCAT TGTCTTGGGT GTGATCCTAA CCAAGACAA CTCGCCCTCT 1980
GAAGAGGTTA TCTGGGAAGC GTTGAAGTGT ATGGGGTGT ATGTTGGGAA GGAGCACATG 2040
70 TTCTACGGGG AGCCCGAGAA GCTGCTCACC CAAGATTGGG TGCAGGAAAA CTACCTGGAG 2100
TACCGGAGG TGCCCGGAGC TGATCTCTGG CACTACGAGT TCCTGTGGGG TTCCAAGGCC 2160
CAGCTGAAA CCAGCTATGA GAAGGTCATA AATTATTGG TCATGCTCAA TGCAAGAGAG 2220
CCCATCTGCT ACCCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAAGA GGGAGTCTGA 2280
GCACAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTGAGG CCCCATCCAG CAGCTGCCCT 2340
75 GCCCATGTG ACATGAGGCC CATCTCTCGC TCTGTGTTT AAGAGAGCAA TCAGTGTCT 2400
CAGTGGCAGT GGGTGAAGT GAGCACACTG TATGTCATCT CTGGGTTCCT TGCTATTGG 2460
GTGATTTGGA GATTATCCT TGCTCCCTTT TGGAAATGTT CAAATGTTCT TTTAATGGTC 2520
AGTTAATGA ACTTCAACAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT 2580
ATGTTATTTA GGAGTAAGAT TCTTGTCTTT GAGTCACATG GGGAAATCCC TGTATTTTG 2640
80 TGAATTGGGA CAAGATAACA TAGCAGAGGA ATTAATAATT TTTTGAAGC TTGAAGTTAG 2700
CAGCAAAATA GAGCTCATAA AGAAATAGTG AAATGAAAT GTAGTTAATT CTGCTCTTAT 2760
ACCTCTTTCT CTCTCTGTA AAATTAAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
TCTTGAGCA TGTAAAGAG AAATAAATTG AAAGAATAAT TTTTCTGTT CACTGGCTCA 2880
TTTTTCTTC AGACACGCAC TGAACATCTG TTATTCGGAA CACCTGGGT T

85

Seq ID NO: 162 Protein sequence:
Protein Accession #: AAA68877.1

1	11	21	31	41	51	
MSLEQRSPHC	KPDEDLEAQQ	EDLGLMGAQE	PTGEEEBETTS	SSDSKEEEVS	AAGSSSPFQS	60
PQGGASSSIS	VYYTILWSQFD	EGSSSQESEE	PSSSVDPAPL	EFMFQEALKL	KVAELVHPLL	120
HKYRVKPEVT	KAEMLESVVK	NYKRYFPVIF	GKASEFMQVI	FGTDVKEVDP	AGHSYILVTA	180
LGLSCDSMLG	DGHSMPKAAAL	LIIVLGVILT	KDNCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
PRKLLTQDWV	QENYLEYRQV	PGSDPAHYEF	LWGSKAHAET	SYEKVINYL	MLNAREPICY	300
PSLYEVLGE	EQEGV					

Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

1	11	21	31	41	51		
GGGGGGGGAG	AGGCCCTGGAG	GACACCAACA	TGAACAAGTT	GAAATCATCG	CAGAAGGATA	60	
AAGTTCGTCA	GTTTATGATC	TTACACAAAT	CTAGTGAAAA	AACAGCAGTA	AGTTGTCTTT	120	
CTCAAAATGA	CTGGAAAGTTA	GATGTTGCAA	CAGATAATTT	TTTCCAAAAT	CCTGAACCTT	180	
ATATACGAGA	GAGTGTAAAA	GGATCATTGG	ACAGGAAGAA	GTTAGAACAG	CTGTACAATA	240	
GATACAAAGA	CCCTCAAGAT	GAGAATAAAA	TGGAATAGA	TGGCATAACAG	CAGTTCTGTG	300	
ATGACCTGGC	ACTCGATCCA	GCCAGCATT	GTGTGTTGAT	TATTGCGTGG	AAGTTCAGAG	360	
CAGCAACACA	GTGCGAGTTC	TCCAAACAGG	AGTTCATGGA	TGGCATGACA	GAATTAGGAT	420	
GTGACGAT	AGAACCACTA	AAGGCCCAGA	TACCCAAGAT	GGAACAAGAA	TTGAAAGAAC	480	
CAGGACGATT	TAAGGATTTT	TACCAGTTTA	CTTTTAATTT	TGCAAGAAT	CCAGGACAAA	540	
AAGGATTAGA	CTTAGAAATG	GCCATTGGCT	ACTGGAACTT	AGTGCTTAAT	GGAAAGATT	600	
AATTCTTAGA	TTTATGGAAT	AAATTTTGT	TGGAACATCA	TAAACGATCA	ATACCAAAAG	660	
ACACTTGGAA	TCTTCTTTTA	GACTTCAGTA	CGATGATGTC	AGATGACATG	TCTAATTATG	720	
ATGAAGAAGG	AGCATGGCCT	GTTCTTATTG	ATGACTTTGT	GGAATTTGCA	CGCCCTCAAA	780	
TTGCTGGGAC	AAAAGTATCA	ACAGTGTAGC	ACTAAAGGAA	CCTTTTAGAA	TGTACATAGT	840	
CTGTACAATA	AATACAACAG	AAAATTGCAC	AGTCAATTTT	TGCTGGCTGG	ACTGAACTGA	900	
AGATCAATCC	TCACAATTCA	GACTGAGGGT	TGAGACAAAA	CTTTAAGGAT	ACATCTTGGG	960	
CCATATCGTA	TTTCAATCTT	CTAATGGTGG	TTTGGGCTTG	TCTTCTAGTC	TGGGCCGCTC	1020	
TAAACATTTA	TAATCCCAAC	ATTGTGGATT	TCATCTTATA	TCTGTGGACC	ATCCTAGTTT	1080	
ATTCTCCCAT	AAGTCTTAGA	AGCTTTATGG	TGATTATTTT	GAGGTTTTCA	TTCTCGCATA	1140	
AAGCACAAATG	CTGCTCTTCAT	CAGAAAAACAG	TTGGCATAAG	AATTAAACAT	ATGAACATCA	1200	
CAAAACAATT	TATAAAAACT	TCTTAAATAT	ACGCTTTGGG	CTAGTTGCAA	AGACTATGCT	1260	
AATAGCACTT	CCAGTGAGAG	TGATATATTT	AAGTGTACTG	GATCTGGAAT	GGTGTTTTGG	1320	
TTTGGGGGGA	ATTTTTTTTT	TTTCTGGCA	AATCACATAT	GTGTTGATG	TGAGTATCTG	1380	
ATGAAAAAAC	AATGTCAGAA	TAACCGACAT	GAAAATTTTT	TAGGATAACT	TGGTGCTTAC	1440	
CTGAAAAATG	TATGTGTTT	TAGACTCTTG	ATTTCAAAAG	GTTCACAGA	ACTAGTCTGC	1500	
GCTTACCTTA	CCCATGTTTA	TATATAGCTG	TCCTACAGGG	AGCTTTTATT	TAGAAAAATG	1560	
CTGCATAATG	TTAGATCTCT	CTCCTGTCTA	CATTATGCAC	TACATAATG	GACTTCATTA	1620	
TGCTTTTGAA	ATGCTTATCT	GCCTGTCCAC	TAAGTTAAAC	TATTTAAATT	GTTTGAATG	1680	
TTTTGGATTG	CTACACAATA	CAATATTCTA	AATTTAGGCA	TGAGGGTTTT	TTTGTTTTAT	1740	
TTTTACTTTT	TTTTGTGCAT	TGCACATGAG	AACACAAATG	AAATCTCTT	AATTTATAAG	1800	
AAGATAGTAG	GAGTTAAAT	TTGAAAATGG	TTGTGATGAG	CCACGAAAT	CAATCTTTAT	1860	
AATATAGGTA	CTGCTCTTTC	AGACAAACAG	TCCATTTTTA	ATGACTTCTT	ATTTTGTGTA	1920	
AATTACTTTA	ACTGCTAATC	ACTGTGGTGG	CCAAATATTT	ACTTCAGAAG	CAAAGATTTT	1980	
CAAAACAAGCA	TACACAGATG	AAAATACCAG	TCTGGCTTCT	AGTCTATTTA	CTGTTTTGT	2040	
TCACTCAGAT	TAGCTCAGTT	TCTCATCAA	AGCAGAAATG	TATCTTGCGT	GTGTGTGTGT	2100	
GTGTGTGTGT	GTGTGTGTGT	GTATGTGTGT	ATATATATAT	ATATATATAT	ATATATATTT	2160	
TTTTTTTTTT	TTTTTTTTAA	ATTACAAAAG	CCATGAGCTG	CTTTATAGCT	GAAAATGGTC	2220	
ATTTCCCTGT	TCACTTACTG	ACATGTGAAG	AAGGGTTTCT	TGCTTCTT	AACATTTCCG	2280	
TAAGGCAGGC	TAGAAATGTA	ATACCTTCAA	TGTTTGATGA	TTATGGTCTT	TTGATAGGAA	2340	
TAGATTCTGC	TTGGGATATA	TATCCAGGCA	CTCTTAAGG	TCTAGGGTTG	ATATTAACAA	2400	
AGGAATGTAC	TTAGAATAGC	AGTACATTTT	ATGCAAAAT	GGAAATTTAT	TTAAGAAACA	2460	
ATGACATATC	AAAACGTGCT	TTTACATGAT	TTTGAATAG	ACTAGAAAGC	TTTCCCTATA	2520	
GACATATTAA	TATTTCAATC	ATAACTTTAA	TTCAAGAATG	CAGTTTTAC	AAAAGAAAAA	2580	
TTGAAAAAT	TCTATTGAG	CTACTGGAAT	TGGTTATTAA	AAGAAAAAGG	AAAAGAGAGA	2640	
ATCTTGCTGC	TTTCAGTATT	TCTGATTTT	TTTGTAAATA	TAAAGAGGAA	CTTCAATTAT	2700	
GAAAAAATTT	TAAAAGATAT	ATATATCTAT	ATATCTATAT	ATATGTACTG	TTTTGTTTCC	2760	
TGCTCTGAAG	ATTTTGAATT	ATGGTTATG	GTTCAGATT	GATTAATTCA	CATATGCTGT	2820	
GTTTCTTTA	AAAGTCATAT	GGGTTGCTGG	CCTAATGCCT	TGGATTTTAC	ATATTTTCTT	2880	
TTTTAAATGC	AAAACCTTTT	CAACAAAATA	GTGTTTGTC	TCAGGTTGGT	ACTAAACATT	2940	
TATAATTACT	GTGTAATTAT	AAACAAAAT	ACATAAAGCT	TTGAATATAA	TTATGTAGCA	3000	
TAAAAGTTAA	GGTTGTTTAC	TATGATGGCA	TCTTAGAATT	AAACAAAAT	TTTACTAGGG	3060	
CTGAAAAGAG	AAGACTGATT	TAATGTGGTG	TGATTATTCT	GAAGATAAAT	GTCTGGCTAC	3120	
AGGGAAATATT	TTGTACTAAA	AAATGATTAC	ACATATGGCT	GTGTGTGTTT	GAGTCTGTGT	3180	
CTGTGAGAGA	GCCAGAGAGA	GTGAGAGAGA	TTGACAGAGA	AAGGGAGAGA	CACACACAG	3240	
CCCCTTGAAT	TGCTTTAACT	CCTAAGTGT	TCAGTCTCA	TTCCGGTAAA	CTCCCCATGC	3300	
TGATTCTTTG	TTTTAAACTG	AACCATAGGT	ACAGTTTCCT	TTTGCCAAA	TGTCAAAACA	3360	
GGTACAAATT	TTAAAATGTA	ATGCTTTT	AATAGAAAAA	TGTATAAAAT	TAGAAGTGCC	3420	
CACATATAAA	AAATACTTGA	GATGAAGATT	ATCTTTAGTG	AATATCATCT	GCATATCTCT	3480	
75	TAAGTTCAA	TTGTGTTTCT	TACAGTCCCT	GTCAATATTAC	CAACAGAGGC	AATAAAGCT	3540
	GCAGTGAAT	TG					

Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

1	11	21	31	41	51	
MNKLKSSQKD	KVRQFMIFTQ	SSEKTAVSCL	SQNDWKLDVA	TDNFFQNPFL	YIRESVKGSL	60
DRKLEQLYN	RYKDPQDENK	IGIDGIQFQC	DDLALDPASI	SVLIIAWKFR	AATQCEFSKQ	120
EFMDGMTELG	CDSIEQLKQ	IPKMEQELKE	PGRFKDFYQF	TFNFAKNPGQ	KGLDLEMAIA	180
YWNVLNGRF	KPLDLWNKFL	LEHHRKRSIPK	DTWNLLLDPS	TMIADDSMNY	DEEGAWPVL	240
DDFVEFARFQ	IAGTKSTTV					

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
CTCCAGTCCG	CATGCTCAGT	AGCTGCTGCC	GGCCGGGCTG	CGGGGCGGCG	TCCGCTGCGC	60
GCCTACGGGC	TGCGGTGGCG	GCGCGCGCGG	CACCCGGCAG	GGCCCGGCCAG	TCCCGGCTTC	120
CCTGCTCCAG	AGCCGCGCGC	TGGGCGGGG	CAGGGCGGGC	CGGGGGCTCC	TCCATGCTGC	180
CAGCGCGCGG	GCTCGGGAGC	CGACCAAGTG	GCTCCTGCGA	TGGCGGCGGA	AGAGGAGGCT	240
GCGGCGGGAG	GTAAGTGTT	GAGAGAGGAG	AACCAAGTGA	TTGCTCCTGT	GGTTTCCAGC	300
CGCGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
TTTCCACGAA	AACGCAAGG	AAGTGATTCA	GACCCATCCC	AAGTGAAGA	TGGTGAACAC	420
CAAGTTAAAT	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
AAAAATGAATA	ACCTGATTGA	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
CGTAACTGG	ACAAACTTAC	AGTTTAAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
GGCTTGACAA	ATCTTATGT	GGGAAGTAAT	TATAGACCAT	CATTCTTCA	GGATAATGAG	660
CTCAGACATT	TAATCCTTAA	GACTGCAGAA	GGCTTCTTAT	TTGTGGTTGG	ATGTGAAAGA	720
GGAAAAATTC	TCTTCGTTC	TAAGTCAGTC	TCCAAAAATAC	TTAATTATGA	TCAGGCTAGT	780
TTGACTGGAC	AAAGCTTATT	TGACTTCTTA	CATCCAAAAG	ATGTTGCCAA	AGTAAAGGAA	840
CAACTTCTCT	CTTTTGATAT	TTCACCAAGA	GAAAAGCTAA	TAGATGCCAA	AACTGGTTTG	900
CAAGTTCACA	GTAATCTCCA	CGCTGGAAGG	ACACGTGTGT	ATTCTGGCTC	AAGACGATCT	960
TTTTTCTGTG	GGATAAAGAG	TTGTAAAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
AACTCAAAGA	AGAAAGGACA	CAGAAAATTC	TATACTATCC	ATTGCACTGG	TTACTTGAGA	1080
AGCTGGCCTC	CAAAATATTGT	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAAACAGT	1140
AAITTTTACCT	GCCTTGTGGC	CATTGGGAAG	TTACAGCCAT	ATATTGTTC	ACAGAACAGT	1200
GGAGAGATTA	ATGTGAAGCC	AACCTGAATT	ATAACCCGGT	TTGCAGTGAA	TGGAAAATTT	1260
GTCTATGTAG	ATCAAAGGGC	AACAGCGATT	TTAGGATATC	TGCCTCAGGA	ACTTTTGGGA	1320
ACTTCTTGT	ATGAATATTT	TCATCAAGAT	GACCACAATA	ATTGACTGA	CAAGCACAAA	1380
GCACTCTTAC	AGAGTATAGG	GAAAATACTT	ACAGATTCTT	ACAAATTCAG	AGCAAAAGAT	1440
GGCTCTTTTG	TAAGTTTAAA	AAGCCAAATG	TTAGTTTCA	CAATCCTTG	GACAAAAGAA	1500
CTGGAATATA	TTGTATCTGT	CAACACTTTA	GTTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
TCATTTTATC	CTGTAGCTC	TCATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
GTACCTGGAA	TGCTTACTGG	AACAGTACTT	GGTGCTGGTA	GTATTGGAAC	AGATATTGCA	1680
AATGAAATTC	TGGATTTACA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTCGAGTCCA	1740
ACAGGTTTAA	TGAAGATATA	TCATCTGTA	AACCTGCAGG	GTATGTCAA	TAAGGAGTTG	1800
TTTCCACCAA	GTCCTTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCCAAA	CCAGAGTACT	1860
GTGTCTGTCC	ACAGCCATGA	GCCACTCCTC	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCATTATAGA	ATTACTTAGA	AGCAGAGGGG	1980
GGCCTGGGAG	ACCCTGGGAG	TTCACTGAC	ATCCAGTGGG	CCCTTAGGCC	TTTGATTTT	2040
AACTCCAAAA	ATGAGAAACA	TTTAAAGCA	TTATTTACGA	AAAACTGTC	TCAACTATTC	2100
TTAAGTACTG	TATTGATATT	GTTTGTATCT	TTTATTAATG	TTCTACCCT	TTTTATAGAT	2160
TTGCATCTTC	CTGTACACAG	GATGTGGGA	AATACGTTT	CCTCCCAAG	GAACCAAGTT	2220
TATTATAGAC	TCCCTTATTC	AGTGAATGG	CTTATAATCC	ACTAGTTGCC	ATATTTTTCG	2280
TAAATATATT	CTAACCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTGA	2340
TGCAGTTTTT	TTTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTTCTTTGT	GTCTAAGATT	2400
GATTATATAAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCCCTGCG	AATTTCTCTA	2460
ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAACAT	TTAAAGGGAC	2520
AGTGCAATTT	ATAGTCATAA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
GATTTCTTGC	TTAAAATCTA	GAAAGTCAA	AGAGTTTCAG	CTTCTCTTAC	AGAAAAGGAA	2700
GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTTAC	TCTTAATAGG	2760
CCAGAGCTGG	TGCTCACGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
CTTGAGGTCA	AGGCTGGGGA	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
AATACAAAAA	AAATTACCCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
TGACAGTCCA	TTGATGAGCG	CAAGGCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
ACTGCTTGGG	AGGCTGAGGC	GAGAGGATTG	CTTGAACCTG	GGAGGCAGAG	GTTCAGTGA	3060
GCGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
AGTAAAAAAA	AAGATTTAAT	ATAATCACTG	AAGATCTCTA	TTATAGATAG	ATTAGGTTTT	3180
TGACATTGGA	AACATATCTA	GGGATAGATT	TGCTCTAAAG	GAAAAAAGTA	GGCCCGGGCA	3240
GATTAAATGT	CTTGTTGTA	GTCAACATT	AAATTCAGTC	ACACATTAAA	TTCATAGAGT	3300
TTTAAATGTT	TAATGTATAT	AAACAGTTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
CACAGATTAA	ATGATTAACT	AACCTGACCA	GGAACCTAGT	GTAGCTTTCT	AAGTAATTAG	3420
GCAATTACAG	TTATTGCCCTG	TAACCAAGG	TAATAAAACA	AAATGACAAG	TACATGTTTA	3480
AAATTATGAG	GCAATGAGAA	ATAATTTAAA	AACCAATTTT	CTAGTTATAA	TTTAAATTT	3540
GGAGAGCATT	TTTAAACAGTA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAATTAAAG	3600
ATTATTTAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTTCTGCT	3660
TCAGTAGCTC	TTCATAGCTT	GCCAAGTATG	CTCCATATT	TTCTCTCTG	TGCTCGCAA	3720
ATGAAAGTCA	GATAGGCTGG	GAACTCATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
AAATCCAGTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTCCAG	AAAATTTCCC	TCAGAGCCCC	3840
TCGCCAAAAA	AAAGCATAT	TTTGACCTG	CATGCTATTT	CTTAGCTGT	AGGTGATAGA	3900
TTAGAACTTC	TGTCAGACAT	GTTAATGACA	AACATACCAA	CAGACAATAA	CCAAAGCAAA	3960
TGTTTCTCTC	AAGTGTGAAA	TGTGCAGGGG	CTCGTGGGCA	AGGATGTATT	GGCACACTGT	4020
CCTCTTGAAC	TGATAGTGT	CCAGCAATGT	TGGAGGTTGG	CACCATTCCT	GGTCCGACAC	4080
TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTACA	AGATGGGGAG	4140
AAATGTGTGT	CAGCAGCCTA	AGTGTATAG	TTAAGTCTAA	AGAAGTATGA	AAGATCCCTC	4200
GTGTTCTCTA	AATTGAGCAG	AGGGGCTGCT	CTACCAATAT	CACCTTTTAG	GGGACTGAAC	4260
CATTGCAGGT	TAGACTTGGC	TTCCAAGAG	TCTGCCTAAG	CCAGGGGTGG	CAGGGTAGGC	4320
CATCATAGCT	GGATGGCCTC	AAAAGCAGAT	GGGGGCGAGC	TTGCCCTCGT	GATGCCAGGA	4380
TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCT	CTCACAGTGG	CAGTTTTC	4440
TCTTTGCAAG	AGGAGGGGCT	GTCAATTCC	ATAGACCAGT	GGGCAGATAG	CCAGTTGAAT	4500
ACTCTGTGCA	TGGTTTGATC	CTTTATTAGT	TOGCTCTAAT	ATTTTCTGT	AGATCCTTTT	4560
GTCCCTGGACT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
GTTCCTCTTA	AAATGTTTTA	GTTCCTTCA	ACTAAATTTG	ATTTTGTCTG	TTAGAGTGA	4680
CATATTTTTA	TGGTATACAC	TATGTTCTCT	TTTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAAACAG	TACTCTAGAG	4800

	CAGCGCTGTC	CAATAGAAAT	ATAATCTGAG	CCACATGTAT	AATTTTATTT	TCTTCTAGCC	4860
	ACATTAAAGA	AGTAAAAAGA	TACAAGTAGA	ACTAATTTTA	ATGTTTAAAT	TCAGTATATC	4920
	CAAAATATCA	TTTGAAACATG	TAATTAATAT	AAAATTATTA	ATGTGATATT	TTACATTCTT	4980
5	TTGGTAATAC	TAGTCTTCAA	AATCTGGTAT	GTATCTTACA	TTGATAGCAC	ATCTCACTTT	5040
	GTACTAGCCA	CATTGCAAGT	GCTCAGTAGC	CACATGTGGC	TAGTGGCTAC	TGCACCTGGAC	5100
	AGCACAATTC	TAGTCTCCAC	CCTAACACCC	AAGTCCGTGG	GATTAGAATC	CCAGAATCAG	5160
	AGCTGGAAGT	AAACATAGAG	ATCAAAACCTC	CTTTTAAAAA	TGAGGACGCT	GAGGCACAGA	5220
	GTTTAAATGG	CTTGCACTAG	GTACATACAG	TAAATTCAGC	CTCAACAGGG	TCTTCTGATT	5280
10	CCAGGCACCT	TTCCCACTCC	ACTACATTAC	TGTAGTGGTA	ATTCTTAGGG	TIAAAAAAAG	5340
	TGTAGAGTAG	GCCGGGGCGCA	GTGGCTCATG	CCTGTAATCC	CAGCAGTTTG	GGAGGCCGAA	5400
	GTGGGCGGAT	CACGAGTGCA	GGAGATCGAG	ACCATCCTGG	CCAACATGGT	GAACCCCGGT	5460
	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCG	5520
	CTGCTCTGGA	GGCTGAGGCA	GAATGGCGTG	AACCCAGGAG	GCAGAGATGG	CAGTGAGCCA	5580
	AGATCGCGCC	ACTGCAACCC	AGCCTGGGCG	ACAGAGCGAG	ACTCCATCTC	AAAAAAAATA	5640
15	AAAAAAAATA	AAGAAAAAG	AAGAAAAATC	TAGAGAACAT	TATATTAAGT	GGTTATTATT	5700
	GAAGTAGACC	AAAGTTTATA	CCATAAGGAT	ATTTTTCTTT	AAATACCATG	TTTGAAGAAC	5760
	AATTATTTAT	TGATCCTTGA	ATCTGTAAGA	TCAAATAACA	AGTCTCTATC	CATGTTACCA	5820
	AATTTAACCT	TTTGAATAA	ATAAACTTTA	AAATATCAGA	TGTTGTATTA	CAGGATGATA	5880
20	CTTGAATCA	AGTGAATGA	GTTATATGGT	CATCACTAAA	TTTAGAAATC	TATTGTGAAA	5940
	CAAAGACAAA	CAGGAAAGTA	CAGAATAGAG	ACTTTTAGTA	AATAAATGGA	ATTTAAAAAG	6000
	AAGTGTTTAT	TTACAGTGTC	ACGACAGAAA	AGGATGTCTT	TGTTGTCTTA	GTCTTTGAGG	6060
	GATCTCCGTA	AAATCTGGGG	CACAGGTACA	AGAAATAGCC	AATATTAGT	TCCAGACCA	6120
	TGTTTAGTAG	TGTCACATTT	CAGATCATGC	TGCCAAGAGG	TATCTCCCCC	TCAGGTGGGT	6180
	CATCACTGAG	CCCTGGAATT	GGAGACTCAT	ACTTGCCGAG	CACAATGTTA	CGGGCAGACA	6240
25	GGCCGACATC	TATGATTAGC	TAGAAGCCAT	AAAGAAAAGC	TGCTAAGTGG	CCAATAGGTG	6300
	CCACTTTTCT	GTTTTGTGAA	TGCTTTTCAT	AGCAGATCTT	TTTTTTCCAA	GCTCCATGGG	6360
	GCCTATGAGA	GGCATTATTG	ATTTTTGTGC	CTACAATAAG	TCAGCCTGTC	TGGTGTGAGT	6420
	TGTTTTATGA	GAATGCTTT	CCAAGGGAGG	TCTAGGAAGA	TCCAGACACA	TAAAGACTTT	6480
	GGCTTAGAGA	GCTTTCCAGG	TGTAGTGCCA	ATAAAAACCTG	ACCTGGAAAG	AAAACCTGCC	6540
30	CAGCAGCGAA	CATGCTTTCT	GAACCTCACT	GAGAGTGTAT	GGTGTATGTC	ACTTCTCATA	6600
	TATTCTTGAG	TTTAGATTGG	TCTTTTATAC	AATTTTATAGC	TCTTTTCCAG	TTCACCTGTG	6660
	CTGCTCTGTA	TATTGGTATT	TTTAAATTTT	TGTGGTAAAT	AATGAAAAGA	GTGAAATTAT	6720
	ATTTTATAAT	TACTCATTTG	TAGTTTTTTT	TTTTAATTTA	ATAAACTTCC	TCCAAAAGT	6780
35	GCTCCCTTAA	AA					

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

40	1	11	21	31	41	51	
	MAAEBAEAAAG	GKVLREENQC	IAPVVSSRV	PGTRPTAMGS	FSSHMTFPPR	KRKGSDSDPS	60
	QVEDGHEQVQK	MKAFREAHSQ	TEKRRRDKN	NLIEELSAMI	PQCNPMARKL	DKLTVLRLMAV	120
	QHLRLSLKGLT	NSYVGSNYRP	SFLQDNELRH	LILKTAEGFL	FVVGCEGRKI	LFVSKSVSKI	180
45	LNVDQASLTG	QSLDFDLHPK	DVAKVKEQLS	SFDISPREKL	IDAKTGLQVH	SNLHAGRTRV	240
	YSGSRSPFC	RIKSKISVQ	EEHGCLEPSK	KKEHRKFYTI	HCTGYLRSWP	PNIVGMEER	300
	NSKDNSTFT	CLVALGRQP	YIVPQNSGEI	NVKPTBFITR	FAVNGKFVYV	DQRATAILGY	360
	LPQELLGTSC	YEFPHQDDNH	NLTDKHKAVL	QSKEKILTDS	YKFRKDGSP	VTLKQWFSF	420
	TNPWTKELEY	IVSVNTLVLG	HSEPGAEASF	PCSSQSSEES	SRQSCMSVPG	MSTGTVLGAG	480
50	SIGTDIANEI	LDLQLQSSS	YLDSSPTGL	MKDTHTVNCR	SMSNKELFPF	SPSEMGELEA	540
	TRQNQSTVAV	HSHEPILLSG	AQLDFDALCD	NDDTAMAAFM	NYLEAEGGLG	DPGDFSDIQW	600
	TL						

Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

60	1	11	21	31	41	51	
	GGTTACTCAT	CCTGGGCTCA	GGTAAGAGGG	CCCGAGCTCG	GAGGCGGCAC	ACCCAGGGGG	60
	GAGCCCAAGG	GAGCAGGACG	GAGCCATGGA	CCCGCCAGG	AAAGCAGGTG	CCCAGGCCAT	120
	GATCTGGACT	GCAGGCTGGC	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGACGA	AAGCAGATGA	CGGATGCTCC	CCGAACAAGA	TGAAGACAGT	240
	GAAGTGCGCG	CCGGCGCTGG	ACGTCTGCAC	CGAGGCCGTG	GGGGCGGTGG	AGACCATCCA	300
65	CGGACAATTC	TGCTGCGCAG	TGCSGGGTTG	CGGTTGCGGA	CTCCCCGGCA	AGAATGACCG	360
	CGGCGCTGGAT	CTTCACGGGC	TTCTGGCGTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
	CTGCAACGCC	AAGCTCAACC	TCACCTCGCG	GGCGCTCGAC	CCGGCAGGTA	ATGAGAGTGC	480
	ATACCCGCCCC	AACCGCGTGG	AGTGCTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCGTGCCA	540
	GGGTACATCG	CCGCGGCTCG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
70	CTTGCACGGC	AACGTCACTT	TGACGGCAGC	TAATGTGACT	GTGTCCTTGC	CTGTCCGGGG	660
	CTGTGTCCAG	GATGAATCTT	GCACCTCGGA	TGGAGTAACA	GGCCCAAGGT	TCAAGCTCAG	720
	TGGCTCCTGT	TGCCAGGGGT	CCCGCTGTAA	CTCTGACCTC	CGCAACAAGA	CCTACTTCTC	780
	CCCTCGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCCACGACTG	TGGCTCAAC	840
	CACATCTGTC	ACCACCTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
75	GCCAGCGCCA	ACCAGTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCCT	CCCGGATGA	960
	GGAGCCCAAG	TGACTGAGG	GCGCCGCTGG	CCACCAGGAC	CGCAGCAATT	CAGGGCAGTA	1020
	TCCTGCAAAA	GGGGGGCCCC	AGCAGCCCCA	TAATAAAGGC	TGTGTGGCTC	CCACAGCTGG	1080
	ATTGGCAGCC	CTTCTGTTTG	CCGTGGCTGC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
80	AAATTTCCCT	CTCACCTACT	TCTCTGGCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTCTGT	1200
	CCCACCACTG	GACTGGGCTG	GCCAGCCCCC	TGTTTTTCCA	ACATTCACCA	GTATCCCCAG	1260
	CTTCTGCTGC	GCTGTTTTCG	GGCTTTGGGA	AATAAAATAC	CGTTGTATAT	ATTCTGGGCA	1320
	GGGTGTTCTA	GCTTTTTGAG	GACAGCTCCT	GTATCCTTCT	CATCCTGTGC	TCTCCGCTTG	1380
	TCCTCTTTTG	ATGTTAGGAC	AGAGTGAGAG	AAGTCAGCTG	TCACGGGGAA	GGTGAGAGAG	1440
	AGGATGCTAA	GCTTCTACTG	CACTTTCTCC	TAGCCAGCCT	GGACTTTTGA	GCGTGGGGTG	1500
85	GGTGGGACAA	TGGCTCCCCA	CTCTAAGCAC	TGCTCCCCCT	ACTCCCCGCA	TCTTTGGGGG	1560
	ATCGGTTCCC	CATATGTCTT	CCTTACTAGA	CTGTGAGCTC	CTCAGGGGCA	GGGACCGTGC	1620
	CTTATGTCTG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

TTGTATAGTG AAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

1 11 21 31 41 51
MDPARKAGAQ AMIWTAGNLL LLLLRRGGAQA LECYSCVQKA DDGCSPNKMK TVKCAPGVVDV 60
CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT 120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCCFDGNVTLT 180
AANVTYSLPV RGCQVDEPCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240
LPPPEPTTVA STTSVTSTST APVRPTSTTK PMPAPTSQTP RQGEHEASR DEEPRLTGGA 300
AGHQDRSNGS QYPAKGGPQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

1 11 21 31 41 51
GAATTCGGCA CGAGCGCGCG GCGAATCTCA ACGCTGCGCC GTCTGCGGGC GCTTCGGGGC 60
CACCAGTTTC TCTGCTTTCC ACCCTGGCGC CCCCCAGCCC TGGCTCCCCA GCTGCGCTGC 120
CCCGGGCGTC CACGCCCTGC GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CGCAGCGCCA 180
CCTCCATGTT GACCAAGCCT CTACAGGGGC CTCGCGCGCC CCGCGGGACC CCCACGCGCC 240
CGCCAGGAGG CAAGGATCGG GAAGCGTTCG AGGCCGAGTA TCGACTCGGC CCCCTCCTGG 300
GTAAGGGGGG CTTTGGCACC GTCTTCGCG GACACCGCCT CACAGATCGA CTCAGGTGG 360
CCATCAAAAT GATTCGCCGG AATCGTGTGC TGGGCTGGTC CCCCTGTGCA GACTCAGTCA 420
CATGCCCACT CGAAGTGCBA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCTTGGCG 480
TGATCCGCCT GCTTGACTGG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTCGAGCGGC 540
CTTTGCCCGC CCAGGATCTC TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC 600
CAAGCCGCTG CTTCTTTGGC CAAGTAGTGG CAGCCATCCA GCACTGCCAT TCCCGTGGAG 660
TTGTCCATCG TGACATCAAG GATGAGAACA TCCTGATAGA CCTACGCGT GGCTGTGCCA 720
AATCATTTGA TTTTGGTTCT GGTGCCCTGC TTTATGATGA ACCCTACACT GACTTTGATG 780
GGACAAGGGT GTACAGCCCC CCAGAGTGGG TCTCTCGACA CCAGTACCAT GCACTCCCGG 840
CCACTGTCTG GTCAGTGGC ATCTCTCTCT ATGACATGGT GTGTGGGGAC ATTCCCTTTG 900
AGAGGGACCA GGAGATTCTG GAACTGAGC TCCACTTCCC AGCCCATGTC TCCCCAGACT 960
GCTGTGCCCT AATCCGCGCG TGCGTGGCCC CCAAACCTTC TCCCGGACCC TCACTGGGAG 1020
AGATCCTGCT GGACCCCTGG ATGCAAAAC CAGCCGAGGA TGTACCCCT CAACCCCTCC 1080
AAAGGAGGCC CTGCCCCCTT GGCCTGGTCC TTGCTACCTT AAGCCTGGCC TGGCCTGGCC 1140
TGGCCCCCAA TGGTCAGGAG AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATTT 1200
GTTGACTTGG TTTTACAGGT CATTACCACT CATTAAAGTC CAGTATTACT AAGGTAAGGG 1260
ATTGAGGATC AGGGGTTAGA AGACATAAAC CAAGTTTGCC CAGTTCCTT CCAATCTCTA 1320
CAAAGGAGCC TTCTCCCGAG AACCTGTGGT CCCTGATTTT GGAGGGGGAA CTTCTTGCTT 1380
CTCATTTTGC TAAGGAAGTT TATTTTGGTG AAGTTGTTCC CATTTTGAGC CCGGGGACTC 1440
TTATTTTGAT GATGTGTAC CCCACATTGG CACCTCCTAC TACCAACACA CAAACTTAGT 1500
TCATATGCTT TTACTTGGCG AAGGGTGCTT TCCTTCCAAT ACCCCAGTAG CTTTATTTT 1560
AGTAAAGGGA CCGTTTCCCC TAGCCTAGGG TCCCATATTG GGTCAAGCTG CTTACTTGCC 1620
TCAGCCGAGG ATTTTATTAT TTGGGGGAGG TAATGCCCTG TTGTTACCCC AAGGCTTCTT 1680
TTTTTTTTTT TTTTTTTTTT GGTGAGGGGA CCTACTTTG TTATCCCAAG TGCTCTTATT 1740
CTGGTGAGAA GAACCTTAAT TCCTAATTTT GGAAGGAAT GGAAGATGGA CACCACCGGA 1800
CACCACCAGA CAATAGGATG GATGATGATG TTTTGTGGG GATGGGCTAG GGGAAATAAG 1860
GCTTGCTGTT TGTTCCTGCG GGGCGCTCCC TCCAATTTTG CAGATTTTGT CAACCTCCTC 1920
CTGAGCCGGG ATTTGCCAAT TACTAAATG TAAATAATCA CGTATTGTGG GAGGGGGAGT 1980
TCCAAGTGTG CCCTCCTTTT TTTTCTGCCC TGGATTATTT AAAAAGCCAT GTGTGGAAAC 2040
CCACTATTTA ATAAAGTAA TAGAATCAGA AAAAAA AAAAAA

Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

1 11 21 31 41 51
MLTKPLQGGP APPGPTPTPP GGDREAFEA EYRLGPLLKG GGFGTVFAGH RLTDRLQVAI 60
KVIPRNRVLG WSPLESDSVTC PLEVALLWKV GAGGGHPGVI RLDDWFETQE GFMLVLERPL 120
PAQDLFDYIT EKGPLGEGFS RCFGQVVAI IQHCHSRGVV HRDIKDENIL IDLRRGCAKL 180
IDFGSGALLH DEPYTDFDGT RVYSPPEWIS RHQYHALPAT VWSLIGILYD MVCGDIPFER 240
DQBILEAEEL FPAHVSPDCC ALIRRCCLAPK PSSRPSLEEI LLDPMWQTPA EDVTPQPLQR 300
RPCPFGVLVA TSLAWPLGA PNGQKSHFMA MSQG

Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

1 11 21 31 41 51
GCGGCGCGGA GCGGGCGTGC TGAGCCCCGG CCGCCGGCCC GGCATGGGCG TCTCCCGCGG 60
GCCCTCCGCC GCGCGGGGCT AGGCGCGGAT GGAGCCGCGG GACCGTAGCC CCGAGGCCCCG 120
GAGCAGCGAC TCCGAGTCGG CTTCGCGCTC GTCCAGCGGC TCCGAGCGCG ACGCCGCTCC 180
CGAGCCGAGC AAGGCGCGCG GCGGACTCAA CAAGCGCGCG TCCCGGGGCG TCGGCTCTT 240
CGGGCAGCAG AAAGCCATCA CCAAGTCGGG CTCCAGCAC CTGGCCCCC CTCCGCCCC 300
CCCTGGGGCC CCGTGCAGCG AGTCAGAGCG GCAGATCCGG AGTACAGTGG ACTGGAGCGA 360
GTCAGCGACA TATGGGAGC ACATCTGGTT CGAGACCAAC GTGTCCGGGG ACTTCTGCTA 420
CGTTGGGGAG CAGTACTGTG TAGCCAGGAT GCTGAAGTCA GTGTCTCGAA GAAAGTGCGC 480
AGCCTGCAAG ATTGTGGTGC ACAGCCCTCG CATCGAGCAG CTGGAGAGAA TAAATTTCCG 540
CTGTAAAGCG TCCTTCCGTG AATCAGGCTC CAGGAATGTC CGCGAGCCAA CCTTTGTACG 600
GCACCACTGG GTACACAGAC GACGCCAGGA CGGCAAGTGT CGGCACTGTG GGAAGGGATT 660
CCAGCAGAAG TTCACCTTCC ACAGCAAGGA GATTGTGGCC ATCAGCTGCT CGTGGTGCAA 720

GCAGGCATAC CACAGCAAGG TGCTCTGCTT CATGCTGCTAG CAGATCGAGG AGCCGTGCTC 780
 GCTGGGGGTC CACGCAGCCG TGCTCATCCC GCCCACCTGG ATCCTCCGCG CCCGAGGGCC 840
 CCAGAAATCT CTGAAGAGCA CCAAGAGAGG GAAGAGGGCA TCCTTCAAGA GGAAGTCCAG 900
 CAAGAAAGGG CCTGAGGAGG GCGCTGGAG ACCCTTCATC ATCAGGCCCA CCCCCTCCCC 960
 5 GCTCATGAAG CCCCTGCTGG TGTATTGTGA CCCCAAGAGT GGGGGCAACC AGGGTGCAAA 1020
 GATCATCCAG TCTTTCCTCT GGTATCTCAA TCCCAGACAA GTCTTCGACC TGAGCCAGGG 1080
 AGGGCCCAAG GAGGCGCTGG AGATGTACCG CAAAGTGAC AACTTGCGGA TCCTGGCGTG 1140
 CGGGGGCGAC GGCACGCTGG GCTGGATCCT CTCCACCCTG GACCAGCTAC GCCTGAAGCC 1200
 10 GCCACCCCTT GTTGCCATCC TGCCCTCTGG TACTGGCAAC GACTTGGCCC GAACCTCAA 1260
 CTGGGGTGGG GGCTACACAG ATGAGCCTGT GTCCCAAGAT CTCTCCCAAG TGGAGGAGGG 1320
 GAACTGTGTA CAGCTGACCC GCTGGGACCT CCAAGCTGAG CCCAACCCCG AGGCAGGGCC 1380
 TGAGGACCGA GATGAAGCGG CCACCGACCG GTTGCCCTCT GATGTCTTCA ACAACTACTT 1440
 CAGCCTGGGC TTTGACGCCC ACGTCACCTT GGAGTTCAC GAGTCTCGAG AGGCCAACCC 1500
 AGAGAAATTC AACAGCCGCT TCGGAATAA GATGTCTTAC GCGGGGACAG CTTTCTCTGA 1560
 15 CTCTCTGATG GGCAGCTCCA AGGACCTGGC CAAGCACATC CGAGTGGTGT GTGATGGAAT 1620
 GGACTTGAAT CCAAGATCC AGGACCTGAA ACCCCAGTGT GTTGTCTTCC TGAACATCCC 1680
 CAGGTACTGT GCGGGCACCA TGCCCTGGGG CCACCTGGG GAGCACCACG ACTTTGAGCC 1740
 CCAGCGGCAT GACGACGGCT ACCTCGAGGT CATTGGCTTC ACCATGAGT CGTTGGCCCG 1800
 20 GCTGCAGGTG GCGGAGACAG GCGAGCGGCT GACGCGAGT GCGAGGTGG TGCTCACCAC 1860
 ATCCAGGGCC ATCCCGGTGC AGGTGGATGG CGAGCCCTGC AAGCTTGACG CCTCAGCAT 1920
 CCGCATGGCC CTGCGCAACC AGGCCACCAT GGTGCAGAG GCGAAGCGGC GGAGCGCCCG 1980
 CCCCCTGCAC AGCGACCCAG AGCCCGTGCC AGAGCAGTTG CGCATCCAGG TGAGTCCGCT 2040
 CAGCATGACG GACTATGAGG CCCTGCACTA CGACAAGGAG CAGCTCAAGG AGGCCCTCTG 2100
 GCGCTGGGC ACTGTGTGG TCCAGGAGA CAGTGACCTA GAGCTCTGCC GTGCCACAT 2160
 25 TGAGAGACTC CAGCAGGAGC CCGATGGTGC TGGAGCCAAG TCCCGACAT GCCAGAACT 2220
 GTCCCCCAAG TGGTGCTTCC TGAGCGCCAC CACTGCCAGC CGTCTCTACA GGATCGACCG 2280
 AGCCAGGAG CACCTCAACT ATGTGACTGA GATCGACAG GATGAGATT ATATCTTGA 2340
 CCCTGAGCTG CTGGGGGCAT CGGCCCGGCC TGACCTCCCA ACCCCACTT CCCCCTCTCC 2400
 30 CACCTCACCC TGCTCACCCA CGCCCGGTC ACTGCAAGGG GATGCTGCAC CCCCTCAAGG 2460
 TGAAGAGCTG ATTGAGCTG CCAAGAGGAA CGACTTCTGT AAGCTCCAGG AGCTGCACCG 2520
 AGCTGGGGGC GACTCTATGC ACCGAGACGA GCAGAGTCCG ACGTCTCTGC ACCAGCAGT 2580
 CAGCACTGGC AGCAAGGATG TGGTCCGCTA CCTGCTGGAC CAGCCCCCCT CAGAGATCCT 2640
 TGATGCGGTG GAGGAAACG GGGAGACCTG TTTGCAACAA CGAGCGGCCCT TGGGCCAGCG 2700
 CACCATCTGC CACTACATCG TGGAGGCCGG GGCCTCGCTC ATGAAGACAG ACCAGCAGGG 2760
 35 CGCACTCCC CGGCAGCGGG CTGAGAAGGC TCAGGACACC GAGCTGGCCG CCTACTTGA 2820
 GAACCGGAG CACTACCAGA TGATCCAGCG GGAGGACCCG GAGACGGCTG TGTAGCGGGC 2880

Seq ID NO: 172 Protein sequence:
 Protein Accession #: NP_003637

1 11 21 31 41 51
 MEPRDGSPEA RSSDSSESASA SSSGSESDAG PEPDKAPRRL NKRRFPGLRL FGHRKAITKS 60
 GLQHLAPPPP TPGAPCSESE RQIRSTVDWS ESATYGEHIW FETNVSGDFC YVGEQYCVAR 120
 45 MLKSVSRKRC AACKIVVHTP CIEQLEKINF RCKPSFRESE SRNVREPTFV RHHVHRRRQ 180
 DGKRCRCHGG PQQKFTPHSK EIVAISSWC KQAYHSKVC FMLQIEEPC SLGVHAAVVI 240
 PPTWILRARR PQNTLKASKK KKRASFRRKS SKKGPEEGRW RPFIRPTPS PLMKPLLVPV 300
 NPKSGGNQGA KIIQSFYLWL NPRQVFDLSQ GGPKEALEMY RKVHNLILA CGGDGTGVGI 360
 50 LSTLDQLRLK PPPPVAILPL GTGNDLARTL NWGGGYTDEP VSKILSHVVE GNVVQLDRWD 420
 LHAEPNPEAG PEDRDEGATD RLPLDVFNNY FSLGFDHVT LEFHESREAN PEKFNRSFRN 480
 KMFYAGTAFS DFLMGSSKDL AKHIRVVCBG MDLTPKIQDL KPQCVPFLNI PRYCACTMEW 540
 GHFGEHDFPE PQRHDDGYLE VIGFTMTSLA ALQVGGHGER LTQCREVLT TSKAIPVQVD 600
 GEPCKLAASR IRIALRQAT MVQAKRRSA APLHSDQPPV PEQLRIQVSR VSMHDEYALH 660
 55 YDKEQLKEAS VPLGTVVVPG DSDLELCRAH IERLQOEPDG AGAKSPTCQK LSPKWCFLDA 720
 TTASRFYRID RAQEHNLNVT EIAQDEIYIL DPELLGASAR DPLPTPSPL PTSPCSPTR 780
 SLQGDAAAPQ GEELIEAAKR NDFCKLQELH RAGGDLMHRD EQSRTLHHA VSTGSKDVVR 840
 YLLDHAPPEI LDAVEENGET CLHQAALGQ RTICHYIVEA GASLMKTDQO GDTPRQRAEK 900
 AQDTELAAYL ENRQHYQMIQ REDQETAV

Seq ID NO: 173 DNA sequence
 Nucleic Acid Accession #: AF232772
 Coding sequence: 1-1662

1 11 21 31 41 51
 ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGCGCA CCAGCCTGTT TGCCCTGGCA 60
 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGAAAGAG 120
 CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACTGCT CATTGAGAGC 180
 70 CTTTTCGCTT TCCTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGCTGCCC 240
 TCCCGCGGC GGGGCTCGGT GGCACGTGTC ATTGCGCAT ACCAGGAGGA CCTGACTAC 300
 TTGCGCAAGT GCCTGCGCTC GGCACGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCTAG 360
 GTGGTGGATG GCAACGCCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
 GCGCGCACCG AGCAGGCCGG CTCTTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
 75 GGTGAGACCG AGGCAGCCTT GCAGGAGGGC ATGGACCGTG TCGGGGATGT GGTGCGGGCC 540
 AGCACCTTCT CGTGATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTGAT GTACAGGCC 600
 TTCAAGGCCCT TCGCGGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTCGA GTCCCTGAGG AGGATCCCCA AGTAGGGGGA 720
 GTCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTCT CTGAGCAGC 780
 80 GTGCGGTACT GGATGSCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900
 GACTGTATCC ATCAGAGTCT CTTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCTCT 1020
 ACAGAGACCC CACTAAGTGA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
 85 TACTTCGGG AGTGCTCTA CAACCTCTCT TGGTTCCATA AGCAACCACT CTGATGAC 1140
 TACGAGTCAG TGGTACCGG TTTCTTCCCC TTCTTCTCTA TTGCCAGGT TATACAGCTT 1200
 TTCTACCGG GCGCATCTG GAACATTCTC CTCTTCTCTG TGACGGTGCA GCTGGTGGG 1260
 ATTATCAAGG CCACCTAGCG CTGCTTCTCT CGGGGCAATG CAGAGATGAT CTTATGTTCC 1320

5 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGCGCA AGATCTTTGC CATTGCTACC 1380
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTCATTGGC 1440
 CTCATTCTCGT TGTCCATCTG GGTGGCAGTT CTCCTGGAGG GGCTGGGCTA CACAGCTTAT 1500
 TGCCAGGACC TGTTTCAGTGA GACAGAGCTA GCCTTCCTTG .TCTCTGGGGC TATACTGTAT 1560
 GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGGCTTTT GCTGAGGTGT GACATGGCCC CCAAGCAGAG 1680
 CGGGTAAAGT GCAATGGGTA AGGGAGGGAA GGGGAATGGA AGAGAAAAGA CAGGGTGGGA 1740
 GGGAGGAGGG AGTGCTGTGT TTTAGTCTCT TAATGGTCCA AAGGACAAAT CTAAATATGA 1800
 AAGAACGGTG ATGTAGTATG GCCTGACAGC TCTGTTTAGA GGAGGCAACA CTGATCCCCC 1860
 10 AGATGCAGGG CTGCAGGGGA TTCTGTGTTT TCAGACTGCC TGTCTGCTTG CATCTGCACA 1920
 TAGGCAGTAG CCTCTCTCTG GGTCCAGAG GGCACCTAGA AGTGTGCTA AACCAAGTTA 1980
 AGTCCCATTG AGTGGCAACT TGTGATAGGT ACCTGAGTGA CGGCAACCTG CGGAAGGAGG 2040
 TTCTCCAGC CCATCTGAAC ACAACCAGAG GTGGCAGGAG AATTTCTACT GAGCGAGGTG 2100
 GGCCGGTTAG TGTATGTAC CCCCACCCCA CCATAAGTA GTCATCAATG CAATAAGATT 2160
 15 GCGCGTGAGA TACAAGGCCC AGAAGCCTGA TCTTTGGGCA TCAGAAAACA GGGTCCAGGA 2220
 ATGGTGCTTT ATGTGAGATA CCCCACCTCA CATCAACATT CCAGGGATGA GCCAAACCAG 2280
 CAGGGAGTTA GCATGAAGT GCTTTTAAAA GTGCACATTA AAAAGGAAAG TTTGCCAGGA 2340
 GGAACAAAGA GATTGTGGTG GTGCTAAAG AGGCCATAAG CTACACAGAG GCCTTGGGTG 2400
 20 TTCCACCTGG AAACCTGCTCA GACGTCTAGA TGGGTTCTTA GCTTGTCTGT GATCTCTGCT 2460
 GGGGAGATAA AAGATTAAAG CCCCACCATG TTCAGAAAAG AAGTGAAGTC TTGGGTATTT 2520
 TAACCTGTAT ACTCTTGAAT TCTCTCAAA TTCAGCTCTG ATCTGAGGCT AAGACACACT 2580
 CCCCACCTCA CTTTCTCAA AGCCACATTT TTTGAGGTAT CACTGCAGTC ACCTCTTCTA 2640
 CCCTCATCAT CATAGGTAA GCTTTTCAAGG TGGCAATTGG GCGGAGCCCC CGGCTTCTTA 2700
 TAGAAGCTTC AGCAGGAGGC AAGCGTGTTC TCAGCACATA TGGGAACAT GAGGAGCCTC 2760
 25 TGATCAAAAT GGCTACAATC TTGGAGCTGC TTGGACGGAT TCCTTGGCAG CCGGTTTAGC 2820
 ATGTGTGACT TTCAGGCTAC TGTTCCTGAC AATCATCTCC AATGGAAGC TTTTCAGTGT 2880
 TCCCAAAGTG AACTCTCAA TCCAAATGG TTATCTTTGA GACCATCCAT TCTCCTCAGT 2940
 GGCTTCTCCA GGAATTTCTT ACAGCCAAGT TGTGACAGTC ACTGCATTG CTGCTTCTT 3000
 30 TCCAGAAACC AAACCTAGGAG ATGAAACTGG TTCCCTACAT CTAAGGTTCT TGCTTTCTCT 3060
 CTCACTGCTC CTGAGGCTGT TTTTGGCTGT TTTCCCTCTG CTGCTTTTGG GGAATGAGGG 3120
 GAAGCCATTT TCCAAGTGAC TTGCAATCCA GGCTGTTCTC AGCGTTTGA GTTTAAACC 3180
 TGGGATCCTG ACTAAGCCTT TGACTTAAGG GTTGCTTGTCT TGCCCTCCAA ATGTCCTTTC 3240
 TCAAAGGGGC CAACTAACCC GTGCAGAAC AGCACTAAGG TGGACAGCA ACAAGAGGGC 3300
 35 AAGCCTCTAA TGTACCAAGT GCTTCTTACA AAGACGCAAG GTGTGCTCCG AACCCAGAT 3360
 GGGCAAAACC TGGTGCTTTC CTTCATCTCC CACGAACTCA AGGTTTTC AAGTGTAGCT 3420
 AACAGTTGCC ACATCACACA GACCTCCAGT TTCTGGTAAG ACTGCTGGTT GACATCAGAC 3480
 CCAACCCATT GAAGGCTGGA AGGCAGCAGG CATTTGCTAA GGCAGCTGAT CCAGGCAATC 3540
 GTTCTGCTGG CCAAGAAGTT AAACATTTT GAGCATTTAGA ATGGAGGAAA TCCGCTCAGC 3600
 40 CAAGTGACAG GTTCAGACTT CGCTAAGGGC TTGTTTTTCT TCAGCATTTA CTTGAAGATT 3660
 AATGTAGGAT GACAGGCTCT CCTGGCTGTC CTACCATCAG CTCTGCCTTG CACTGTGGTC 3720
 GTCACATTTT CTCAATCAA AAACAGGCAG GTACAGGTAG TGGGCTCACA ACGTTTGACC 3780
 TCGACTGGTT TTTCTAAGTT ATTTTGTACA TTTTTCAGCA GCAAAACCAA ACTGGGCTT 3840
 CAGCTTTATC CCGGTTTCTT GCAAGGGAAG AGCCTTTATA CAATTGGACG CATTTTGGTT 3900
 45 TTTCTCATG GAGAATTCAA ATCCTCTTTT GTATTGTTTC TACAATAATT TGTAAACATA 3960
 TTTATTTTTA CTGCTTTTTT TTTTTTTTTT TAATTTTCAG GTCAGTTTTT TTATACTGCA 4020
 CTTATTGTG AAAATAAAGA TTCTCACAT

Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

50 1 11 21 31 41 51
 | | | | | |
 MPVQLTTLALR VVGTSPLPALA VLGGILAAAYV TGYQFIHTEK HYLSFGLYGA ILGLHLLIQS 60
 LFAFLERHRM RRAGQALKLP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVV 120
 55 VVDGNRQEDA YMLDIFHEVL GGTEQAGFPV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSCIMQKW GSKREVMYTA PKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQLFLE 300
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS 360
 YFREWLYNSL WFKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRINIL LFLLTVLQVG 420
 60 IIKATYACFL RGNAMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFPG 480
 LIPVSIWVAV LLEGLAYTAY CQDLFSETEL AFLVSGAILY GCVWVALLML YLAIIARRCG 540
 KKPEQYSLAF AEV

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

65 1 11 21 31 41 51
 | | | | | |
 CCAGGAGCCC CAGTTACCGG GAGAGGCTGT GTCAAAGGCG CCATGAGCAA GATCAGCGAG 60
 GCCGTGAAGC GCGCCCGCGC GGCCTTCAGC TCGGGCAGGA CCCGTCGCT GCAGTCCGA 120
 70 TTCCAGCAGC TGGAGGCGCT GCAGCGCCTG ATCCAGGAGC AGGAGCAGGA GCTGGTGGGC 180
 GCGCTGGCCG CAGACCTGCA CAAGAATGAA TGGAAACGCT ACTATGAGGA GGTGGTGATC 240
 75 GTCCTAGAGG AGATCGAGTA CATGATCCAG AAGCTCCCTG AGTGGGCGC GGATGAGCCC 300
 GTGGAGAAGA CCCCCAGAC TCAGCAGGAC GAGCTCTACA TCCACTCGGA GCCACTGGGC 360
 GTGGTCTCTG TCATTGGCAC CTGGAATAC CCCTTCAACC TCACCATCCA GCCCATGGT 420
 GCGCGCATCG CTGACGGGAA CGCAGTGGTC CTCAAGCCCT CGGAGCTGAG TGAGAACATG 480
 80 GCGAGCCTGC TGGCTACCAT CATCCCCAG TACCTGGACA AGGATCTGTA CCCAGTAATC 540
 AATGGGGGTG TCCTTGAGAC CACGGAGCTG CTCAAGGAGA GGTTCGACCA TATCCTGTAC 600
 ACGGGCAGCA CCGGGGTGGG GAAGATCATC ATGACGCTG CTGCCAAGCA CCTGACCCCT 660
 GTCACGCTGG AGCTGGGAGG GAAGAGTCCC TGCTACGTGG ACAGAACTG TGACCTGGAC 720
 GTGGCCTGCC GACGCATCGC CTGGGGGAAA TTCTGAACA GTGGCCAGAC CTGCGTGGCC 780
 85 CCAGACTACA TCCTCTGTGA CCCCTCGATC CAGAAACAAA TTGTGGAGAA GCTCAAGAAG 840
 TCACTGAAG AGTTCTACGG GGAAGATGCT AAGAAATCCC GGGACTATGG AAGAATCATT 900
 AGTGCCCGGC ACTTCAGAG GGTGATGGGC CTGATTGAGG GCCAGAAGGT GGCTTATGGG 960
 GGCACCGGGG ATGCCGCCAC TCGCTACATA GCCCCACCA TCCTCACGGA CGTGGACCCC 1020

CAGTCCCCGG TGATGCAAGA GGAGATCTTC GGGCCTGTGC TGCCCATCGT GTGCGTGC GC 1080
 AGCCTGGAGG AGGCCATCCA GTTCATCAAC CAGCGTGAGA AGCCCTGGGC CCTCTACATG 1140
 TTCTCCAGCA AGCACAAGGT GATTAAGAAG ATGATTGCAG AGACATCCAG TGGTGGGGTG 1200
 GCGGCCAAGC ATGTCTATGT CCACATCAAC TTGCACTCTC TGCCCTTCGG GGGCGTGGGG 1260
 AACAGGGGCA TGGGATCCTA CCATGGCAAG AAGAGCTTCG AGACTTTCTC TCACCCCGGC 1320
 TCTTGCTG TGAGGCCTCT GATGAATGAT GAAGGCCTGA AGGTCAGATA CCCCCGAGC 1380
 CCGGCCAAGA TGACCCAGCA CTGAGGAGGG GTTGCTCOGC CTGGCCTGGC CATACTGTGT 1440
 CCCATGGGAG TGGCGACCAC CCTCACTGGC TCTCTGGGCC CTGGAGAATC GCTCCTGCAG 1500
 CCCAGCCCCA CCCCCATCCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCACAT 1560
 GGGCCAGGCC CTCACCATTC CAAGTCTCCA CCCCTTTCTA GACCAATAAA GAGACAAATA 1620
 CAATTTTCTA ACTCGG

Seq ID NO: 176 Protein sequence:
 Protein Accession #: NP_000682

1 11 21 31 41 51
 MSKISEAVKR ARAAPSSGRT RPLQFRFQQL BALQRLIQEQ EQELVGLAA DLHKNEWNAV 60
 YEEVVVLEE IEYMIQKLPE WAADEPVEKT PQTQDELYI HSEPLGVVLV IGTWNYPFNL 120
 TIQPMVGAIA AGNAVVLKPS ELSENMAALL ATIIPOYLK DLYPVINGGV PETTELLKER 180
 FDHILYTGST GVGIKIMTAA AKHLTPVLE LGGKSPCYVD KNCOLDVACR RIAWGKFMNS 240
 GQTCVAPDYI LCDPSIQNQI VEKLKSLKE FYGEDAKSR DYGRISARH FQRVMGLIEG 300
 QKVAYGGTGD AATRYIAPTI LTDVDPQSPV MQEEIFGPVL PIVCVRSLEE AIQFINQREK 360
 PLALYMFSSN DVIKKMIAE TSSGGVAAND VIVHITLHSL PFGVGNSGM GSYHGKKSFE 420
 TFSHRRSCLV RPLMNDGLK VRYPPSPAKM TQH

Seq ID NO: 177 DNA sequence
 Nucleic Acid Accession #: NM_001067.1
 Coding sequence: 108-4703

1 11 21 31 41 51
 CTAACCGACG CGCGTCTGTG GAGAAGCGGC TTGGTGGGGG GTGGTCTCGT GGGGTCTGTC 60
 CTGTTTAGTC GCTTTACAGG TTCTTGAGCC CCTTCACGAC CGTCACCATG GAAGTGTCTAC 120
 CATTCGAGCC TGTAATGAA AATATGCAAG TCAACAAAT AAAGAAAAAT GAAGATGCTA 180
 AGAAAAAGCT GTCTGTTGAA AGAATCTATC AAAAGAAAAAC ACAATTGGAA CATATTTTGC 240
 TCCGCCAGCA CACCTACATT GGTCTGTGG AATTAGTGAC CCAGCAATG TGGGTTTACG 300
 ATGAAGATGT TGGCATTAA TATAGGGAAG TCACTTTGT TCCTGGTTTG TACAAATCT 360
 TTGATGAGAT TCTAGTTAAT GCTGCGGACA ACAAACAAAG GGACCCAAAA ATGCTCTGTA 420
 TTAGAGTCAC AATTGATCCG GAAACCAATT TAATTAGTAT ATGGAATAAT GAAAAAGGTA 480
 TTCCTGTTGT TGAACACAAA GTTGAAAAGA TGTATGTCCC AGCTCTCAT TTTGGACAGC 540
 TCCTAAGTTC TAGTAAGTAT GATGATGATG AAAAGAAAGT GACAGGTGGT CGAAATGGCT 600
 ATGGAGCCAA ATTGTTGTAAC ATATTAGTAT CCAAAATTTAC TGTGGAACA GCCAGTAGAG 660
 AATACAAGAA AATGTTCAAA CAGACATGGA TGGATAATAT GGAAGAGCT GGTGAGATGG 720
 AACTCAAGCC CTTCAATGGA GAAGATTATA CATGTATCAC CTTTCAGCCT GATTGTCTA 780
 AGTTTAAAT GCAAAGCCTG GACAAAGATA TTGTTGCACT AATGGTCAGA AGAGCATATG 840
 ATATTGCTCG ATCCACCAA GATGTCAAAG TCTTCTTAA TGGAAATAAA CTGCCAGTAA 900
 AAGGATTCG TAGTTATGTG GACATGTATT TGAAGACAA GTTGGATGAA ACTGTAAT 960
 CCTTGAAGT AATACATGAA CAAGTAAACC ACAGGTGGGA AGTGTGTTTA ACTATGAGTG 1020
 AAAAAGGCTT TCAGCAAAAT AGCTTTGTCA ACAGCATGTC TACATCCAAG GGTGGCAGAC 1080
 ATGTTGATTA TGTAGCTGAT CAGATTGTGA CTAACTTGT TGTGTTGTG AAGAAGAAGA 1140
 ACAAGGGTGG TGTGTCAGTA AAAGCACATC AGGTGAAAA TCACATGTGG ATTTTGTAA 1200
 ATGCCCTAAT TGAAACCCCA ACCTTTGACT CTCAGACAAA AGAAAAACATG ACTTTACAAC 1260
 CCAAGAGCTT TGGATCAACA TGCCAATTGA GTGAAAAAT TATCAAGCT GCCATTGGCT 1320
 GTGGTATTGT AGAAAGCATA CTAACTGGG TGAAGTTAA GGCCCAAGTC CAGTTAAACA 1380
 AGAAGTGTTC AGCTGTAAAA CATAATAGAA TCAAGGGAAT TCCCAAACTC GATGATGCCA 1440
 ATGATGCAGG GGGCCGAAAC TCCACTGAGT GTACGCTTAT CCTGACTGAG GGAGATTGAG 1500
 CCAAACTTT GGCTGTTTCA GGCCTTGGTG TGGTGGGAG AGACAAATAT GGGGTTTCC 1560
 CTCTTAGAGG AAAAATACTC AATGTTGAG AAGCTTCTCA TAAGCAGATC ATGAAAAATG 1620
 CTGAGATTAA CAATATCATC AAGATTGTGG GTCTTCAGTA CAAGAAAAAC TATGAAGATG 1680
 AAGATTCATT GAAGACGCTT CGTTATGGGA AGATAATGAT TATGACAGAT CAGGACCAAG 1740
 ATGGTTCCCA CATCAAAGGC TTGCTGATTA ATTTTATCCA TCACAACCTG CCCTCTCTTC 1800
 TGGCAGATCG TTTTCTGGAG GAATTTATCA CTCCCATGT AAAGGTATCT AAAACAAGC 1860
 AAGAAATGGC ATTTTACAGC CTCTCTGAAT TTGAAGAGTG GAAGAGTTCT ACTCCAATC 1920
 ATAAAAAATG GAAAGTCAAA TATTACAAAG GTTTGGGCAC CAGCACATCA AAGGAAGCTA 1980
 AAGAATACTT TGCAGATATG AAAAGACATC GTATCCAGTT CAAATATTCT GGTCTGAAG 2040
 ATGATGCTCG TATCAGCCTG GCCTTTAGCA AAAACAGAT AGATGATCGA AAGGAATGGT 2100
 TAATAATTT CATGGAGGAT AGAAGACAAC GAAAGTTACT TGGGCTTCT GAGGATTACT 2160
 TGTATGGACA AACTACCACA TATCTGACAT ATAATGACT CATCAACAAG GAACCTATCT 2220
 TGTCTCAAAA TTCTGATAAC GAGAGATCTA TCCCTTCTAT GGTGGATGGT TTGAAACAG 2280
 GTCAGAGAAA GGTTTTGTGT ACTTGCTTCA AACGGAATGA CAAGCGAGAA GTAAAGGTTG 2340
 CCCAATTAGC TGGATCAGTG GCTGAAATGT CTCTTATCA TCATGGTGAG ATGTCACTAA 2400
 TGATGACCAT TATCAATTTG GCTCAGAAAT TTGTGGGTAG CAATAATCTA AACCTCTTG 2460
 AGCCCATTTG TCAGTTTGGT ACCAGGCTAC ATGGTGGCAA GGATTCTGCT AGTCCAAGAT 2520
 ACATCTTTAC AATGCTCAGC TCTTTGGCTC GATTGTTATT TCCACCAAAA GATGATCACA 2580
 CGTTGAAAGT TTTATATGAT GACAACCAGC GTGTGAGGCC TGAATGGTAC ATTCCTATTA 2640
 TTCCCATGGT GCTGATAAAT GGTGCTGAAG GAATCGGTAC TGGGTGGTCC TGCAAAATCC 2700
 CCAACTTTGA TGTGCGTGAA ATTGTAATA ACATCAGGCG TTTGATGGAT GGAGAAGAAC 2760
 CTTTGCCAAT GCTTCCAAGT TACAAGAACT TCAAGGTGAT TATTGAAGAA CTGGCTCCAA 2820
 ATCAATATGT GATTAGTGGT GAAGTAGCTA TTCTTAATTC TACAACCAT GAAATCTCAG 2880
 AGCTTCCCGT CAGAATATGG ACCAGACAT ACRAAGAACA AGTTCTAGAA CCCATGTTGA 2940
 ATGGCACCGA GAAGACACCT CCTCTCATA CAGACTATAG GGAATACCAT ACAGATACCA 3000
 CTGTGAAATT TGTGTGAAG ATGACTGAAG AAAAAGTGGC AGAGGCAGAG AGAGTTGGAG 3060
 TACACAAGT CTCAAACTC CAAACTAGTC TCACATGCAA CTCTATGGTG CTTTGTGACC 3120
 ACGTAGGCTG TTTAAAGAAA TATGACACGG TGTGGATAT TCTAAGAGAC TTTTGTGAAC 3180
 TCAGACTTAA ATATTATGGA TTAAGAAAAG AATGGCTCCT AGGAATGCTT GGTGCTGAAT 3240
 CTGCTAAACT GAATAATCAG GCTCGCTTTA TCTTAGAGAA AATGATGGC AAAATAATCA 3300

	TTGAAAATAA	GCCTAAGAAA	GAATTAATTA	AAGTCTTGAT	TCAGAGGGGA	TATGATTCCG	3360
	ATCCTGTGAA	GGCCTGGAAA	GAAGCCCAGC	AAAAGGTTCC	AGATGAAGAA	GAAAATGAAG	3420
	AGAGTGACAA	CGAAAAGAAA	ACTGAAAAGA	GTGACTCCGT	AACAGATTCT	GGACCAACCT	3480
5	TCAACTATCT	TCTTGATATG	CCCCTTTGGT	ATTTAAACCA	GGAAAAGAAA	GATGAATCTT	3540
	GCAGGCTAAG	AAATGAAAAA	GAACAAGAGC	TGGACACATT	AAAAAGAAAG	AGTCCATCAG	3600
	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCAAGG	3660
	AAAAACAAGA	TGAACAAGTC	GGACTTCTCT	GGAAAGGGGG	GAAGGCCAAG	GGGAAAAAAA	3720
	CACAAATGGC	TGAAGTTTGT	CCITCTCCGC	GTGGTCAAAG	AGTCATTCCA	CGAATAACCA	3780
10	TAGAAATGAA	AGCAGAGGCA	GAAGAAGAAA	ATAAAAAGAA	AATTAAGAAT	GAAAATACTG	3840
	AAGGAAGCCC	TCAGAAGAGT	GGTGTGAAC	TAGAAGGCCT	AAAACAAGA	TTAGAAAAAG	3900
	AACAGAAAAG	AGAACCAGGT	ACAAAGACAA	AGAAACAAAC	TACATTGGCA	TTTAAGCCAA	3960
	TCAAAAAAG	AAAGAAGAGA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGAGC	4020
	AAAGTAATTT	TGATGTCCCT	CCACGAGAAA	CAGAGCCACG	GAGAGCAGCA	ACAAAAACAA	4080
	AAATTCACAT	GGATTGGATG	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAACCTGATG	4140
15	ATGAAGATTT	TGTCCCATCA	GATGCTAGTC	CACCTAAGAC	CAAAACTTCC	CCAAAACCTTA	4200
	GTAACAAAGA	ACTGAAACCA	CAGAAAAGTG	TCGTGTGAGA	CCTTGAAGCT	GATGATGTTA	4260
	AGGGCAGTGT	ACCACCTGCT	TCAGGCCCTC	CTGCTACACA	TTTCCCAGAT	GAAACTGAAA	4320
	TTACAAACCC	AGTTCCTAAA	AAGAATGTGA	CAGTGAAGAA	GACAGCAGCA	AAAAGTCAGT	4380
	CTTCCACCTC	CACCTACCGT	GCCAAAAAAA	GGGCTGCCCC	AAAAGGAACT	AAAAGGGATC	4440
20	CAGCTTTGAA	TTCTGGTGTG	TCTCAAAAGC	CTGATCCTGC	CAAAACCAAG	AATCGCCGCA	4500
	AAAGGAAGCC	ATCCACTTCT	GATGATTCTG	ACTCTAATTT	TGAGAAAATT	GTTTCGAAAG	4560
	CAGTCACAAG	CAAGAAATCC	AAGGGGAGAG	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
	CTGTGGCTCC	TCGGGCAAAA	TCTGTACGGG	CAAAGAAACC	TATAAAGTAC	CTGGAAGAGT	4680
	CAGATGAAGA	TGATCTGTTT	TAAAATGTGA	GGCGATTATT	TAAAGTAATT	ATCTTACCAA	4740
25	GCCCAAGACT	GGTTTTAAAG	TTACCTGAAG	CTCTTAACIT	CCTCCCCTCT	GAATTTAGTT	4800
	TGGGGAAGGT	GTTTTTAGTA	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGC	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCGTGTTTTT	GAGTCTGCTT	TCITTTGTCT	TTAAACCTG	ATTTTTAAGT	TCTTCTGAAC	4980
	TGTAGAAATA	GCTATCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTTATTAA	CCATCCACTA	5040
30	AGCTAAAACT	AGACAGCTTT	GATTTAAAG	TGTCCTCTT	CCTCCTTTTC	TACTTTCAGT	5100
	AGATATGAGA	TAGAGCATAA	TTATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACCATCA	5160
	GATAGAACTT	TATGGTTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AAATGCTCAT	GTTCTTCATC	TTCTCAAAATC	ATCAGAGGCC	5280
	AAAGAAAAAC	ACTTTGGCTG	TGCTATAAC	TTGACACAGT	CAATAGAAATG	AAGAAAAATTA	5340
35	GAGTAGTTAT	GTGATTATTT	CAGCTCTTGA	CCTGTCCCCT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAAA	GAGAGAAACC	AAATTTCTAAG	AGGACTGGAT	TGCAGAAGAC	TCGGGGACAA	5460
	CATTTGATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCAATTTGG	GAAATCTCAA	TAAATTTCAAT	TTGTAAACTT	TGTTAAGACC	TGCTACATTT	5580
40	GTTATATGTG	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATATTTT	ACTATGTTTT	5640
	TCATATTAGT	AAATTCACAC	AAATTTGTAC	TTAATAAAA	TGTTCTAAAC	ATTGC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

45	1	11	21	31	41	51	
	MEVSPLOPVN	ENMQVNKIKK	NEDAKKRLSV	ERIVQKKTQL	EHILLRPDTY	IGSVELVTQQ	60
	MWVYDEEDVG	NYREVTVPFG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWV	120
50	NGKGIPVVEH	KVEKMYVPAL	IFGQLLTSSN	YDDDEKKVTG	GRNGYGAKLC	NIFSTKFTVE	180
	TASREYKKMF	KQTMWDMNGR	AGEMELKPFN	GEDYTCITFQ	PDLSPKFMQS	LKDIDVALMV	240
	RRAYDIAGST	KDQVFLNGN	KLPVKGFRSY	VDMLKDKLD	ETGNSLKVH	EQVNRHWEVC	300
	LTMSEKFPQQ	ISFVNSIATS	KGGRHVDYVA	DQIVTKLVDV	VKKQKKGQVA	VKAHQVKNHM	360
	WTFVNALIEN	PTFDSQTKEN	MTLQPKSFGS	TCQLSEFIK	AAIGCGIVES	ILNWWKFKAQ	420
	VQLNKKCSAV	KHNRIKGIPIK	LDDANDAGGR	NSTECTLILT	EGDSAKTLAV	SGLGVVGRDK	480
55	YGVFPLRGKI	LNVRASHKQ	IMENAEINNI	IKIVGLQYK	NYEEDSLKT	LRYGKIMIMT	540
	DQDQDQSHIK	GLLINFIHNN	WPSLLRHRFL	EEFITPIVKV	SKNKQEMAFY	SLPEFEWKS	600
	STPNHKKWV	KYYKGLGTST	SKEAKEYFAD	MKRHRIOFKY	SGPEDDAAIS	LAFSKQIDD	660
	RKEWLTNFM	DRQRKLLGL	PEDYLYGQTT	TYLTYNDFIN	KELILFSNSD	NERSIPSMVD	720
60	GLKPGQRKVL	FTCFKRNDRK	EVKVAQLAGS	VAEMSSYHHG	EMSLMMTIIN	LAQNFVGSNN	780
	LNLLQPIGQF	GTRLHGKQDS	ASPRYIFTML	SSLARLLFPP	KDDHTLKFY	DDNQVRPEPW	840
	YPIIIPMVL	NGABIGITGW	SCKIPNFDVR	EIVNNIRRLM	DGEPEPLMLP	SYKNFKGTIE	900
	ELAPNQYVIS	GEVAILNSTT	IEISELEVRT	WTQTYKEQVL	EPMLNGTEKT	PPLITDYREY	960
	HTDITVKFVV	KMTBEKLAEA	ERVGLHKVFK	LQTSLTCSNM	VLFHDHVGCLK	KYDITVLDILR	1020
	DPFELRLKYY	GLRKEWLLGM	LGESAKLNN	QARFILEKID	GKIIENKPK	KELIKVLIQR	1080
65	GVDSDFVKA	KEAQKQVDE	EENEESDNEK	ETEKSDSVTD	SGPTFNVLDD	MPLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPSDLWKED	LATFIELEA	VEAKEKQDEQ	VGLPGKGGKA	1200
	KGKKTQMAEV	LPSPRGQRVI	PRITIEKAE	AEKKNKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTTL	AFKPIKKGKK	RNPWPDESSED	RSSDESNEFDV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFSDFD	EKTDEDFDVP	SDASPPKTKT	SPKLSNKLK	PQKSVVSDLE	1380
	ADDVKGSVPL	SSSPPATHFP	DETEITNPVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSQKPDPAKT	KNRRKRKPST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDPHM	1500
	DFDSAVAPRA	KSVRAKKPIK	YLEESDEDDL	P			

Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

80	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGCAGACCG	TCTGTGAAATG	CGAATCCTAA	AGCGTTTCTT	CGCTTGCAAT	180
	CAGCTCCTCT	GCTTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	CTGTGTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420

	AACACATTCA	TTCCATAACAC	TGGGAAAACA	GTGGAATA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCAGTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCTACT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TGTTTGTAGG	TTGGGACAGA	AGAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTITTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TGATCTGCTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
10	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTITTTTGTG	AAGTTCCTAC	AATGCAACAA	960
	TCTGGTTATG	TGATGCTGAT	GGACTACTTA	CAAAAACATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAAGGAA	AGATTTCATGA	AGCAGTTTGT	1080
	AGTTCCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTGACA	1140
	TGGGAAAGAC	CTCAGTCTGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
15	CAGTTGGATG	GAGAGGACCA	AAACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATT	TCAATAATTT	GCTACCCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGAGCAT	GCCTACTGAT	1380
	AATCCTGAAC	TGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
20	GAAGAGGGA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AAACCAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCACC	TCACACTGTG	1740
	GAGGTACTTT	CAGCTCTTTT	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCCATATG	1800
25	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AAATATATCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	AGACAAATAC	ATATGATGTC	CTTATACAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
30	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAACTTA	CAGTGAGATA	CGTGTGATG	AATCTGAGAA	GACACCAAG	2220
	TCCTTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTGCGAGAC	AACCCAAACG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCTACAGTA	GTGAAGTCTT	TCCCTAGTTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCTCT	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGAGTG	TGTCATTGTA	ATCCATCTCT	2580
	TCTTCTATG	ATGCTGACCC	TTTGCTTCCA	TTTCTCTCTG	CTTCTCTCAG	TAGTGAAATG	2640
40	TTTCGCCATC	TGCATACAGT	TTCTCAATC	CTTCCACAAG	TTACTTTCAG	TACCGAGAGT	2700
	GATAAGGTGC	CCTTGCAATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTGCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATCTGTA	TGCTGCTGCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGTGTAGT	AATCTGTGTG	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCGTCAAT	ACCTGTGCAT	3000
45	GATTCTGTGG	GTGCTAACTTA	TCAGGGTTCC	TTATTTAGCG	GCCTAGGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TCTTCAACCT	GTTCCTGTAG	CTGAATTTAC	ATATACAACA	3240
50	TCGTGTTTGG	GTGATGATAA	TAAGGGGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAAGTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAGGGGCAT	GTTCACAGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATCTGTCT	3540
55	TCTCAAGCAT	CTGGTGACAC	TTGCTTAA	CCTGTGCTTA	TGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAT	TGAAGTATTG	CTACAACCTT	CCTTTGAGG	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACCTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGATTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
60	AGTGAAAAA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTITTTGTTAA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCAATTT	GGAGATTAA	CAGGCCCATC	CCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCCAACAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
65	ATTCCAACAG	TTGCTCTGTA	TACATTTGTA	TCTACTGATC	ATTTCTGTTC	TATAGGAAAT	4260
	GGGCAATGTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTGAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGCT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCAT	GCTCATCTTA	TAGAGAATCA	4500
70	CAGGAAAAAG	TAATGAATGA	TTCAGACACC	CACGAAAACA	GTCTTATGGA	TCAGAAATA	4560
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATT	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
75	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATT	CAGTTTGTCA	4860
	GACACTAATG	AAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCACGCTT	4980
	TCAGAGGAC	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCGAT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
80	CTAGTGGTTC	TTGTTGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAAGTG	ATGTCGAGG	AAATCCAATA	AAGCACTTTC	CAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAG	5400
85	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	5580
	TGGAGAATGA	TATGGGAACA	TAAATGGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640

	AAAGGAAGGA	AAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
5	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGTC	5940
	CACGTGCAGT	CTGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTC AAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCCACA	6060
	AGAAATTAAT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTTATGATAC	ACTGGTTGAG	6120
10	GCCATACTTA	GTAAGAAGAA	TGAGGTGCTG	GACAGTCATA	TTTATGCTTA	TGTTAATGCA	6180
	CTCCTCATTC	CTGAGACCAG	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
	AATCGAAGCT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTT	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTCATCATTA	CCCAGCAGCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
15	GACCATTAAT	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	GAGGAAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAACTT	TTTGAACCTA	TAAAGTGTAT	AAAAGAAAGAA	6780
20	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTTTCTGTG	CTCTGACAA	CCTTATGCAC	CAACTAGAAA	AAGAAAAATC	CGTGGATGTT	6900
	TACCAAGTAG	CCAAGATAGT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
25	TCCACCTCTC	TGGACAGTAA	TGGTGCAGCA	TTGGCTGATG	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACACG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
	TTCTTAAAT	TAGCAGGAA	AATCAGTCTA	GTTCTGTTAT	CTGTTGATT	CCCATCACTT	7200
	GACAGTAAT	TTATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTAA	CAATGTGTGC	7260
	CTTTTTGCAA	GACTTGAAT	TTACTTATTA	TGTTTGAAT	AAAATGATTG	AATTTTACAG	7320
30	TATTTCTAAG	AATGGAATTG	TGTTATTTT	TTCTGTATTG	ATTTTAAACG	AAAAATTCAG	7380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAAATTTTA	7440
	GCTGTATTGG	TAGCAATTTT	CAGGTTTGCT	AGAAATATAA	CTTTTAAATC	AGTAGCCTGT	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAAATACT	GCCCTAGTGT	CTCCATGGAC	CAAAATTTATA	7620
35	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
	GTTTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAGTTTTC	TGACATTGTA	7740
	TTGTGTTACC	TAACTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAAATA	7800
	GAAATACCTT	CATTTTGAAA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
	AATGGTTTTT	ATCCAAGGAA	TTGCAAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAATA	7920
40	AAAAAAAATA	AAAAAAAATA	AAAA				

Seq ID NO: 180 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MRILKRFLAC	IQLLCVCRLD	WANGYYRQOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKLKL	KFQGWKTSLS	ENTFIHNTGK	TVEINLTNDY	RVSQGVSEMV	120
	FKASKITFW	GKCMNSDGS	EHSLEQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDPKAIIDGV	BSVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
50	TDVVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNFREQQY	KFSRQVFSSY	300
	TGKEEHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTGYDQ	LGAILLNLLP	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLPFE	420
	LIGTEEIKE	EEEGKDIIEG	ATVNPGRDSA	TNQIRKKEPQ	ISTTHYNRI	GTYNEAKTN	480
	RSPTRGSEFS	GKGDVNPNTS	NSTSQPVTKL	ATEKDISLTS	QTVTELPFHT	VEGTASASND	540
55	GSKTVLRSPH	MNLSTGAEAL	NTVSIIEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITTD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAFFP	720
	TEVTPHAFTP	SSRQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
60	LNTPPAASSS	DSALHATPVF	PSVDVSFESI	LSSVDGAPLL	PFSSASFSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGGDLLLE	PSLAQYSDDL	STTHAASETL	EFSGESGVLY	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
	SLFSGSPSHIP	IPKSSLTITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIYGN	ETELQIPSFN	EMVYPSESTV	MPNMYDNVKN	1080
65	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTHT	VSQASGDTSL	1140
	KPVLSANSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLKTLVLP	1200
	AVPSDPLIVE	TPKVDKISST	MLHLIVNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPSTLYSD	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDHSPVIG	NGHVAITAVS	1380
70	PHRDGSVTST	KLLFPKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDSD	THENSMDQON	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAAQDSEIT	PGFPQSPSTSS	VTSENSEVPH	VSEAEASNSS	1620
	HESRIGLABG	LESEKKAVIP	LVIVSALTPI	CLVVLVGILI	YWRCKFQTAH	FYLEDSTSPR	1680
75	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTTE	FETLKEPYQE	VQSCVTDLGI	1740
	TADSSNHPDN	KHKRYINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPRAYTAA	1800
	QGPLKSTAE	FWRMIVHEVN	EVIVMITNLV	EKGRKCDQY	WPADGSEYEG	NPLVTQKSVQ	1860
	VLAYYTVRNF	TLRNTKIKKG	SQGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAV	1920
	AKRHAVGPVV	VHCASAGVRT	GTIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
80	QYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIIQSDY	2040
	SAALKQCNRE	KNRTSSIIIF	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIIITQHPL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCESPKVT	LMAECHKCLS	2160
	NEEKLIIQDF	ILEATQDDYV	LEVRFQCPK	WPNPDSPISK	TFELISVIKE	EAANRDGPMI	2220
	VHDEHGGVTA	GTFCALTTLM	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVL	2280
85	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 181 DNA sequence
Nucleic Acid Accession #: Eos sequence

	1	11	21	31	41	51	
5	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAACC	ATTTCCCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10	CTTGTTGAAG	AGATTGGCTG	GTCCATATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCTAATCAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
15	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTC	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATATCTCT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
20	AATGGCTCAT	TGACATCTCC	TCCTGTCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAGG	CCAGTTGGCT	GTTCCTTTTG	AAGTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GCACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACCAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCTT	TCTTGTTTACA	1140
25	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGACGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTG	TCAATAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
30	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTCTAC	1500
	AACCAAAATC	GGAAGAAAGG	ACCCACAGAT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGAAT	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACGTCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
35	AACTTGTGCG	GGACTGCGAG	ATCCTTAAAT	ACAGTTTCTA	TACACAGAAT	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAACCCAG	AGACAAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
40	GAAGATTCAA	CTTCATCAGG	TTCAGAAAG	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTGAATTA	CATGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
45	TCACAGCAAC	AGGATTTTGGT	CTCCACGGTC	AACGTGGTAT	ACTGCGAGAC	AACCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAAATAGTAG	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGTCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
50	CCAATTTCAG	ATGATGTCGG	AGCAATTCOA	ATAAGCACT	TTCCAAGACA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAGAGTTC	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CAAACCTGAC	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
55	TACAACAGAC	CAAAAGCTTA	TATTGTCTGC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTT	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAATG	TGATCAGTAC	TGGCCTGCCC	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCC	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACAAAAGGGC	TCCAGAAAG	GAAGACCCAG	TGGACGTTGT	TGGACGTTGT	3240
60	GTACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCACTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	TGCTGAGAGT	TGCTGAGTAT	TTGTGCTAGA	CAGTATGTTG	CAGTATGTTG	3420
	CAGCAGATTC	AACACGAAGG	AACCTGTCAAC	ATATTGGGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAGAAATTT	ATTGTGTACA	AACCTGAGGAG	CAATATGTCT	TCATTCTATG	TACACTGGTT	3540
65	GAGGCCATAC	TTAGTAAAGA	AACCTGAGGTG	CTGGACAGTC	ATATTCTATG	CTATGTTAAT	3600
	GCACTCCTCA	TTCTTGAGCC	AGCAGGCAAA	ACAAGCTAG	AGAAACAAAT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTATCCCTCG	3780
	AGTGAGAGAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
70	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCCT	GAGGATGATA	3900
	TGGGACCATA	ATGCCCAACT	GGTGGTTATG	ATTCCTGATG	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGTCTATCT	AATGAGGAAA	AACCTTAAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGTCTTAAA	4140
75	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTCATGATG	AGCATGGAGG	AGTGACGCCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCCCTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCCT	AGCCTTGTGA	GCACAAGGCA	GGAAGAGAAAT	4440
80	CCATCCACCT	CTCTGGACAG	TAAATGGTGA	GCATTGCTCT	ATGGAATATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCAG	GAAATCAGT	CTAGTTCTGT	TATCTGTGTA	TTTCCCATCA	4620
	CTGACAGTGA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
	TGCCCTTTTG	CAAGACTTGT	AAATTTACTTA	TTATGTTTGA	ACTAAATATG	TTGAATTTTA	4740
85	CAGTATTTCT	AAGAAATGGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
	CAATTTATAG	AGGTAGAGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTATAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATAATA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980

AGTAGAAATA ATCTGTTACT TATGTGTAAT ACTGCCCTAG TGTCTCCATG GACCAAAATT 5040
 ATATTTTATAA TTGTAGATTT TTATATTTTA CTACTGAGTC AAGTTTCTA GTTCTGTGTA 5100
 ATTGTTTAGT TTAATGACGT AGTTCATTAG CTGGTCTTAC TCTACCAGTT TTCTGACATT 5160
 GTATTGTGTT ACCTAAGTCA TTAACCTTGT TTCAGCATGT AATTTTAACT TTGTGGGAAA 5220
 ATAGAAATAC CTTCAATTTG AAAGAAGTTT TTATGAGAAT AACACCTTAC CAAACATTGT 5280
 TCAATGGTT TTTATCCAAG GAATTGCAAA AATAAATATA AATATTGCCA TTAACAAAAA 5340
 AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 182 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRID WANGYYRQOR KLVEEIGWSY TGAALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITTFHW GKCMNSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRLALS 180
 ILFEVGTEN LDPKAIIDGV ESYSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DIVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEHEAV CSSEPEVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
 HEFLTGDYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGYK SQDLIVDMPT DNPFLDLFPE 420
 LIGTEELIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDPVNTSL NTSQPVTKL ATEKDISLTS QTVELPPHT VEGTSASLND 540
 GSKTVLRSPH MNLGGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETTYD VLIPE SARNA SEDSTSSGSE ESLKOPSMEG NVWFPSSTDI 660
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
 TEVTPHAPT SSRQDLVST VNVVYSQTTQ PVYNAEASNS SHESRIGLAE GLESEKKAVI 780
 PLVIVSALT F ICLVVLGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDVGAI 840
 PIKHFPKHA DLHASSGFTE EFETLKEFYQ EVQSCVDLQ ITADSSNHPD NXHKWRYINI 900
 VAYDHSRVLK LQALEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMWEHN 960
 VEVIVMITNL VEKGRKCDQ YWPADGSEY GNFLVTQKSV QVLAYTYVRN FTLRNTKIKK 1020
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCASAGVR 1080
 TGTIYVLDLM LQIQHEGTV NIPGFLKHIR SQRYNLVQTE EQYVPIHDTL VEAILSKETE 1140
 VLDSHIHAV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSALKQCNR EKNRTSSIIP 1200
 VERSRVGISS LSGEGTYIN ASYIMGYQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
 MIPDGNMAE DEFVWPNKD EPINCESFKV TLMAEHKLCL SNEEKLIQD FILEATQDDY 1320
 VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCAITFL 1380
 MHQLEKENS DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
 AALPDGNIAE SLESILV

Seq ID NO: 183 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4494

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAAC ATTTCCCTCG CTCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CCGCAGACCG TCTGGAATG CGAATCTTAA AGCGTTTCTC CGCTTGCAAT 180
 CAGCTCCTCT GTGTGTGCGC CCGTGGATTG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTGTGTTGAAG AGATTGCGTG GTCCATATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAACAA TCTCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420
 AACACATCCA TTAATACAC TGGGAAAAA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTACGCGGAG GAGTTACAGA AATGGTGT TAAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGACAGC CGATTTCCTA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTGAGG TTGGGACAGA AGAAAATTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTAGTC GTTTTGGGAA GCAGGCTGCT 780
 TTAGATCCAT TCATCTGTT GAACCTTCTG CCAAACTCAA CTGACAGTA TTACATTTAC 840
 AATGGCTCAT TGACATCTCC TCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAG CAGTTGGCT GTTTTGTG AAGTCTTAC AATGCAACAA 960
 TCTGGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA ACAGTACAAG 1020
 TTCTCTAGAC AGGTGTTTTT CTATACACT GGAAAGGAAG AGATTCTATGA AGCAGTTTGT 1080
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTACA 1140
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTG TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTGCACAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCTGGAATTA ATTGGAAC TGAGAAATAAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGCTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGAAG ACCCCAGATT TCTACCACAA CACTACAA TCGCATAGG 1560
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
 AAGGGTGATG TTCCCAATAT ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTCTCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAAC TGCTTAGATC TCCACATATG 1800
 AACTTGTGCG GGACTGCGA ATCTTAAAT ACAGTTTCTA TAACAGAAATA TGAGGAGGAG 1860
 AGTTTATGGA CAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGTATAT ATTTTCTCTC 1980
 GAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTATCAGG TCCAGAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAT 2100
 GTGTGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
 TCCTTTCTG CAGCCCGAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAAATGCCA 2280
 CATTATTCTA CTTTGCCTA CTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340
 TCCAGACAAC AGGATTGGT CTCCACGGTC AACGTGGTAT ACTGCAGAC AACCCAACCG 2400
 GTATACAATG AGGCGATTA TAGTAGCCAT GAGTCTCGTA TTGCTCTAGC TGAGGGGTTG 2460

5	GAATCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520
	CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580
	TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 2640
	ATTTCAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700
	CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGGAAGTGC AGAGCTGTAC TGGTGACTTA 2760
	GGTATTACAG CAGACAGCTC CAACCAACCA GACAACAAGC ACAAGAATCG ATACATAAAT 2820
	ATCGTTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC TTGCTGAAAA GGATGGCAAA 2880
	CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA ACAGACCAAA AGCTTATATT 2940
10	GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCTT GGAGAAATGAT ATGGGAACAT 3000
	AAATGTGGAAG TTATTGTGAT GATAACAAAC CTCGTGGAGA AAGGAAGGAG AAAATGTGAT 3060
	CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAAC TCTGGTTCAC TCAGAAAGAT 3120
	GTGCAAGTGC TTGCCTATTA TACTGTGAGG AATTTTACTC TAAGAAACAC AAAAATAAAA 3180
	AAGGGCTCCC AGAAAGGAAG ACCCAGTGGG CGTGTGGTCA CACAGTATCA CTACACGCAG 3240
	TGGCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC TGACCTTTGT GAGAAAGGCA 3300
15	GCCTATGCCA AGCGCCATGC AGTGGGCGCT GTTGTCTGTC ACTGCAGTGC TGGAGTTGGA 3360
	AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC AGATTCAACA CGAAGGAACT 3420
	GTCAACATAT TTGGCTTCTT AAAACACATC CGTTCACAAA GAAATTATTT GGTACAAACT 3480
	GAGGAGCAAT ATGCTCTTAT TCATGATACA CTGTTGAGG CCATACCTAG TAAAGAAACT 3540
20	GAGGTGCTGG ACAGTCATAT TCATGCCTAT GTTAATGCAC TCCTCATTC TGGACCAGCA 3600
	GGCAAAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGCC AGTCAAATAT ACAGCAGAGT 3660
	GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAGAA ATCGAACTTC TTCTATCATC 3720
	CCTGTGAAA GATCAAGGGT TGGCATTTC TCCCTGAGTG GAGAAGGCAC AGACTACATC 3780
	AATGCCTCCT ATATCATGGG CTATTACCAG AGCAATGAAT TCATCATTAC CCAGCACCTT 3840
	TCCTTCATA CCATCAAGGA TTTCTGGAGG ATGATATGGG ACCATAATGC CCAACTGGTG 3900
25	GTTATGATT CTGATGGCCA AAACATGGCA GAAGATGAAT TTGTTTACTG GCCAAATAAA 3960
	GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACTCTTA TGGCTGAAGA ACACAAATGT 4020
	CTATCTAATG AGGAAAAACT TATAATTGAG GACTTTATCT TAGAAGCTAC ACAGGATGAT 4080
	TATGTACTTG AAGTGAGGCA CTTCAGTGT CCTAAATGGC CAAATCCAGA TAGCCCCATT 4140
	AGTAAAACTT TTGAACCTAT AAGTGTATTA AAAGAAGAAG CTGCCAATAG GGATGGGCTT 4200
30	ATGATTGTTT ATGATGAGCA TGGAGGAGTG ACGGCAGGAA CTTTCTGTGC TCTGACAACC 4260
	CTTATGCACC AACTAGAAAA AGAAAAATCC GTGGATGTTT ACCAGGTAGC CAAGATGATC 4320
	AATCTGATGA GGCCAGGAGT CTTTGTCTGAC ATTGAGCAGT ATCAGTTTCT CTACAAAGTG 4380
	ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT CCACCTCTCT GGACAGTAAT 4440
	GGTGAGCAT TGCCTGATGG AAATATAGCT GAGAGCTTAG AGTCTTAGT TTAACACAGA 4500
35	AAGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCTCT TCCTAAAT AGGCAGGAAA 4560
	ATCAGTCTAG TTCTGTATAT TGTGATTTT CCATCACCTG ACAGTAACCT TCATGACATA 4620
	GGATTCTGCC GCCAAATTTA TATCATTAAC AATGTGTGCC TTTTGTCAAG ACTTGTAAAT 4680
	TACTTATTAT GTTTGAACTA AATGATTGA ATTTTACAGT ATTTCTAAGA ATGGAATTGT 4740
40	GGTATTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT TTATAGAGGT TAGGAATTCC 4800
	AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTAG CTGTATTGT AGCAATTATC 4860
	AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA AATAAAACAC TCTTCCATAT 4920
	GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980
	GTAATACTG CCCTAGTGTG TCCATGGACC AAATTTATAT TTATAATTGT AGATTTTAT 5040
45	ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG TTTAGTTTAA TGACGTAGTT 5100
	CATTAGCTGG TCTTACTCTA CCAGTTTCTT GACATTGTAT TGTGTTACCT AAGTCATTAA 5160
	CTTTGTTTCA GCATGTAATT TTAACTTTGG TGGAAAAATG AAATACCTTC ATTTTGAAAG 5220
	AAGTTTATAT GAGAAATAAC CCTTACCAAA CATTGTTCAA ATGGTTTTTA TCCAAGGAAT 5280
	TGCAAAAAATA AATATAAATA TTGCCATTAA AAAAAAATAA AAAAAAATAA AAAAAAATAA 5340
50	AAA

Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

55	1 11 21 31 41 51	
	MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGAALNQXNWG KKYPTCNSPK 60	
	QSPINIDEDL TQVNVNLKKL KFGGWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120	
	FKASKITFWH GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKLRRLS 180	
60	ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240	
	TDVVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVLMMDY LQNNFREQQY KFSRQVPSY 300	
	TGKEEHEAV CSSEFENVQA DPNYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360	
	HEPLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPELDLPFE 420	
	LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480	
65	RSPTRGSEFS GKGVDVNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540	
	GSKTVLRSPH MNLGTAESL NTWSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600	
	ENISQGYIFS SENPETIYD VLIPESARNA SEDSTSSGSE ESLKDPMEG NVWPPSSTDI 660	
	TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGSPVTDLEM PHYSTFAYFP 720	
	TEVTPHAFTP SSRQDVLST VNVVYSQTTQ PVYNBASNS HESRIGLAEG LESEKKAVIP 780	
70	LVIVSALTPI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840	
	IKHFPKHVAD LHASSGFTEE FEEVQSTVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900	
	KLAQLAEKDG KLTDYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMIWE HNVEVIVMIT 960	
	NLVEKGRRC DQYWPADGSE EYGNPLVTQK SVQVLAYYTV RNFTLRNTKI KKGSKGRPS 1020	
	GRVVTQYHYT QWPDGMVPEY SLPVLTFRK AAYAKRHAVG PVVVHCSAGV GRTGYIVLD 1080	
75	SMLQQIQHEG TVNIFGFLKH IRSQRNVLVQ TEEQVVFVHD TLVEAILSKE TEVLDSHIHA 1140	
	YVNALLIPGP AGKTKLEKQF QLLSQSNIQQ SDYSALKQC NREKNTSSI IPVERSRVGI 1200	
	SSLSGEGTDY INASYIMGYI QSNFIIQTH PLLHTIKDFW RMIWDHNAQL VVMIPDGQNM 1260	
	AEDEFVYWN KDEPINCESP KVTLMAEHKK CLSNEEKLI QDPFILEATQD DVLVLRHFQ 1320	
	CPKPNPDSP ISKTFELISV IEKAAANRDG PMIVHDEHGG VTAGTFALT TLMHOLEKEN 1380	
80	SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440	
	AESLESLV	

Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

85	1 11 21 31 41 51	
----	------------------	--

	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAACC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
5	CGGCGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCTC	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGGAAG	AGATTGGCTG	GTCCATATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGAAGA	300
	AATATCCAAC	ATGTAATAGC	CCAAAAACAAT	CTCCTATCAA	TATTGATGAA	GATCTTACAC	360
	AAGTAAATGT	GAATCTTAAG	AAACTTAAAT	TTCAAGGGTG	GGATAAAACA	TCATTGGAAA	420
10	ACACATTCAT	TCATAACACT	GGGAAAAACG	TGGAAATTA	TCTCACTAAT	GACTACCGTG	480
	TCAGCGGAGG	AGTTTCAGAA	ATGGTGTGTTA	AAGCAAGCAA	GATAACTTTT	CACTGGGGAA	540
	AATGCAATAT	GTCACTCTGAT	GGATCAGAGC	ATAGTTTAGA	AGGACAAAAA	TTTCCACTTG	600
	AGATGCAAAAT	CTACTGCTTT	GATGCGGACC	GATTTTCAAG	TTTTGAGGAA	GCAGTCAAG	660
	GAAAAGGGAA	GTTAAGAGCT	TTATCCATTT	TGTTTGAGGT	TGGGACAGAA	GAATTTTGG	720
15	ATTTCAAGC	GATTATTGAT	GGAGTCGAAA	GTGTTAGTCG	TTTTGGGAAG	CAGGCTGCTT	780
	TAGATCCATT	CATACCTGTTG	AACCTTCTGC	CAAACTCAAC	TGACAAGTAT	TACATTTACA	840
	ATGGCTCATT	GACATCTCCT	CCTGCACAG	ACACAGTTGA	CTGGATTGTT	TTTAAAGATA	900
	CAGTTAGCAT	CTCTGAAAGC	CAGTTGGCTG	TTTTTGTGTA	AGTTCTTACA	ATGCAACAAT	960
	CTGGTTATGT	CATGCTGATG	GACTACTTAC	AAAACAATTT	TCGAGAGCAA	CAGTACAAGT	1020
20	TCTCTAGACA	GGTGTTTTCC	TCATACACTG	GAAAGGAAGA	GATTTCATGAA	GCAGTTTGTA	1080
	GTTCAAGAAC	AGAAAATGTT	CAGGCTGACC	CAGAGAATTA	TACCAAGCCTT	CTTGTTACAT	1140
	GGGAAGGACC	TCGAGTCGTT	TATGATACCA	TGATTGAGAA	GTTTGCAGTT	TTGTACCAGC	1200
	AGTTGGATGG	AGAGGACCAA	ACCAAGCATG	AATTTTGTAC	AGATGGCTAT	CAAGACTTGG	1260
	GTGCTATTCT	CAATAATTTG	CTACCCAATA	TGAGTTATGT	TCTTCAGATA	GTAGCCATAT	1320
25	GCACATATGG	CTTATATGGA	AAATACAGCG	ACCAACTGAT	TGTCGACATG	CCTACTGATA	1380
	ATCTGAACT	TGATCTTTTC	CCTGAATTA	TTGGAATCGA	AGAAATAATC	AAGGAGGAGG	1440
	AAGAGGGAAA	AGACATTTGAA	GAAGGCGCTA	TTGTGAATCC	TGGTAGAGAC	AGTGCTACAA	1500
	ACCAAAATCAG	GAAAAGGGAA	CCCCAGATTT	CTACCAACAAC	ACACTACAAT	CGCATAGGGA	1560
	CGAAATACAA	TGAAGCCAA	ACTAACCGAT	CCCCAACAA	AGGAAGTGAA	TTCTCTGGAA	1620
30	AGGGTGAATG	TCCCAATACA	TCTTTAAAT	CCACTTCCCA	ACCACTCACT	AAATTAGCCA	1680
	CAGAAAAAGA	TATTTCTCTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
	AAGGTACTTC	AGCTCTCTTA	AATGATGGCT	CTAAAACCTG	TCTTAGATCT	CCACATATGA	1800
	ACTTGTGCGG	GACTGCAGAA	TCCTTAAATA	CAGTTTCTAT	AACAGAATAT	GAGGAGGAGA	1860
	GTTTATTGAC	CAGTTTCAAG	CTTGATACG	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
35	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCCCG	1980
	AAAACCCAGA	GACAATAACA	TATGATGTCC	TTATACCAGA	ATCTGCTAGA	AATGCTTCCG	2040
	AAGATTCAAC	TTATCAGAGT	TCAGAAGAAT	CACATAAGGA	TCCTTCTATG	GAGGGAATG	2100
	TGTGGTTTCC	TAGCTCTACA	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
	GCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
40	CCTTTTCTGC	AGGCCAGTGG	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	GAATGCCAC	2280
	ATTATTCTAC	CTTTGCTCAT	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCTT	2340
	CCAGACAACA	GGATTGCTGC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCAAACCGG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
	AATCCGAGAA	AGAGGCAAGT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
45	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTATC	CAGGAAGTGC	2760
	AGAGCTGTAC	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCAACCA	GACAACAAGC	2820
50	ACAAGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGTGAAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTTCT	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTGAT	GATAACAAAC	CTCGTGAGAA	3060
55	AAGGAAGGAG	AAAATGTGAT	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAC	3120
	TTCTGCTCAC	TCAGAAGAGT	GTGCAAGTGC	TTGCCATTAT	TACTGTGAGG	AATTTTACTC	3180
	TAGAAACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGG	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGCG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGCTCT	GTTGTGCTCC	3360
	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
60	AGATTCAACA	CGAAGGAACT	GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTACAAA	3480
	GAAATTAATT	GGTCAAACT	GAGGAGCAAT	ATGTCCTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACCTAG	TAAAGAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCAT	GTTAATGCAC	3600
	TCCTCATTCC	TGGACCAGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	3660
	AGTCAAAAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAAG	3720
65	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCCTGAGTG	3780
	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTAC	CCAGCACCCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAACCTGGT	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
	TTGTTTACTG	GCCAAATAAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACCTTCA	4020
70	TGGCTGAAGA	ACACAAATGT	CTATCTAATG	AGGAAAAACT	TATAATTCAG	GACTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAATCCAGA	TAGCCCCATT	AGTAAACTT	TTGAACCTAT	AAGTGTATA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCTT	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
75	CTTCTGTGC	TCTGACAACC	CTTATGCACC	AACTAGAAAA	AGAAAAATTC	GTGGATGTTT	4320
	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTGTGCTAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	4440
	CCACCTCTCT	GGACAGTAAT	GGTGACGAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TAAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTCTCTCT	4560
	TCCTAAAAAT	AGGCAGGAAA	ATCAGTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACCTG	4620
80	ACAGTAACCT	TCATGACATA	GGATTCTGCC	GCCAAATTTA	TATCATTAA	AATGTGTGCC	4680
	TTTTTGCAAG	ACTTGTAATT	TACTTATTAT	GTTTGAACCTA	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATTGT	GGTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAAT	4800
	TTATAGAGGT	TAGGAATTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTAG	4860
	CTGTATTGTT	AGCAATTATC	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
	AATAAACAC	CTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
85	GAAATAATCT	GTTACTTATT	GTAATACTG	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCT	GACATTGTAT	5160

TGTGTTACCT AAGTCATTAA CTTTGTGTTCA GCATGTAATT TTAACITTTTG TGGAAAATAG 5220
 AAATACCTTC ATTTTGAAGG AAGTTTATAT GAGAATAACA CCTTACCATA CATTGTTCAA 5280
 ATGGTTTTTA TCCAAGGAAT TGCAGGATAA AATATAATAA TTGCCATTAA AAAAAAATAA 5340
 AAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

1	11	21	31	41	51	
MVFKASKITF	HWGKCNMSSD	GSEHSLEGQK	FPLEMQIYCP	DADRPSSFEE	AVKKGKGLRA	60
LSILEFVGTE	ENLDPFKAID	GVESVSRFGK	QAALDPFILL	NLLPNSTDKY	YIYNGSLTSP	120
PCTDITVDNIV	FKDTSVSISES	QLAVFCEVLT	MQQSGYVMLM	DYLNQNFREQ	QYKFSRQVFS	180
SYTGKEEIEH	AVCSSEPENV	QADPENYTSI	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240
TKHEFLTIDGY	QDLGAILNML	LPMMSYVLQI	VAICTNGLYG	KYSDQLIVDM	PTDNPFLDLF	300
PELIGTEBII	KEEBEGKDIE	EGAIVNPGRD	SATNQIRKKE	PQISTTTHYN	RIGTKYNEAK	360
TNRSPTRGSE	FSGKGDPVNT	SLNSTSQPVT	KLATEKDIDL	TSQTVTELPP	HTVEGTSASL	420
NDGSKTVLRS	PRHNLSTGAE	SLNTVSITEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIPP	480
ISENISQGYI	FSSSEPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	BGNVWPPSST	540
DITAQPDVGS	GRESFLQTNV	TEIRVDESEK	TTKSFSAGPV	MSQGPSVTDL	EMPHYSTFAY	600
FPTEVTPHAF	TPSSRQQLDV	STVNVVYSQT	TQPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
IPLVIVSALT	FICLVVLVGI	LIYWRKCFQT	AHFVLEDSTS	PRVISTPPTP	IFPISDDVGA	720
IPIKHFPKHV	ADLHASGSFT	EEFETLKEFY	QEVQSCITVDL	GITADSSNHP	DNKHKNRYIN	780
IVAYDHSRVK	LAQLAEKDGK	LTDYINANYV	DGYNRPKAYI	AAQGPKLSTA	EDFWRMIWEH	840
NVEIVIMITN	LVEKGRKKCD	QWPADGSEE	YGNFLVTQKS	VQVLAYTIVR	NFTLRNTKIK	900
KGSQKGRPSG	RVVTQYHYTQ	WEDMGVPEYS	LPVLTFRVKA	AYAKRHAVGP	VVVHCSAGVG	960
RTGTIYVLDS	MLQQIQHEGT	VNIFGFLKHI	RSQRNYLVQT	EEQYVFIHDT	LVEAILSKET	1020
EVLDSHIIHAY	VNALLIPGPA	GKTKLEKQFQ	LLSQSNIQQS	DYSAAALKQCN	REKNRTSSII	1080
PVERSRVGIS	SLSGEGTDYI	NASYIMGYIQ	SNFIIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
VMIPDQGNMA	EDEFVYWPKN	DEPINCSEFK	VTLMAEHEKC	LSNEEKLIQ	DFILEATQDD	1200
YVLEVRHFQC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIWDEHGGV	TAGTFCALTT	1260
LMHQLEKENS	VDVYQVAKMI	NLMRPGVFAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
GAALPDGNIA	ESLESILV					

Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

1	11	21	31	41	51	
CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
CAAAAAAAGC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
CGCGAGGGGG	CCCGACACCG	CTCGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCAAT	180
CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGGAAAG	300
AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
AACACATCA	TTCATACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTITTTGAGGA	AGCAGTCAAA	660
GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTCT	GTITTTGGGAA	GCAGGCTGCT	780
TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTCAC	840
AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTITTTTGTG	AAGTCTTCTAC	AATGCAACAA	960
TCTGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTATGA	AGCAGTTTGT	1080
AGTTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTGTACA	1140
TGGGAAAGAC	CTGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
TGCACTAATG	GCTTATATGG	AAATACACAG	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
ACAGAAAAAG	ATATTTCTTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCACC	TCACACTGTG	1740
GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACGT	TTCTTAGATC	TCCACATATG	1800
AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
AGTTTATIGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
GAAGATTCAA	CTTCATCAGG	TTCAGAAAGG	TCACTAAAGG	ATCTTCTAT	GGAGGGAAT	2100
GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
AGCTTCTCTC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
TCCTTTCTCG	CAGGCCCATG	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCAACCG	2400
GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCAGAC	TGCACACTTT	2580
TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
ATTTTCAGATG	ATGTCGGAGC	AATTTCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
CATGCAAGTA	TGCGGTTTAC	TGAAGAAATT	GAGACACTGA	AAGAGTTTAA	CCAGGAAGTG	2760
CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	2820

5
10
15
20
25
30
35
40
45

CACAAGAATC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCACAG 2880
CTTGCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGAATGGCTAC 2940
AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTC 3000
TGGGAATGA TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 3060
AAAGGAAGGA GAAATGTGCA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 3120
TTTCTGGTCA CTCAGAAAGAG TGTGCAAGTG CTTCGCTATT ATACTGTGAG GAATTTTACT 3180
CTAAGAAACA CAAAAATAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 3240
ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 3300
CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTCTGTC 3360
CACTGCAGTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 3420
CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 3480
AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGCTTCA TTCATGATAC ACTGGTTGAG 3540
GCCATACCTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTAAATGCA 3600
CTCCTCATTC CTGGACCAAG AGGCAAAACA AAGCTAGAGA AACATTCCA GGGTCTCACT 3660
CTGTCAACCA GGCTGGAGTG CAGAGGCACA ATCTCGGCTC ACTGCAACCT TCCTCTCCCT 3720
GGCTTAACTG ATCCTCCTAC CTCAGCCTCC CGAGTGGCTG GGACTATACT CCTGAGCCAG 3780
TCAATATATC AGCAGAGTGA CTATTCTGCA GCCCTAAAGC AATGCAACAG GGAAGAAGAT 3840
CGAACTTCTT CTATCATCCC TGTGAAAGA TCAAGGGTTG GCATTTTATC CCTGAGTGGG 3900
GAAGGCACAG ACTACATCAA TGCCCTCTAT ATCATGGGCT ATTACCAGAG CAATGAATTC 3960
ATCATTACCC AGCACCCTCT CCTTCATACC ATCAAGGATT TCTGGAGGAT GATATGGGAC 4020
CATAATGCCC AACTGGTGGT TATGATTCCT GATGGCCAAA ACATGGCAGA AGATGAATTT 4080
GTTTACTGGC CAAATAAAGA TGAGCCTATA AATTGTGAGA GCTTTAAGGT CACTCTTATG 4140
GCTGAAGAAG ACAAATGTCT ATCTAATGAG GAAAACTTA TAATTTCAGGA CTTTATCTTA 4200
GAAGCTACAC AGGATGATTA TGTACTTGAA GTGAGGCACT TTCAGTGTCC TAAATGGCCA 4260
AATCCAGATA GCCCATTAG TAAACTTTT GAACCTATAA GTGTTATAAA AGAAGAAGCT 4320
GCCAATAGGG ATGGGCTTAT GATTGTTTAT GATGAGCATG GAGGAGTGAC GGCAGGAATC 4380
TTCTGTGCTC TGACAAACCT TATGCACCAA CTAGAAAAAG AAAATTCGGT GGATGTTTAC 4440
CAGGTAGCCA AGATGATCAA TCTGATGAGG CCAGGAGTCT TTGCTGACAT TGAGCAGTAT 4500
CAGTTTCTCT ACAAAGTGAT CCTCAGCCTT GTGGGCACAA GGCAGGAAGA GAATCCATCC 4560
ACCCTCTCTG ACAGTAATGG TGCAGCATTG CCTGATGGAA ATATAGCTGA GAGCTTAGAG 4620
TCTTTAGTTT AACACAGAAA GGGGTGGGGG GACTCACATC TGAGCATTGT TTTCTCTTTC 4680
CTAAAATTAG GCAGGAAAAA CAGTCTAGTT CTGTTATCTG TTGATTTCCT ATCAGCTGAC 4740
AGTAACCTTC ATGACATAGG ATTCTGCCGC CAAATTTATA TCATTAACAA TGTGTGCCCT 4800
TTTGCAAGAC TTGTAATTTA CTTATTATGT TTGAACATAA ATGATTGAAT TTTACAGTAT 4860
TTCTAAGAAT GGAATTGTGG TATTTTTTTC TGTATTGATT TTAACAGAAA ATTTCAATTT 4920
ATAGAGGTTA GGAATTCCAA ACTACAGAAA ATGTTTGTGT TTAGTGTCAA ATTTTTAGCT 4980
GTATTGTAG CAATTATCAG GTTGTCTAGA AATATAACTT TTAATACAGT AGCCTGTAAA 5040
TAAACACTC TTCCATATGA TATCAACAT TTTACAACCT CAGTATTAC CTAAGTAGA 5100
AATAATCTGT TACTTATTGT AAATACTGCC CTAGTGTCTC CATGGACCAA ATTTATATT 5160
ATAATTGTAG ATTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTG TGTAAATGTT 5220
TAGTTTAATG ACGTAGTTCA TTAGCTGGTC TTACTCTACC AGTTTCTGGA CATTGTATTG 5280
TGTTACCTAA GTCAATTAAT TTGTTTCAGC ATGTAATTTT AACTTTGTG GAAAATAGAA 5340
ATACCTTCAT TTTGAAAGAA GTTTTATGA GAATAACACC TTACCAACA TGTTCAAAT 5400
GGTTTTATC CAAGGAATTG CAAAAATAA TATAAATATT GCCATTAAAA AAAAAAATA 5460
AAAAAATAA AAAAAAATA A

Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

50
55
60
65
70
75
80

1 11 21 31 41 51
| | | | |
MRILKRFLAC IQLLCVCRID WANGYYRQQR KLVEEIGWSY TCAINQKNWG KKYPTCNPK 60
QSPINIDEDL TQVNVNLKKL KFGWDKTSLS ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGLRLALS 180
ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVLMMDY LQNNFREQQY KFSRQVFSY 300
TGKEIHEAV CSSEPENQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
HEFLTGYQD LGAILNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
LIGTEBIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
RSPTRGSEFS KGKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540
GSKTVLRSPH MNLSTGAESL NTVSITEYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSESGE ESLKDPMEG NVWFPSSTDI 660
TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSPSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
TEVTPHAFPT SSRQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780
LVIVSALTFI CLNVVLGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCVTDLGI TADSSNHPDN KHKNRYINIV 900
AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAE FWRMIWEHNV 960
EVIVMITNLV EKGRKCDQY WPADGSEYGF NFLTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRVKAAY AKRHAVGPV VHCAGVGRT 1080
GTIYVLDSML QQIQHEGTVN IFGLKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKETEV 1140
LDSHIHAYVN ALLIPGPAGK TKLEKQFOGL TSPRLCEGR TISAHCNLF PLGLDPPTSA 1200
SRVAGTILLS QSNIIQSDYS AALKQCNREK NRTSSIIFVE RSRVGISSLS GEGTDYINAS 1260
YIMGYQSNF FIITQHPLH TIKDFWRMIW DHNAQLVVM PDGQNMAGE FVYWPKNDEP 1320
INCESPKVTL MAEEHKCLSN EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPIKST 1380
FELISVIKEE AANRDGPMIV HDEHGGVTAG TPCALITLMH QLEKENSVDV YQVAKMINLM 1440
RPGVFADIEQ YQFLYKVLIS LVGTQRQENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 189 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304..831

85

1 11 21 31 41 51
| | | | |
CCGTTTCCCA AAGAAGCTGA CTTACAGAGG GGAACCTTTC TTCTTTTAGG AGGCGGTTAG 60
CCCTGTTCCA CGAACCCAGG AGAAGCTGCT GCCAGATTAA TTAGACATTG CTATGGGAGA 120
CGTGTAAACA CACTACTTAT CATTGATGCA TATATAAAAC CATTTTATT TCGCTATTAT 180

5
10
15
20
25

TTCAGAGGAA GCGCCTCTGA TTGTGTTCTT TTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
GTTTGGAGAA AGCACAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCGAGC GCGAGCGGAG 300
ACGATCGAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCCTGCT GAGCTACGGG 360
GTGCCCTCCT GCGGGCGGTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT 420
GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTTC 480
CTTCACCATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC 540
CCTAACTCCA AGCCCTCTCC CAACACAAAG AACCAACCCG TCCGATTGGG GTCTGATGAT 600
GAGGGCAGAT ACCTAACTCA GGAACCTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC 660
AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCGGGGAAAC GCAAGGAGCA GGAAAAAGAA 720
AAACGGCGAA CTGCTCTGCG CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG 780
GACCACCTGT CTGACACCTC CACAACGTCG CTGGAGCTCG ATTCACGSTA ACAGGCTTCT 840
CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTTT GGAGCCTCCC TTCTGCCTTG 900
GCTTGGACAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA 960
CAGAGAATAA CTCAGAATAT TGCTGCTCTT AAAGCAGTAC CCCCCTACCA CACACACCCC 1020
TGTCCTCCAG CACCATAGAG AGGCGCTAGA GCCCATTCTT CTTTCTCCAC CGTCACCCAA 1080
CATCAATCCT TTACCACCTT TTCTCCCTTT ATCATATTCA AGCTTCAGAA GCTAGTGACC 1140
ATCTTCATAA TTGCTGAGAG AAGTGTATTT CTTCCTCTTA CTCTCACACC TGGGCAAACT 1200
TTCTTCAGTG TTTTTCATTT CTACGTTCTT TTCATTCAA GGGAGAATAT AGAAGCATTT 1260
GATATTATCT ACAAACTCTG CAGAACAGCA TCATGTCTAA AACGATTCTG AGCCATTAC 1320
ACTTTTTATT TAAATAAATG TATTTAATTA AATCTCAAAT TTATTTTAAAT GTAAAGAACT 1380
TAAATTATGT TTTAAACACA TGCTTAAAT TTGTTTAAAT AAATTTAACT CTGTTTCTA 1440
CCAGCTCATA CAAAATAAAT GGTTCCTGAA AATGTTTAA TATTAACCTA CAAGGATATA 1500
GGTTTTTCTC ATGTATCTTT TTGTTCAATG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
CCGTAGGAAA AATAAACTT CACATTTAAA AAAAA

Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

30
35

1 11 21 31 41 51
| | | | | |
MQRRLLVQWS VAVFLLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRFFL 60
HHLIAEIHITA EIRATSEVSP NSKPSPTNKN HPVRFSGDDE GRYLTOETNK VETYKEQPLK 120
TPGKKKKGKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEBD HLSDTSTTSL ELDSR

Seq ID NO: 191 DNA sequence
Nucleic Acid Accession #: XM_059328
Coding sequence: 52..1023

40
45
50
55
60
65

1 11 21 31 41 51
| | | | | |
GGGCTGTCCG GCCCACTCCC CTGGGAGCGC GAGCGGTGGA CCCAGGCGGC CATGTCCCGC 60
CCTCGCATGC GCCTGGTGGT CACCGCGGAC GACTTTGGTT ACTGCCCGCG ACGCGATGAG 120
GGTATCGTGG AGGCCTTTCT GGCCTGGGCT GTGACCAGCG TGTCCTGCTT GGTCAACGGT 180
GCGGCCACGG AGAGCGCGGC GAGAGCTGGCC CGCAGGCACA GCATCCCCAC GGGCCTCCAC 240
GCCAACCTGT CCGAGGGCCG CCCCCTGGGT CCGGCCCGCC GTGGCGCCTC ATCGCTGCTC 300
GGCCCCGAAG GCTTCTTCTT TGCAAGATG GGATTCCGGG AGGCGGTGGC GGGCGGAGAC 360
GTGGATTTCG CTCAGGTGCG GGAGGAGCTC GAGGCCCAAC TAAGCTGCTT CCGGGAGCTG 420
CTGGGCGAGG CCCCCACGCA CGCGGACGGG CACCAGCAAG TGCACTGCTT CCCAGCGCTG 480
TGCCAGGTGT TCGCCGAGGC GCTGCAGGCC TATGGGTGTC GCTTTACGCG ACTGCCGCTG 540
GAGCGCGGTG TGGGTGGCTG CACTTGGCTG GAGGCCCCCG CGCGTGCCCT CGCCTGCGCC 600
GTGGAGCGCG ACGCCCGGGC CGCGGTGGGC CCCTTCTCCC GCCACGGCCT GCGGTGGACA 660
GACGCCTTCG TGGGCTGAG CACTTGCGGC CGGCACATGT CCGCTCACCG CGTGTCCGGG 720
GCCCTGGCGC GGGTCTCTGA AGGTACCTTA GCGGGCCACA CCCTGACAGC CGAGCTGATG 780
GCGCACCCCG GCTACCCAG TGTGCTCTCC ACCGGCGGCT GCGGTGAAGG CCCCAGCGCT 840
TTCTCTTGCT CTTGGGAGCG GCTGCATGAG CTGCGCGTCC TCACCGCGCC CACGCTGCGG 900
GCCCAGCTTG CCCAGGATGG CGTGCAGCTT TGCGCCCTCG ACGACCTGGA CTCCAAGAGG 960
CCAGGGGAGG AGGTCCCTCT TGAGCCCACT CTGGAAACCT TCCTGGAACC CTCCTACTC 1020
TGACCCCTTA CAGACAACA AGCACTAATC CCCTTAGTAC CAAGAAAGGG GAGCCAGGAT 1080
TTAGTCTGG CCAAGCCAG AGCTGGGACC TGGAGCAGA TCTGTTGACT TCCTGGGTA 1140
GGACACTGCC ACCTCTGGGC TCAGGTCTCT ATGCCTCCAA ATGGCATCTA GAGTTTGAGC 1200
AGCCTTCTTG GCTGCAGGCA GGCTAGCCT GTGGCAGCGG GCTAGGGCCC GCAGAGCAT 1260
TGGTGCCCT CCATGTTGCA ATGCAACAC CTTCAACACT GGGGCAGTGG GGAGAGATGG 1320
CTATATTAAT AAAATAACGT GTGTCTTTC

Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

70
75

1 11 21 31 41 51
| | | | | |
MSRPRMLV V TADDFGYCPR RDEGIVEAPL AGAVTSVSL L VNGAATESAA ELARRHSIPT 60
GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMGFREAVA AGDVDLPQVR EELEAQLSCF 120
RELLGRAPH TH ADGQHVVHVL PGVCQVFAEA LQAYGVPRTR LPLERGVGGC TWLEAPARAP 180
ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
ELMAHPGYFS VPPTGGCGEG PDAFSCSWER LHELRLVTAP TLRLAQLAQDQ VQLCALDDLD 300
SKRPGEVPC EPTLEPFLEP SLL

80
85

Seq ID NO: 193 DNA sequence
Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

1 11 21 31 41 51
| | | | | |
CCGGGCAGGT GGCTCATGCT CCGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC 60
AGGGGCGCAG GAATCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCGCTCAG 120

	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CGGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
5	TCCTCTTGA	TGCCTCCATG	CACTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACACAG	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCT	GIATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGGAAG	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGGGAA	GGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAGCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTCT	CTCCTGACCG	AAATCGTGG	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAAATTACCGA	ACCGGTGTCC	GCTTGGGGGG	GGCCATCCTA	ACCATGGCAT	900
15	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CAGTGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTGGG	ATCAGCTGTT	TTTATCTCT	TTTACCCAGC	AATGATGTTT	GCATCAACGC	1140
20	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTCATAT	GACCCCTGGG	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATT	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
25	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTCATATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCCAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCACGCG	ACTGAGCATC	1740
	AGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCCAAGT	1800
30	CCGAAGAGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCCTGAGATC	CAAGAGGGTA	AACCTGGTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAGAAC	CTCTCTCAT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
35	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTCTGTA	2100
	ACAGCTGTG	CCTGAGGCTT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGAGATTG	2160
	GAGAGCGAG	AGCCAACTTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCTG	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
40	TTGTTACCCA	CAGTTTACAG	TACCTGGTTG	ACTGTGATGA	AGTATCTTCT	ATGAAGAGAG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACCTGTGG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCACTGG	TGACAGAAAG	AAGTCAACA	ACAAGGGTCC	TAAACACGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGGTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
45	TCCTGGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACACAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTAATATGCC	AGCATCTAAG	2880
	CCCTCTCCAT	GGCAGTCTAG	CTGATCCTGA	AAGCCATTGC	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
50	CTATGAAGTT	TTTTGACAGC	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGCGG	CTGCGGTTC	AGGCGGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCCCTGT	CATCCTCTTT	TCAGTCTCTC	ACATTTGCTC	CAGGGTCTCT	ATTCCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	AOCGAGTCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATAC	3300
55	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTCTCTGCAC	AGATACCAGG	3360
	AGCTGTGGA	TGACAACCAA	GCTCCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	GCAGATCTCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
60	TAAAGGGGCT	GTTCAGGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAGCACCT	GCCAGAATTA	3660
	AGAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGAG	3720
	AGATGAGGTA	CCGAGTAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAA	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
65	GTGATATTGG	CCTTGCAGAC	CTCCGAAGCA	AACCTCTCTA	CATTCCTCAA	GAGCCGGTGC	3960
	TGTTCACTGG	CATGTCTAGA	TCAAATTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAAATGAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGATGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
70	CCATGGACAC	AGAGACAGAC	TTATTGATT	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCTGCTGC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC	TCCTTCTCTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
75	CCCTCATCG	CGTCTCTCTA	CCGAAACCTT	GCCTTCTCTG	ATTTTATCTT	TGCGACAGCA	4560
	GTTCGGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGTTTCA	4680
	GGGAACCGGT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TACCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
80	TATTAATAA	AGCACTGTGC	TAATAACAGT	GCATATCTCT	TTCTATCATT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCATTCTT	4920
	CTCTAGCTGG	TGTTTCTACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCGGTGA	GTCTCTAGGG	CTCCTGCCTT	5100
85	CTGTCTGTGT	GTCTCTTACT	TTTCTGTCTA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTTCTTTTT	GCTGTTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCCCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTTGAGG TGGCACTTTT TCATTTCGCT 5400
 ATTCACACAC CTCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT 5460
 CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAAGTCTG CAACTTTAAG 5520
 CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580
 ACCTCAGGTT GCTGGTTGCT GTGTGGTTCC GCAAACCCCT TTTGTGCTGT 5640
 GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCTATC AGTTGAATGG TCACGCTTGC 5700
 ATGTCGTGAC CAACTAGACA TTCTGTGCGC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
 CAAAAATCTG AAAATGTGAA TAAATATTAT TTGGATTTTG TAAAAAATAA AAAAAAATAA 5820
 AAAAAAATAA AAAAAAATAA

Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS 60
 LDASMHSQLR ILDEEHPKKG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEEELNEV GPDAASLRV VWIFCRTRLI 180
 LSIVCLMITQ LAGFSGPAFM VKHLLYTOA TESNLQVSL LVLGLLLTEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF LGSVFIIFY PAMMFASRLT AYFRKCVAA TDERVQKMNE 360
 VLTYIKFIKM YANVKAQSQS VQKIREEEER ILEKAGYFQG ITVGVAPIVV VIASVVTFSV 420
 HMTLGFDLTA AQAPTUVTVF NSMTFALKVT PFSVKSLSSEA SVAVDRFKSL PLMBEVHMIK 480
 NKPASPHIKI EMKNATLAWD SSHSIQNSP KLTPKMKDK RASRGKKEKV RQLORTEHOA 540
 VLAEQKHLL LDSDERPSPE EEEGKHIHLG HLRQLRTLHS IDLEIQEKL VGICGSGVSG 600
 KTSLSIAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
 CCLRDLAIL PSSDLTEIGE RGANLGGQR QRIARALY SDRSIYILD PLSALDAHVG 720
 NHIFNSAIRK HLKSKTVLTV THQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
 FNNLLGETP PVEINSKET SGSQKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGGGS 840
 VPWSVGVYI QAAGGLPFL VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900
 VSDSKMDNPH MQYYIAIYAL SMAVLMILKA IRGVVFKGT LRASSRLHDE LFRILRSPM 960
 KFFDTPTGR ILNRFSKMD EVDVRLPFQA EMFIQNVILV PFCVGMIAVG PFVPLVAVGP 1020
 LVILFSLVLI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQTTVRLA SETEARETSV ERINHVIKTL SLEAPARIKN KAPSPDWQPE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLMGAL FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSLNLP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
 MLTIAHRLHT VLGSDRMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKVG

Seq ID NO: 195 DNA sequence
 Nucleic Acid Accession #: NM_006470
 Coding sequence: 228..1922

1 11 21 31 41 51
 GCTGTCTCTGA GCCTGAGTAC TCTAGCTGCC TTGTGCGCAT CGCATCTGGC TGCCATCCAG 60
 CGCCAGCACA CAGTAATGAG TGGCCGAGCT TCCTCTGGGA GGGAGGAAAC AGTAAAAATC 120
 TTGCAGCAGC TGCAATCATC TAGGCGTGGT TCTCTGTCT GACTTGGGCT GCACAGATCC 180
 TGGGCCAAGG GACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCAGATG GCTGAGTTGG 240
 ATCTAATGGC TCCAGGGCCA CTCGCCAGGG CCACTGCTCA GCGCCAGGCC CCTCTCAGCC 300
 CAGACTCTGG GTCACCCAGC CCAGATTCTG GGTACGCCAG CCCAGTGGAA GAAGAGGACG 360
 TGGGCTCCTC GGAGAAGCTT GGCAGGAGGA CGGAGGAACA GGACAGCGAC TCTGCAGAGC 420
 AGGGGGATCC TGCTGGTGAG GGAAGAAGAG TCCTGTGTGA CTTCTGCTTT GATGACACCA 480
 GAAGAGTGAA GGCAGTGAAG TCCTGTCTAA CTTGATGTT GAATTACTGT GAAGAGCACT 540
 TGCAGCCGCA TCAGGTGAAC ATCAAACTGC AAAGCCACCT GCTGACCGAG CCAAGTGAAG 600
 ACCACAATCG GCGATACTGC CCTGCCACCC ACAGCCACT GTCTGCTTT TGTGCGCCTG 660
 ATCAGCAGTG CATCTGCCAG GACTGTGTC AGGAGCAGAG TGGCCACACC ATAGTCTCCC 720
 TGGATCGAGC CGCAGGAGAC AAGGAGGCTG AACTCCAGTG CACCCAGTTA GACTTGGAGC 780
 GGAAACTCAA GTTGAATGAA AATGCCATCT CAGGCTCCA GGCTAACCA AAGTCTGTT 840
 TGGTGTGCGT GTCAGAGGTC AAGCGGTGG CTGAAATGCA GTTTGGGGAA CTCTTGTCTG 900
 CTGTGAGGAA GGCCAGGCCC AATGTGATGC TCTCTTAGA GGAGAAGGAG CAAGCTGCGC 960
 TGAGCCAGGC CAACGGTATC AAGGCCACCC TGGAGTACAG GAGTCCCGAG ATGGAGAAGA 1020
 GCAAGCAGGA GCTGGAGAGG ATGGCGGCCA TCAGCAACAC TGTCCAGTTC TTGAGGAGT 1080
 ACTGCAAGTT TAAGAACACT GAAGACATCA CCTCCCTAG TGTTTACGTA GGGCTGAAG 1140
 ATAACTCTC GGGCATCCGC AAAGTTATCA CGGAATCCAC TGTACACTTA ATCCAGTTGC 1200
 TGGAGAATA TAAGAAAAAG CTCAGGAGT TTTCCAAGGA AGAGGAGTAT GACATCAGAA 1260
 CTCAAGTGTC TGCGTTGTT CAGCGCAAAT ATTGGACTTC CAAACCTGAG CCCAGCACCA 1320
 GGGAAACAGT CCTCCAATAT GCGTATGACA TCACGTTTGA CCCGACACA GCACACAAGT 1380
 ATCTCCGGCT GCAGGAGGAG AACCGCAAGG TCACCAACAC CACGCGCTGG GAGCATCCCT 1440
 ACCCGGACCT CCCAGCAGG TTCTGTCACT GCGCGCAGGT GCTGTCCAG CAGAGTCTGT 1500
 ACCTGCACAG GTACTATTTT GAGGTGGAGA TCTTGGGGC AGGCACCTAT GTTGGCCTGA 1560
 CCTGCAAGG CATGACCGG AAAGGGGAGG AGCGCAACAG TTGCATTTC GGAACAACCT 1620
 TCTCTGGAG CTTCCAATGG AACGGGAAGG AGTTCACGGC CTGGTACAGT GACATGGAGA 1680
 CCCCACTCAA AGCTGGCCCT TTCCGGAGGC TCGGGTCTA TATCGACTTC CCGGGAGGGA 1740
 TCCTTTCTCT CTATGGCGTA GAGTATGATA CCATGACTCT GGTTCACAAG TTTGCTGCA 1800
 AATTTTCAGA ACCAGTCTAT GCTGCTTCT GGCTTTCCAA GAAGGAAAAA GCCATCCGGA 1860
 TTGTAGATCT GGGAGAGGAA CCCGAGAAGC CAGCACCGTC CTGGGGGTG ACTGCTCCCT 1920
 AGACTCCAGG AGCCATATCC CAGACCTTTG GGTAGCTGGC TTTTGAAATC CTATGGGGTC 2040
 GGTGATTGT GGGCAGAAAT AACTGCTGAT GGTAGCTGGC TTTTGAAATC CTATGGGGTC 2100
 TCTGAATGAA AACATTCTCC AGCTGCTCTC TTTTGTCTCA TATGTGCTG TTCTCTATGT 2160
 GTTTGACGTA ATTCTTTTTT TTTTGTGGA GACGGAGTCT CGCACTGTTG CCCAGGCTGG 2220
 AGAGCAGTGG CGGATCTTGG GCTCACTGCA AGCTCCGCT CCCAGATTCA AGCAATCTC 2280
 CTGCTCAGC CTCGAGTA GCTGGGATTA CAGGTGCTG CCACCAACCC CAGCTAATGT 2340
 TTTGTATTTT TAGTAGAGAT GGGGTTTAC CATGTGGCC AGGCAGATCT CAACTCCTG

ACCTGCTGAT GCACCCACCT CGGCTCCCA AAGTGTGGG ATTACATGCG TGAGCCACTG 2400
CGCCCTGCCT GTTTGTAGTA ATTTTATAGC ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460
CTCCTCTCTG TTCAGGTAAA TGTACACTG TGCCACGAAT GGATGACGAC GAACCTTAAA 2520
GAGTGGCTGA AAGATTGCA GAGTTATCAT AATAAATTGC TAACTTGCCT

Seq ID NO: 196 Protein sequence:
Protein Accession #: NP_006461

1 11 21 31 41 51
MAELDLMAPG PLPRATAQPP APLSPDSGSP SPDSGSASPV EEDVGSSEK LGRETEEQDS 60
DSAEQGDPAE EGKEVLCDFF LDDTRRVKAV KSCLTCMVNY CEEHLQPHQV NIKLQSHLLT 120
EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCCQEHSGH TIVSLDAARR DKEAELQCTQ 180
LDLERKLN ENAISRLQAN QKSVLVSVSE VKAVAEMQFQ ELLAAVRKAQ ANVMLFLEER 240
EQAALSQANG IKAHLEYRSA EMEKSKQELE RMAAISNTVQ FLEBYCKFKN TEDITFFSVY 300
VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEFSEKEE YDIRTQVSAV VQRKYWTSKP 360
EPSTREQFLQ YAYDITDFPD TAHKYLRLQE ENRKVTNTTP WEHPYDLPSS RFLHWRQVLS 420
QQSLYLHRYF FEVEIFGAGT YVGLTCKGID RKGEERNSCI SGNFNSWSLQ WNGKEFTAWY 480
SDMETPLKAG PFRRLGVYID FPGGILSFYG VEYDITMTLVH KFAKPFSEPV YAAFWLSKKE 540
NAIRIVDLGE EPEKPAPSLG VTAP

Seq ID NO: 197 DNA sequence
Nucleic Acid Accession #: NM_004316
Coding sequence: 433-1149

1 11 21 31 41 51
CCCGAGACCC GCGCAAGAG AGCGCAGCCT TAGTAGGAGA GGAACGCGAG ACGCGGCAGA 60
GCGCGTTTCA CACTGACTTT TGCTGCTGCT TCTGCTTTTT TTTTCTTAG AAACAAGAAG 120
GCGCCAGCGG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCGGAAGCCA ACCCGGAAG 180
GGAGGAGGGG AGGGAGGAGG AGGCGGCGTG CAGGGAGGAG AAAAGCATT TTCACCTTTT 240
TTGCTCCAC TCTAAGAAGT CTCGCGGGA TTTGTATAT ATTTTAAAC TTCGTCAGG 300
GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
GTCCCCCTCG CGGGCCCCGC ACCTCGCGTC CGGATCGCT CTGATTCCGC GACTCCTTGG 420
CGCGCGCTGC GCATGGAAAG CTCTGCCAAG ATGGAGAGCG GCGGCGCGG CAGCAGCGCC 480
CAGCGCGAGC CCCAGCAGCC CTTCCTCGCG CCGCAGCCT GTTCTTTTGC CACGCGCGCA 540
GCGCGCGCGG CCGCAGCGCG CGCAGCGGCA GCGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
CAGCAGCAGC AGCAGCAGCA GCAGGCGCGG CAGCTGAGAC CGGCGGCGCA CGGCCAGCCC 660
TCAGGGGGGG GTCAAGATG AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC 720
GAACTGATGC GCTGCAACAG CCGGCTCAAC TTCAGCGGCT TTGGCTACAG CCGTCCGCGC 780
CAGCAGCGCG CCGCGTGGC GCGCGCAAC GAGCGCGAGC GCAACCGCGT CAAGTTGGTC 840
AACCTGGGCT TTGCCACCTT TCGGGAGCAC GTCCCAACG GCGCGGCCAA CAAGAAGATG 900
AGTAAGGTGG AGACACTGCG CTCGGCGGTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
GACGAGCATG ACGCGGTGAG CGCCGCTTTC CAGGCGGCG TCTGTGCGC CACCATCTCC 1020
CCCAACTACT CCAACGACTT GAACTCCATG GCGGCTCGC CGGTCTCATC CTACTGCTCG 1080
GACGAGGGCT CTTACGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTACCAAC 1140
TGGTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGGCAA TGGACTTTGG AAGCAGGGTG 1200
ATGCAACAAC CTGATCTTTT AGTCTTTTCT TGTCAGTGGC GTTGGGAGGG GGAGAAAAGG 1260
AAAAAGAAAA AAAAGAGAAA GAAGAAGAAA AGAGAAGAA AAAAAACGA AAACAGTCAA 1320
CCAAACCCAT CGCAACTAA GCGAGGCATG CCGAGAGAC ATGCTTTCA GAAACCGGGA 1380
AGCGCTCAGA ACAGTATCTT TGCACTCAA TCATTACCG AGATATGAAG AGCAACTGGG 1440
ACCTGAGTCA ATGCGCAAAA TGCACTTGT GTGCAAAAGC AGTGGGCTCC TGGCAGAAAG 1500
GAGCAGCACA CGCGTTATAG TAACCTCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT 1560
GCTCGGGTCC CTTACCTCC CCGCCCTTTC TTAGAGTGCA GTTCTTAGCC CTCTAGAAAC 1620
GAGTTGGTGT CTTTC

Seq ID NO: 198 Protein sequence:
Protein Accession #: NP_004307

1 11 21 31 41 51
MESSAKMESG GAGQFPQPP QPFPLPFAAC FFATAAAAAA AAAAAAQSA QQQQQQQQQQ 60
QQQAPQLRP AADQPSGGG HKSAPKQVKR QRSSPELMR CKRRLNFSGF GYSLPQQQPA 120
AVARRNERER NRVKLNVLGF ATLREHVPNG AANKMKSVE TLRSAVEYIR ALQQLLDEHD 180
AVSAAFQAGV LSPTISPNYS NDLNSMAGSP VSSYSSDEGS YDPLSPPEQE LLDFTNWF

Seq ID NO: 199 DNA sequence
Nucleic Acid Accession #: NM_007015
Coding sequence: 1-1005

1 11 21 31 41 51
ATGACAGAGA ACTCCGACAA AGTTCCTTCC GGCCTGGTGG GACCTGATGA CGTGGAAATTC 60
TGACAGCCCC CGGCTAGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
AAGGTGGGAG CCGTGGTCTT CATTTCCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
TTTAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360
ACAGGAATTC GTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
ATTCTGAGG TGGGCGCGCT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480
ATGCCAGTCA AATATGAAGA AATTTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
GACCAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTCTCG 600
CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAAA GAGAGTGGT AAGAAAAATT 660
GTTCCAACTA CCACAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA 720
CTGAATAATG AAACCAAGAC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780

CCTTATCATC AGCAGGAAGG GGAAAGCATG ACATTGACC CTAGACTGGA TCACGAAGGA 840
ATCTGTTGTA TAGAATGTAG GGGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCTCG CAGAGTCATC 960
ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTTATATAT 1020
CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG 1080
ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAATGCA CTGAAAGGGT 1200
AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTGTATT TTTTATTGCG ATTGATTGTC 1260
CATAGTCTT CCCTTGCTG CATCTCCAA AGCTATTG AAATAAACAC GAAATTTTAC 1320
AGTTTGCC

Seq ID NO: 200 Protein sequence:
Protein Accession #: NP_008946

1 11 21 31 41 51
MTENSDKVPI ALVGPDDVEP CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
APYFWKGS DS HIYNVHYTMS INGKLQDGS EIDAGNNLET FKMGSAGEEA IAVNDFQNGI 120
TGIRFAGGEK CYIAQVKAR IPEVGAVTKQ SISKLEKGI MPVKYEENSL IWVAVDQPVK 180
DMSFLSSKVL ELCDLPIFW LKPTYPKEIQ RERREVRKI VPTTKRPHS GFRSNPGAGR 240
LNNETRPVSQ EDSQAFNPDN PYHQEGESM TDFPRLDHEG ICCIECRRSY THCQKICEPL 300
GGYYPWFYNY QGCRSACRVI MPCSMWVARI LGMV

Seq ID NO: 201 DNA sequence
Nucleic Acid Accession #: NM_000728.2
Coding sequence: 112..495

1 11 21 31 41 51
GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCACAGC AGGTGTGGTG TTCATCCCGG 60
GTCGACCGGC CGCTCGCGCT GCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
CGGAAGTTCT CCCCTTCTT CCCTCTCAGT ATCTTGGTCC TGTACCAGCG GGGCAGCCTC 180
CAGGCGGCGC CATTAGGTC TGCCCTGGAG AGCAGCCAG ACCCGCCAC ACTCAGTAAA 240
GAGGACGCGC GCCTCTGCT GGCCTGCACTG GTGCAAGACT ATGTGCAGAT GAAGGCCAGT 300
GAGCTGAAGC AGGAGCAGGA GACACAGGC TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
AACACTGCCA CCTGTGTGAC TCATCGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTGGCAG GCGCCGACG 480
GACCTTCAAG CCTGAGCAGA TGAATGACT CAGGAAGAAG GTGTGCTCTA AATCCAATGA 540
CATATCCTTA TAAGAGATTC ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
TGGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAAGTGTGA 720
GAGAATAATT TCTGTGTTT TAAGCCACAA AGTTTGTGGT AATTGTATT GACAGCCCTA 780
GGAACTAAT ACAATACATT TTCACTTATT TTGGGTAAT GCCTTGGAGT GGGATTGCTG 840
GGTTATTGG AAGTGTGTA TTTAACTCTG TAAGAACTG CCAAATATT TTCTGAAATG 900
ACTGTACCAC TTGCGCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATTT CCACAAATAG 960
GTATGTAGCA GTATCTCATT GCTGTTTAA TTTGTATTTC CCAATGACT AATGACGTTG 1020
AGCATCTATT TTACCATATG TTTATCACCT TTATTGAAGG GTCTGTATA ATCTCTGCT 1080
AAATTTTGT TGGCTTGCTT GCTTATTAG TGTGAGTTT TTAGAGCTCT TTATATGTTG 1140
TGGATGCAAG ATGTGTTTCA GATATATAGT TTGGAACCTT CCTTCCCTG AATCTGCGGA 1200
TTGCTTTTTC ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
TCCAATCAT CTTTTTTTTT CTTTATGTA TTGTGCTTTT AGTTTATGTC TAAGAACTCT 1320
TTGCTTAAT AAGGTCCCAA GGTCAACAATA ACCTTATTCT ATACTTTCTT GTAAAAAGTT 1380
TATAGTTTAT TATTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
TGAGAGGTGT AGGTTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
TTTGTAAAA AGACTGTTAT TTCAACATTT AATTGCCCTT GCACCTTGT CAAAAAGCAA 1560
CTGATCATAT TTGTGTGGGT ATATTCTGG GTTCTCAATT CTGTCTCATT GATTGATTG 1620
ACCATCTTT TGCCAAATGC ATACTGCCTT GATTAGTGA GTGTAAAGT GAATCTCAAA 1680
ACCAGATAAT GTGGGTCTAC CAACATTGTT CATTCTGTTT CAAAAAGATT TTAGCTACAT 1740
CTAAATATT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
TTCTGATGAG ATTTTAAATG GGATGTGTT AAATCAGTGG GTTAATTTTG GGAGAAATTAG 1860
CATATTAATA ATATTAGTC GTTCAATTCA TGAACACAAT ACATGTTTTC ACTTATTAG 1920
GTTTCTCTG TTTTTTTTT TTTAACAGTG TTCTCAGTTT TCAACAGAAA TATTCTACAC 1980
ATATCTGTT AGATTTTTAA CTATTTTATT TTTTGGTGT AATGTAAATG GTACTTAAAC 2040
ATTTTGTGT TTAATGTTT ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
Protein Accession #: NP_000719.1

1 11 21 31 41 51
MGFRKFSFPL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
KASELKQEQE TQSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKS NFVP TNVGSKAFGR 120
RRRLDQA

Seq ID NO: 203 DNA sequence
Nucleic Acid Accession #: NM_001741
Coding sequence: 71..496

1 11 21 31 41 51
CTCTGGCTGG ACGCCGCGC CGCCGCTGCC ACCGCTCTG ATCCAAGCCA CCTCCCGCCA 60
GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTT 120
GTTGCAGGCA GGCAGCCTCC ATGCAGCACC ATTCAGGTCT GCCCTGGAGA GCAGCCAGC 180
AGACCCGCCC ACGCTCAGTG AGGACGAAGC GCGCTCTCTG CTGGCTGCAC TGGTGCAGGA 240
CTATGTGCAG ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC 360
 GCAGGACTTC AACAAAGTTTC ACACGTTCCC CCAAAGTGA ATTGGGGTTG GAGCAGCTGG 420
 AAAAGAAAGG GATATGTCCA GCGACTTGGG GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
 CCAGAAATGCC AACTAAACTC CTCCTTTCC TTCTTAATTT CCCTTCTTGC ATCCTTCCTA 540
 TAACTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
 TTCTTGTGG CAGAGGATGT CTCAAACTTC AGATGGGAGG AAAGAGAGCA GGACTCACAG 660
 GTTGAAGAG AATCACCTGG GAAAAATACCA GAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCTCT GTCTGCTTC TGAATGTGCT GATCATTGA GGAATAAAAT 780
 TATTTTCCC C

Seq ID NO: 204 Protein sequence:
 Protein Accession #: NP_001732

1 11 21 31 41 51
 MGFKQFSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKPHFTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSMQPNA N

Seq ID NO: 205 DNA sequence
 Nucleic Acid Accession #: NM_005361
 Coding sequence: 1-945

1 11 21 31 41 51
 ATGCCCTCTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA 60
 GAGGCCCTGG GCCTGGTGGG TGCGCAGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT 120
 TCCTCTTCTA CTCTAGTGGG AGTTACCTCG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 CCTCCCCACA GTCTCTCAGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGCTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTCCCGAC 300
 CTGGAGTCCG AGTTCCAAGC AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AAATGCTGGA GAGTGTCTCT 420
 AGAAATTGCC AGGACTTCTT TCCCGTGATC TTCAGCAAAG CCTCCGAGTA CTGTCAGCTG 480
 GTCTTTTGCA TCGAGGTGGT GGAAGTGGTC CCCATCAGCC ACTTGATACAT CCTTGTCAAC 540
 TGCTTGGGCC TCCTCTACGA TGGCTGCTG GCGGACAATC AGGTCATGCC CAAGACAGGC 600
 CTCCTGATAA TCGTCTGGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGAGAG AGCTGAGTAT GTTGGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCACGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG 780
 GTGCCCGGCA GTGATCTCTG ATGCTACGAG TTCCTGTGGG GTCCAAGGGC CCTCATTGAA 840
 ACCAGCTATG TGAAGTCTCT GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTC 900
 TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
 Protein Accession #: NP_005352

1 11 21 31 41 51
 MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 PPHSPQASS PSTTINTTLW RQDEGSSNQ EEEGRMFPD LESEFQAAS RKMVELVHFL 120
 LKLYRAREPV TKAEMLESLV RNCQDFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKGT LLIIVLAIIA IEGDCAPEEK IWEELSMLEV FEGRSDSVFA 240
 HPRKLLMQDL VQENYLEYRQ VPGSDPACYE FLWGPRLALIE TSYVKVLHHT LKIGGEPHIS 300
 YPPLHERALR EGEE

Seq ID NO: 207 DNA sequence
 Nucleic Acid Accession #: NM_021115
 Coding sequence: 743-2893

1 11 21 31 41 51
 AAAGGAAGGG AGGGAGGGAG AAAGGAGAAG TTGGTTTAGA GGCCAGCCGG ACGAGCTTTG 60
 GGCACCGCCC TTAGGAGGGC CACCCCTCAGA GTCTGACAGC AGGTGAAGGT CCTAAATCTC 120
 CCCAAACTAA CTGGTGTCTT TTCTCTCTTT CCAAGATGCT CTTCCGAGG GAGATGCTAG 180
 CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
 GCACCCTGAA GAGAGAGTGG TAACAGCGCC CCCAGTTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCGAGCTG GTGCTGGATG GGACCGCACC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACOGCTGCTT CCAGAGGAGG CCGCCCCAA GCACGCCTTG CCCCCAAGA AGAAACTGCC 420
 TTGCTCAAG CAGGTGAACT CTGCCAGGAA GCAGCTGAGG CCCAAGGCCA CCTCCGCAGC 480
 CACTGTCCAA AGGGCAGGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTCTC 540
 CACGAGAAG CCTGGCCAC CGGGGGACCC GGACCCCATC GTGGCTCCG AGGAGGCATC 600
 AGAAGTGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCCTG CCTACACAC CCGCACCCCT 660
 GCAAAATCTCC CCTTCACTT GCAGCCCTA TGTGGCCAC ACACCTCCCC AGAGGCCAGA 720
 ACCCGGGGAG CCTGGGCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCAT 780
 GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
 GACCACTACC TCCACCATTA TCACCACAC GGTCAATCACC ACCGAGCAGG CACCAGCTCT 900
 GTGAGTGTG AGCTTCTCCA ATCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
 GCCCTCAAC AACTTCTGG AGTGACATA CAACGTGACA GTCTACACTG GCTATGGGGT 1020
 GGAGCTCCAG GTGAAGAGTG TGAACCTGTC CGATGGGGAA CTGCTCTCCA TCCGCGGGGT 1080
 GGACGCGCCT ACCCTGACCG TCTTGGCCAA CCAGACATCT CTGTTGGAGG GGCAGGTAAT 1140
 CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCCGACC TTCCAGGACC ACGGCTTTGG 1200
 GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCCC GCGGCGCTGA 1260
 CTCCTGGGAT GTACCGGTGA TGGACCTGCA CTCAGGTGGG GTGGCCCACT TTCACTGCCA 1320
 CCTGGGCTAT GAGCTTCCAG GCGCTAAGAT GCTGACATGC ATCAATGCCT CCAAGCCGCA 1380
 CTGGAGCAGC CAGGAGCCCA TCTGCTCAGC TCCTTGTGGA GGGGCGAGTC ACAATGCCAC 1440
 CATCGGCGC GTCTCTCTCC CAAGTTACCC TGAACAACCA AATGGGAGCC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTTGCT 1560

5 GCATGACAAG GACAGGATGA CGGTTCACAG CGGGCAGACC AACAGTCAG CTCTTCTCTA 1620
 CGACTCCCTT CAACACGAGA GTGTCCCTTT TGAGGGCCTG CTGAGCGAAG GCAACACCAT 1680
 CGGCATCGAG TTCACTGCTG ACCAGGCCCC GGCGGCTCC ACCTTCAACA TCGATTGTA 1740
 AGCGTTTGAAG AAAGGCCACT GCTATGAGCC CTACATCCAG AATGGGAAT TCACTACATC 1800
 CGACCCGACC TATAACATTG GGAATATAGT GGAGTTCACC TGCGACCCCG GCCACTCCCT 1860
 GGAGCAGGGC CGGGCCATCA TCGAATGCAT CAATGTGCGG GACCCATCT GGAATGACAC 1920
 AGAGCCCTG TGCAGAGCCA TGTGTGGTGG GGAGCTCTCT GCTGTGGCTG GGTGGTATT 1980
 GTCCCCAAG TGGCCCGAGC CCTACGTGGA AGGTGAAGAT TGTATCTGGA AGATCCACGT 2040
 10 GGGAGAGAG AAACGGATCT TCTTAGATAT CCAGTTCCTG AATCTGAGCA ACAGTGACAT 2100
 CTTGACCATC TACGATGGCG ACGAGGTCAT GCCCCACATC TTGGGGCAGT ACCTTGGGAA 2160
 CAGTGGCCCC CAGAACTGT ACTCCTCCAC GCCAGACTTA ACCATCCAGT TCCATTCCGA 2220
 CCTGCTGGC TCTCTTTG GAAAGGCCA GGGATTATC ATGAACTACA TAGAGGTATC 2280
 AAGGAATGAC TCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAAAA CCACTTCTCA 2340
 CACGAGTTG GTGCGGGAG CCGAATCAC CTACCACTGT GACCCCGGCT ATGACATCGT 2400
 15 GGGGAGTGAC ACCCTCACCT GCCAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTG 2460
 TGAGAAAAAT ATGTAAGTCA CCGACCCCGG AGAGGTGGAT CACTCGACCC GCTTAATTTT 2520
 GGATCCTGTG CTGCTGGTGG GGACCACCAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
 TGAAGGGAGT TCTCTTCTGA CCTGCTACAG CCGTGAAACA GGGACTCCCA TCTGGACGTC 2640
 TCGCCTGCC CACTGCGTTT CAGAAGCGGC AGCAGAGACG TCGCTGAAG GGGGGAACAT 2700
 20 GGCCTTGGCT ATCTTCATCC CGGTCTTCAT CATCTCCTTA CTGCTGGAG GAGCCTACAT 2760
 TTACATACA AGATGTCGCT ACTATTCCAA CCTCGCCTG CCTCTGATGT ACTCCACCC 2820
 CTACAGCCAG ATCAGCGTGG AAACCGAGTT TGACAAACCC ATTTACGAGA CAGGGGGAAC 2880
 CCAAAAGGTT TAGGTTTCA TTTAAAGA GGTACCCTTT AAAAAGGGC TTGTGAATC 2940
 25 AACCCCAATT TCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
 AAAGGCGGCT GTTTTTTGGT TAAACTTTT AACAAAGGT TACGGGTTT TTCCCGGAT 3060
 TTTATAAATT TAAAGATG

Seq ID NO: 208 Protein sequence:
Protein Accession #: NP_066938

30 1 11 21 31 41 51
 35 MAQEAPEQEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
 PEGYIDSSDY PLLPLNNFLE CTYNVTVTG YGVELQVKS NLSDGELLSI RGVDPGLTLV 120
 LANQTLLEVG QVIRSPNTTI SVVFRTQDD GLGTQLLHYQ AFMLSCNFPR RPDSDGVTVM 180
 DLHSGGVAHF HCHLGYELQG AKMLTCINAS KPHWSSQEP CSAPCGGAVH NATIGRVLSP 240
 SYPENTNGSQ FCIWTIEAPE GQKLHLHFER LLLHDKDRMT VHSQGTNKS LLYDSLQTES 300
 40 VPPEGLLSBG NTIRIEFTSD QARAASTFNI RFEAFKHC YEPYIQNGNF TTSDDTYNIG 360
 TIVEFTCDPG HSLEQGPAIL ECINVRDPY NDTEPLCRAM CGGELSAVAV VVLSPNWPEP 420
 YVEGEDCINK IHVGEKRIPL LDITQFLNLSN SDILTIYDGD EVMPHILGQY LGNSGPKLY 480
 SSTPDLTIQF HSDPAGLIFG KQGQFIMNYI EVSRNDSCSD LPEIQNGWKT TSHTELVRGA 540
 RITYQCDPGY DIVGSDTLTC QWDLWSDDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG 600
 45 TTIQYTCNPG VLEGSSLLT CYSRETGTPI WTSRLPHCVS EAAAEETSLEG GNMALAIPIF 660
 VLIISLLGG AIYIYITCRY YSNLRLPLMY SHPYSQITVE TEFDNPIYET GGTQKV

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89-631

50 1 11 21 31 41 51
 55 AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
 CTGAGAGCCG GGCAGAGGCT CCGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
 GACGGGCGAT GCTGATGGCC CAGGAGGCC TGGCATTCCT GATGGCCAG GGGCAATGC 180
 TGGCGGCCA GGAGAGCGCG GTGCCACGG CGGCAGAGGT CCCCGGGCG CAGGGGCAGC 240
 AAGGGCCTCG GGGCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTCAGS 300
 GCTGAATGGA TGTGTCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCGCTG TTAGTTCTA 360
 60 CCTCGCCATG CCTTTCGCGA CACCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
 GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGT GTGCCGCAA 480
 CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
 CTGCTCCAG CAGCTTCCCG TGTGTATGTG GATCAGCGAG TGCTTCTGCG CCGTGTGTTT 600
 GGCTCAGCCT CCCTCAGGCG AGAGCGGCTA AGCCAGCGCT GCGGCCCTT CCTAGTTCAT 660
 65 GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCTATTGTG GGCCTGATT 720
 GTTGTGCGCT GGAGGAGGAC GGCTTACATG TTGTTTCTG TAGAAAATAA AACTGAGCTA

Seq ID NO: 210 Protein sequence:
Protein Accession #: NP_001318.1

70 1 11 21 31 41 51
 75 MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
 PRGPHCGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEIARRSLA QDAPPLVPVG 120
 VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSQRR

Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52-459

80 1 11 21 31 41 51
 85 CCTCGTGGGC CTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
 GAAGGCCAGG GCACAGGGGG TTCCAGGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
 CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGAGA 180
 GGTCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
 CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGTGCC CCTGCGGGC CAGGAGGCCG 300

GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTTC 480
 TAGGTATGTC CTCTCCCT AGGGAATGGT CCGACACGA GTGGCCAGTT CATTTGTTGG 540
 GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAATAAAG 600
 CTGAGCTA

Seq ID NO: 212 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGCA RRPDSRLLOF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLVPFLAQAP SQQRR

Seq ID NO: 213 DNA sequence
 Nucleic Acid Accession #: NM_000555
 Coding sequence: 416..1498

1 11 21 31 41 51
 CTTATTTTAT ATGAATGTG GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTTGATGAAT 60
 AGCACAAGA CACTGGCTGT TCCCTGGAGG CTGTCCCTTT AAAGGAGAAT CTTAGTTTAT 120
 TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGAATA AAATGAAAAC 180
 ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTAAGC TGGAGATGCT 240
 AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAAGCTA TGGATTCATT 300
 TACAACGTGT AGTCATGTGG GCATGTGTGA GGAACAGAT GCCAGTTTAT ATGATTTTAG 360
 CCCGAAGTTC CAATTTGATA GGAGCCACTG TCAGTCTCTG AGGTTCCACC AAAATATGGA 420
 ACTTGATTTT GGACACTTTG ACGAAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCG 480
 GATGAATGGG TTGCTAGCCG CCATCTCAGC CGCCCACTGT AGCTTCTACC GAACCCAGAAC 540
 CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
 CCGCTACTTC AAGGGGATTG TGTACGCTGT GTCTCTGAC CGTTTTCTGCA GCTTTGACGC 660
 CTTGCTGGCT GACCTGACGC GATCTCTGTC TGACAACATC AACCTGCCTC AGGAGTGGC 720
 TTACATTTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
 GGAAGCTAT GTCTGTTCTT CAGACAACCT CTTTAAAAAG GTGGAGTACA CCAAGAATGT 840
 CAATCCCAAC TGGTCTGTCA ACGTAAAAAC ATCTGCCAAT ATGAAAGCCC CCCAGTCTCT 900
 GGCTAGCAGC AACAGTGCAC AGGCCAGGGA GAACAAGGAC TTTGTGCGCC CCAAGCTGGT 960
 TACCATCATC CGCAGTGGGG TGAAGCCTCG GAAGGCTGTG CGTGTGCTTC TGAACAAGAA 1020
 GACAGCCAC TCTTTTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
 CGGGGTTGTC AAAAAACTCT ACCTCTGGA TGGAAAAACG GTAACCTGTC TCCATGATT 1140
 CTTTGTGAT GATGATGTGT TTATTGCTGT TGGTCTGAA AAATTTGCT ATGCTCAGGA 1200
 TGATTTTCT CTGGATGAAA ATGAATGCCG AGTCATGAAG GGAACCCAT CAGCCACAGC 1260
 TGGCCCAAAG GATCCCCCAA CACCTCAGAA GACTTCAGCC AAGAGCCCTG GTCCTATGCG 1320
 CCGAAGCAAG TCTCCAGCTG ACTCAGCAA CGGAACCTCC AGCAGCCAGC TCTCTACCCC 1380
 CAAGTCTAAG CAGTCTCCCA TCTCTACGCC CACGAGTCTG GGCAGCCTCC GGAAGCACA 1440
 GGACCTGATC CTGCTCTGCT CTTGGATGA CTCGGACTCG CTTGGTGATT CCATGTAAAG 1500
 GAGGGGAGAG TGCTCAGAGT CCAGAGTACA AATCCAAGCC TATCATTTGA GTAGGGTACT 1560
 TCTGCTCAAG TGTCCAACAG GGTATTGGT GCTTCAAGT TTTTATTTTG TTTTGTGTTG 1620
 TATTTTGAAA AACACATTGT AATATGTTGG GTTATTTTC CTGTGATTTC TCCTCTGGGC 1680
 CACTGATCCA CAGTATACAA TTATGAGAGA TAGATTGATA ACCATCCTTT GGGGAGCAT 1740
 TCCAGGGATG CAAAATGTGC TAGTCCATGA CCTTCAATG GAAAGCTTAG GGGCCTGGGG 1800
 TAAATTTGCC CCGTTTAAAT TTGCCCAAAC AGTTTTCCTT TTGTAGAGGG GTGTTTAAAT 1860
 ATACAGCAAT TAAAGATTTT GTGTGGGGAA AAAAAAACT CATTTGGCAGA TCCAAGAAATG 1920
 ACAAAACACA GTGCCCTTT TCTCTGATC TCAAGAATGG TGGAGGACCC TGAAGGACA 1980
 GCAAGGCAGC TCCCCAGCCT CACTCTTAC TCCTGATTGA GGGCCGGGTT TGTGTCCAG 2040
 CACCAATTCT GGCTGTCAAT GGGGAGAAAT AAACCAACAA CTTATAATTG TGACACCAGA 2100
 TGCTTAGGAT CTTGTGCTGT GGTAGCTAA GAGAATAGAC AGAATTGGAA AATACTGCAG 2160
 ACATTTCCGA AGAGTTTATA AAGCAGATG AATTCCTGGT CAATCTCTCC ACTGAGGCAA 2220
 TTTGGAATCA ATAAGCAATT GATAATAGTT TGGAGTAAGG GACTTCATAT ACCTGATTCC 2280
 TCTGAAGGC TGTCTAACAT ACCACATGAT TACATGAAT GTATGGTATC CATCTATCTC 2340
 TGTCTATTG AATGCTTGT TAACAGCCAA CACTGAAAAC ACTGTGAGAA TTTGTTTTCA 2400
 GGTCTGACAC CTTTCAGTCT CTTTATATAG CAAGAAATCA ATATCCTTTT TATAAAAAAT 2460
 CATGTCTGTA TTTCAAGGAC AAACCTCTCA GGCTCCTTTT TTATAAATG GTGATTTTTC 2520
 TTTTGTCTAA AAAACACATG AAGAAAATTT ACCAGAAAAA AAAAAAAAG CCGAAGAAAT 2580
 ATGTTATTTA GAAATTATGC TGTCACTGCC AAACAGTAAC CTCAGGAGA AAACAAGATG 2640
 AATAGCAGAG GCCAATTCAA TAGAATCAGT TTTTGTATAG CTTTAAACA GTTATGCTTG 2700
 CATTAAATAT TTCAATGTGG ACCAGACATT CTAATTATAT TTTAAATGAA ATGTTACAGC 2760
 ATATTTTAAG CAATCTTTT TATCTATAAT CCTAATATT CATACTGAAG ACACAGAAAT 2820
 CTTTCACTTG TCTTTAATAT TAGAAAGGAT TTCTCTTTAC TAAGGACTGA TCATTTGAAA 2880
 TAGTTTTCAG TCTTTTGAGA TACAGGTTTA TAACACTGCT TTTTCTTCC TGTAAACATA 2940
 GCCATAATG GCAAAAACAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCCTGTGTTG 3000
 GCTTTNACCA AATATAAAAA TTCCCTTATT CTTTGGTAAT GGTGCAATN TTTGAAAAGG 3060
 CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAATGG CTGTCAGTTG TTCTCCACT 3120
 CTAATGGA TGAAGCTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGATGT 3180
 GTGTGTGTGT GTGTGCATCT GCAGCTGCTT CAAAATTAAG AAATACTACA AGACACCCCT 3240
 GTAATGGATT GGTGGCACT GGGTGGCACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
 GTGGTGGTGG GGTATCTCAA ATGCCCTTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
 ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTGTGTG AAATTGAAAA 3420
 ACCCCAAATG ATGAGGATCT CTTTGTGCC CCTCTCCTTT TTTTGTAAAC CCATTCAAAA 3480
 CCATTAATAA GCTATCTTTA CTAANCCCT ATTTCTTTCT AGAAGCTCAG GGTTTNCCTA 3540
 GTGCCTCCCA NAACATTTTG TAGTTAATTG GGAATAAGTG ATACTTGGAT TAGGGGGTGT 3600
 GGGCATAAAG AATGGTGGGA GGCCTGATTT TAAATTCAG GCCAGAACCC CCAATGACTC 3660
 CACCCATAGT NTCATTTAG GTCTCATTCA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
 TGGAGGCTGG TAAAGAGCAG GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCTCT 3780
 ACCTAGCTC TNGAGTATT TCCTTGATTG CGGTATATGT ACTACTAGAA AATACCAAT 3840
 GGATATATTT TCTTAGGAT AACCTTTGAA CCAACAATNT TCAATAACAA TAGTACATCT 3900

	TCCATCTTAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATT	TGGAGGGAGC	3960
	AGGGGATGAG	GCTTGGCATA	GTCCAAAATT	TAAGNCTCCA	ATAATTAATT	GCATTTTAAA	4020
	TTGTTTTAAA	TTGGCCCACT	TTCAAGGCAA	TTTTTTTTGT	GTGTCGTGAA	CTGAGCTCCT	4080
5	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAATT	TTAGCACTCA	AGTTCCATTG	4140
	TGTTAATTTT	TGCACGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACTCCCTAT	4200
	ACTTCTCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACAAATCCAT	CTCTTGCTTG	4260
	TTCTACCTC	CTGATTTTTT	CTTCCCTACA	GAATAGAGAA	TAGGGACAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGCTGGG	CTGAACAACT	AACCTCATAA	GTAGTATTAA	CTAGGGGTAA	4380
	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
10	GCTTTGTGTC	CTTATGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTTCTAGCT	4500
	GAAGGAACCT	TAAATACACA	TCATCTACTC	CTCTACTCCA	AATTTCTCAT	TCTTCAGGCC	4560
	AGGAAACCGA	GACACAGAGG	TAAAGTAATT	TCCCCAAGGT	CACACAGCTG	GCTGGGGCAG	4620
	GATTGGGTGT	ACAAGCCACA	TCTCCTGGCT	CTTATTCAG	GGCCTTTTCC	CACTAAGTAG	4680
	TATTGGCTTC	CATTAGGCTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTGCA	TCTTGGAGCC	4740
15	ACATGTGCT	GCCCCGATCT	CAGTGGGAAA	TNCACCCAGC	AACCTAATAC	AGCCCCCTTT	4800
	CCCTGCATTC	CATCCACATG	GGTTGCAGAT	GTCCCTGAAG	AGAGTGAGGC		4860
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TGGCCTTGTC	CATCTGATTC	AGGAGATCAC	4920
	TGCTCCATCG	TGAGAGAGCC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCT	TGCCCAATG	4980
20	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTCACCTTGT	GTCTCTCAT	AATGGTTGGT	5040
	CTTTCAGGCG	TGAGGGAAT	GTTCCTTGT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAAAC	5100
	ATANCITTTG	TCTATCTAAC	TTTCTGAGAT	GGCTTTTCAA	CATTAAAAAA	AAACTAGTGT	5160
	GGTACCATTG	ACTGGCANGA	TTTNTTTTAG	AATATGGGAG	TAAGATGAGG	TAGAGAAAAT	5220
	AACTGGGTCT	CACGTGTGTT	GGCCTCATCC	ACAATGTCCC	CAAAGCCATC	CTGCTNTGAT	5280
25	GAGGACAAAT	TAGGAGTATA	AGCAAGGGGC	TTTGTGACAA	AAATGTACCC	TGGCTGATGT	5340
	TAAACATTGG	CTCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
	CATCGTCTTG	TGTACATGCG	TCCTGTGGCC	TTCCACAGCA	GAAGCCAGGG	CAAAAGGGTC	5460
	CAACACATG	GTTCCTCTG	CTGCAAGGCT	NTTCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTCACTTNTA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCAGGTACTT	CTCTCTCCTT	5580
30	CCTCCTTCTC	TCCACAGCTC	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
	TGAAGAAGGC	AAGGAACCTC	GAGATTCTTC	TTTGAATCCT	TTAGTCCAAG	TCTTAGACCA	5700
	GTGATTGGTG	CTTACCTTGA	ACAAAATTTT	GTCTGTGTTT	CTAATCCCTT	CAATACNTG	5760
	GGTACAATGC	TCCCAATCAC	CCTGCACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
35	TGATGGGAAT	GATCCCAANG	ATCACCCAC	CTCAGAAAAC	GTCTGTGCCA	ANAGACTTCC	5940
	CCAGATAGAA	NCACTGGGAC	AGTGGTTTGA	ACGACTTCTT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAAATAA	AAGGCATTTA	TTTTTTAAAA	AAGATGATTG	GAACCTGTCT	TTGGCCACAT	6060
	AGGGCCACTT	GGATCCATTT	CCAGGCCCTA	CTCATATATT	GCCTTCACTG	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCAATAGT	GTTTTGGAGC	TCATCTGGGG	6180
40	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGGCTTC	CCTCCCTTTC	6240
	TCCTAAAGCC	TGGTCCCAAA	AAATGTGTTT	TGTCTCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTG	CGTCTGCCT	TGTTTCTTGT	TAAAGGATCT	ATGCANACCT	6360
	CCCGCTTTGG	CTTAGCTAGC	GTGACATTGG	CTATCATTGG	ACAAGACTAA	CTTTTTTTTT	6420
	TTTTTTTTTT	ACTGAGTCTC	CCTCTGTGAC	CTAGGCTGGA	GTGCACTGGC	ACAATCTTGG	6480
45	CTCGCTGCAA	CCTTCACCTT	TCACCTCCCA	GGTGAAGCG	ATTCTCTGCT	CTCAGTCTCC	6540
	CGAGTAGCTG	GGATTACAGG	CGTGCGCCAC	CAAATCTGGC	TATTTTTTTA	TTATTATTAT	6600
	TTTTAGTAGA	GATGGGGTTT	CACCATGTTG	GCCAGACTGG	TCTTGAATCT	TTGGCCCTCA	6660
	ATTATCTGCC	CACCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
	GCTGACAAGA	CTAATTTTTT	ATCCCTTGGT	TTATTGGCTT	CAACATCTTC	TGGAATCAGA	6780
50	GGTGATTTTT	TCTTACCTTG	GATGCGCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTGGTAA	6840
	TTAAGGCATC	TTCTGCTTCC	TGATCAGAA	GGCAGGTTAG	TTGGGAGAGG	TCAGATGGCA	6900
	CAACAGAAAT	CACCTGTGAA	GTAAAGGCAA	GACTTGAAG	GCATTAGCGT	TTCTCATTAC	6960
	TTAGGTCAAT	AACCTTGAGG	GAATCAATGG	CTTTTTTGCC	GCTCTACCTC	TTTGTGTATC	7020
	TCCTTGACTT	TTCTTCTCT	GTCTAGTTTC	CTCTGTTCTC	AGTTTATATT	CTATGTTATC	7080
55	AGTCTCTCTT	TCCACAGTAC	AAACATCCAT	CCTTCTCTCT	GTGCAATTCT	GTCTCTCCCT	7140
	CTTATTATCT	TTAATTTGAC	TTTTTCCCTC	CTCCCTGTCT	AGGCATTGGG	CATGTGCCTC	7200
	TTCTTAGCCT	GTGATTTTGC	TTTGGGACTG	ATGATAAATT	ATTTCAGAT	TCAATCAGCC	7260
	CTGGTCTTAC	CCCAGTCCAA	TGCAAGATAT	GTGGTGGGG	AATCAACCTG	ATCCTGGCCC	7320
	TTTCTTCTTC	TCCATTTTCA	TTCTGAATCC	CCCTCAGCAG	ATCTTTACAA	GCAGTTTCTT	7380
60	TATAGCTCAT	GTATCTTTAG	GTCTTTGCTT	TCCAAGCACT	GTACAGAATA	CTTTGTGGTT	7440
	CCTTTTTAGT	CTGACATTTT	GTGGAGCAGT	GAAGCGTGCT	CAGAGACATA	ATCAGCTGAA	7500
	GAGAAAAAAT	CCACCCATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTGTTAT	7560
	GTGCCCATAA	TTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGGT	AATTTCTCCT	7620
	GTCAATTTGT	TGCTCTGAT	GGGGGTGGGG	GAGTAATTGC	TTAAAGTTTT	ACCATTACAC	7680
65	ATTAAACTCT	TTCTGCTTCC	CTTGTGTTGG	GCTTGCTAAC	TGTTGAGCTG	TTTTAACTAA	7740
	ACTGGTAGGC	AATCGGAGTT	GATTTAAATG	AAAAGATAAT	TTAACAAATC	TATACTATAA	7800
	AAAGAGACAT	TGCTTAAATT	GACATGTATT	TTTTCTTCTT	GAGTCACCTA	AACATTACT	7860
	CTTGACACCA	ACTGTTTCATG	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TAAAGAAGCC	AGATTGTAGG	TGTTAATTTA	TTAAACAGAA	TTGCAAGGCC	CTTGGAATG	7980
70	TCAGTCTTGG	GCAATACCAT	ATGGCATGCC	AAAATTTACA	ATGACTTTTC	TTTATAAGTT	8040
	ATCCAAAAGG	GATTTGAACA	AGTAAGAGGT	TATGCCAAAA	TGCTCTCAAT	GTATGGTCTC	8100
	GTAATATATT	GCAGCTTGAA	GCCAATGATC	CCTTATGACT	TGTATACAAC	TAATGCATGT	8160
	TTTATTGAAT	TTTGCAATTC	CCAGCTGTGG	TAAGTCTTTA	AAATGTTTTT	GATCACCTTT	8220
	NTGTGCCATT	AACTTGTGAC	AGAAAAATGT	TTTATGGCCA	TTTTCAAAGG	GAGAAAGTTT	8280
75	AAAATGGAAA	CAGCCACCCC	TTTCTGCCCT	ATAGCTGTAG	TTAGAATTGA	GTACCTGTAG	8340
	CAAAACAGCT	GTAATTGGTG	GTTGTAGTGT	TAGAGGTGTT	AGCTTGTCTAG	TGACTAGCTT	8400
	TGGAGAGTAA	ATGCATGGTA	TTGTACATCA	CATTTCCTAA	CTCGTTTTAA	CCTCTGAAAA	8460
	GAATATATTG	TTCTTTGTAG	TCTTCTTCC	CACCCCTTGG	CCCTCTCCCT	CTCCCTGTCT	8520
	CCAGTTGTCT	TACAGTTGTA	AATATCTGAT	TTGAGGCCCA	ATAACTCTTG	CCAAGTAAAG	8580
80	TCAGCAAAACA	ACAACAAAC	CAAAATGTGG	GGAAAAGGCA	TTTCTCAACC	ATCTCTCAGC	8640
	AGTTATTGAT	CATTCTTAA	GGACACAGAT	TGTATCAAAA	GACTCAACTT	TACGTAATAA	8700
	TCAGTGGTAA	ATTGGGGTTG	TATTGGCCAT	TGATTACATT	CAGGATTGAA	TAGTTTTTCA	8760
	AATCAGATGT	AATCCAAAGA	CAGTAGGTAG	TGATGTCCCT	TATCCCTGCA	GCTGTTTTAA	8820
	GATAGAGACC	TCAGAGACT	CTGCTTGACC	GATGACCAAT	AATTATTGTA	AAAAAAGAGA	8880
85	AAAAATGAGA	GAAATAAAAC	AGATATTATA	GAACCTTAGC	CACCTATTTA	GAATAGTTAT	8940
	AGCCAGAAAA	AAAAACAAGG	GCATGAGTTC	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTAACCTA	CTCTGAAATT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCTTTTTT	9060
	TGTTTGTGCT	ACCCCACTTG	GACTGGTAGG	TTTGGTGAGG	CCCCATAAAA	CCAGCTGGAG	9120

CAGACCCCTT TCATCTCTCG TGCCTGTAAC ACCCCTCTTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TCTTGGGTC AGAGGACTTC AAGGTTGTCT AGAGAAGTTT GCCATGTGTG 9240
 TAAGGTGCTG TGAACGTGTA GTGCTGAAGA TTCCAGCAT TCAATACCAG GCAGCCAAAG 9300
 AGCTGCTCTT GCAATTATT TGGCTCTCAA GCTCTGTCTT TCATCGCATT CTCAATTTCTG 9360
 TGTACATTTG CAAGATGTGT GTAATGTCAT TTTCCAAAAA TAAATTTGA TTTCAAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDFGHFDE RDKTSRNMRG SRMNGLPSP T HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
 GDRYFKGIVY AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYITDGS RKIGSMDELE 120
 EGESYVCSDD NFFKKVEYTK NVNPNWSVNV KTSANMKAFQ SLASSNSAQA RENKDFVRPK 180
 LVTIIRSGVK PRKAVRVLN KKTASHSFEQV LTDITEAIKL ETGVVKKLYT LDGKQVTCILH 240
 DFFGDDDVPI ACGPEKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS ANGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DSDSLGDSM

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
 GGCACGAGGC AGAGCTCTGC AAGGAGAGGT TGTGTCTTCG TTTCTTCCGC CATCTTCGTT 60
 CTTTCCAACA TCTTCGTCTT TTCTCACTGA CCGAGACTCA GCCGGTAGGT CTGCAGAGTG 120
 GTCTTCCTGG TAATTTAGTT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCTGTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCCT CCGGTGGTCC TCCGCCCTCC 240
 CCCAGTCTGT GATGCAGGCG CCATGGGCCG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAATGACC 360
 AAGAGTCTTC CCAGCCAGTT GGAACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAT GGGACTGATG TGGAGCTTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATGTA GGAATGCACCT GGAGATGGTC CTGATGTGAG GGAGGGGACT CTGCCCACTT 600
 TTGATCCAC TAAAGTGTCT GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATGAAGACTG AAACCAAGAA TATTGTCTT ATGCTGGAAA TTTGACTGCT AACATTCTCT 720
 TAATAAAGTT TTACAGTTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGPVIVQQ PTEEKREEE PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDEAF QQELALLKIE DAPGDGPDVR EGTLPFTDPT KVLEAGEGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTTCTCTTAC 60
 TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA 120
 CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCTTA TGGCGCCCGA GCAGTTCAGT 180
 GATGAAGTGG AACCAAGCAAC ACCTGAAGAA GGGGAACCA CAACTCAACG TCAGGATCCT 240
 GCAGCTGCTC AGGAGGGAGA GGAATGAGGA GCATCTGAG GTCAAGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTCTAT 360
 GGGCAGGAGG TGGACCCGCC AATCCAGAG GAGGTGAAAA CGCTGAAGA AGGTGAAAAG 420
 CAATCACAGT GTTAAAAGAA GACACGTTGA AATGATGAG GCTGCTCCTA TGTGGAAT 480
 TTGTTCAATTA AATTTCTCCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDPF NPEEVKTPEE GEKQSQ

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90-3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CCTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCG GGCACCGCCA TGCCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCTGCCG GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAAATGGT 240
 TCCGCTGCTT CAACTGCAT GACAACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTCGCCCT CAATTGTAAC TCCAAAGGTT 360

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80

```

CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
CCAGATGGGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCCAAG 480
ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTA CTGGAGA ACGCTGTGAT AGGTGTGAT 600
CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
GGCATTGACG CAGCTGCCCG AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
TTCATCAAGA TGTGTATGGC TGGAAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
TTGTGGCTCC TGCCAAATTT CTGCGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTC 900
TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG 960
GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTGTGGGGC 1020
TCACCAAGAC TTACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC 1080
TGAGTTACTT TGAGTTACTG AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA 1140
CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTC A G C C C C C C T G 1200
TCTCTGGAGC CCCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC 1260
AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTG AGCGAGACTG GGGCCTTTTG 1320
GCACCTGTAT TCCTGTGAAC TGTCAAGGGG GAGGGGCTG TGAATCCAGAC ACAGAGAGATT 1380
GTTATTTCAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTCCTACA 1440
ACGATCCGCA CGACCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT 1500
CAGTGATGCC GGAGACGGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCACCGGTG 1560
CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGA CATGGCCAG 1620
TGAGGCCTTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCAGTGCC TCTGGGAATT 1680
GTGACCGGCT GACAGGCAGG TGTTTGAAGT GTATCCACAA CACAGCCGGC ATCTACTGCG 1740
ACCACTGCCA AGCAGGCTAC TTGCGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGT 1800
GAGCTTGCAA CTGTAAACCC ATGGGCTCAG AGCCTGTAGG ATGTGGAAGT GATGGCACCT 1860
GTGTTTGCAA GCCAGGATTT GGTGGCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG 1920
CTTGCTATAA TCAAGTGAAG ATTCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980
AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG 2040
GCAGGATGCA CAGAGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTTCA 2100
AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGGT GAGGAGCCAA GAGAACAGCT 2160
ACCAGAGCCG CCTGGATGAC CTCAAGATGA CTGTGGAAAG AGTTCGGGCT CTGGGAAGTC 2220
AGTACCAGAA CCGAGTTCCG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCCTGG 2280
CAGAAAGTGA AGCTTCCCTT GGAAACACTA ACATTCTGCT CACAGCCAC TACGTGGGGC 2340
CAAAATGGCTT TAAAGTCTG GCTCAGGAGG CCACAAGATT AGCAGAAAGC CACGTTGAGT 2400
CAGCCAGTAA CATGGAGCAA CTGACAAGGG AAACAGGGA CTATTCCAAA CAAGCCCTCT 2460
CACTGGTGGC CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520
CTGTGGTGCA AGGGCTGTG GAAAATTTGG AGAAAACCAA GTCCCTGGCC CAGCAGTTGA 2580
CAAGGGAGGC CACTCAAGCG GAAATTTAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCC 2640
TCCTGGATTG AGTGTCTCGG CTTAGGGGAG TCAGTGATCA GTCCCTTCAG GTGGAAGAAG 2700
CAAAGAGGAT CAACAAAAA GCGGATTAC TCTCAACGCT GGTAAACGAG CATATGGATG 2760
AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAGA AGAAGCACAG CAGCTCTTAC 2820
AGAATGGAAA AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA 2880
AAGCAGAGC ACAGAGAGCA CTGAGTATGG GCAATGCCAC TTTTATGAA GTTGAGAGCA 2940
TCCTTAAAAA CCTCAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG 3000
AAGCCATGAA GAGACTCTCC TACATCAGCC AGAAGGTTTC AGATGCCAGT GACAAGACCC 3060
AGCAAGCAGA AAGAGCCCTG GGGAGCGCTG CTGCTGATGC ACAGAGGGCA AAGAATGGGG 3120
CGGGGAGGC CCTGGAATC TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACCTGG 3180
AAGCCAATGT GACAGCAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA 3240
GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300
TGGATGCAGT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG 3360
CTGGGGTTAC AATCCAAGAC AACTCAACA CATTAGACGG CCTCTGCA TGTATGGACC 3420
AGCCTCTCAG TGATAGTGA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA 3480
AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTGAGA GCTGGAAGAG AGGGCACGTC 3540
AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA 3600
AGAACTTGA GAACATTAGG GACAACCTGC CCCCAGGCTG CTACAATACC CAGGCTCTTG 3660
AGCAACAGTG AAGCTGCCAT AAATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG 3720
GGCTCGGGAG CCATGTCTATG TGAAGTGGTG GGTATGGGAC ATTTGAACAT GTTTAATGGG 3780
TATGCTCAGG TCAACTGACC TGACCCCATT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT 3840
TGCACCATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900
ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG 3960
ATGTTTGCTT CATAATAGTC GTAAGTGGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT 4020
ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCCAGGC 4080
ATGAAATCTT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCACTAAAAT 4140
ACTATTGCTC CATATTGTCC TCTGCAAGCT TCTTGCTGAT CAGAGTTCTT CCTACTTACA 4200
ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTGAGAGTG 4260
AGGACCTGTA AGGCAGGCCC ATTCAGAGCT ATGGTGCTTG CTGGTGCTG CCACCTTCAA 4320
GTCTCTGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC 4380
ATTTTATTA AAGCATTTCC TACCAGCAA GCAATGTTG GGAAGTATT TACTTTTTCG 4440
GTTTCAAGT GATAGAAAA TGTTGGCTTG GCATTGAAAG AGGTAAATTT CTCTAGATT 4500
ATTAGTCTTA ATTCAATCCT ACTTTTCGAA CACCAAAAAT GATGCGCATC AATGTATTTT 4560
ATCTTATTTT CTCAATCTCC TCTCTCTTTC CTCCACCAT AATAAGAGAA TGTTCCTACT 4620
CACACTTCAG CTGGGTCACA TCCATCCCTC CATTATCCTT TCCATCCATC TTTCCATCCA 4680
TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG 4740
GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800
AGCATTTTAA AAAAATAAAT TTAACCTTAC AAACCTTTGT TGTCAAGT GGTGTTTATT 4860
GCAATAACCG CTGGTTTTC AACCTCTTG CTCAACAGAA CATATGTTGC AAGACCTTCC 4920
CATGGGGGCA CTGAGTTTT GGCAGGCTG ACAGAGCTCT GGGTTGTGCA CATTCTTTTG 4980
CATTCAGCT GTCACCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
TAACACCACT GGAATTGCT GAGGCACTTC CACCTTGCTT GGAAGACTA 5100
TGGTGTGCTC TTGCTCTGT ATTTCTTGG ATTTCTCTGA AAGTGTTTT AAATAAGAA 5160
CAATTGTTAG ATGCC
  
```

Seq ID NO: 220 Protein sequence:
 Protein Accession #: NP_005553

85

1 11 21 31 41 51
 | | | | | |

	MPALWLGCCCL	CFSLLLPAAAR	ATSRREVCD	NGKSRQCFD	RELHRQTGNG	FRCLNCNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCNSKG	SLSARCDNSG	RCSCRPVGTG	ARCDRCCLPGF	120
	HMLTDAGCTQ	DQRLLDSDKD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYNNLDGGN	180
5	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWQQRHQDVF	240
	SSAQRLLDPVY	FVAPAKPLGN	QQVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTYTFRLLN	EHPNNWSPQ	LSYFEYRRL	RNLTLALIRA	TYGEYSTGYI	360
	DNVTLISARP	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGP	GTCIPCNCGG	420
	GGACDPDTGD	CYSGDENPDI	ECADCP1GFI	NDPHDPRSC	PCPCHNGFSC	SVMPEEEVV	480
10	CNNCPGVTG	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSASGN	CDRLTGRCCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAFNPADKC	RACNCNPMGS	EPVGCRCSDGT	CVCKPGFGGP	600
	NCEHGAFSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQJAL	660
	QDILRDAQIS	EGASRSLGLQ	LAKVRSQENS	YQSRLLDLKM	TVERVRALGS	QYQNRVRDTH	720
	RLITQMQLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHSVE	SASNMEQLTR	780
15	ETEDYSKQAL	SLVRKALHEG	VSGSGSPDGG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
	ADRSYQHSRL	LDSVSFQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG		900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL	960
	QVDNRKAEAE	EAMKRLSYIS	QKVSADSDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
	IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMREVEGEL	ERKELEFDTN	MDAVQMVITE	1080
20	AQKVDTRAKN	AGVT1QDTLN	TLDGLLHMD	QPLSVDEEGL	VLEQLKLSRA	KTQINSQRLP	1140
	MMSELEBERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQQ	

Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: NM_016529
Coding sequence: 13-1854

	1	11	21	31	41	51	
	GTCAAGAAAA	GAATGCTGT	AATTGTTTGA	ACTCCTTCAG	GACGACTTCG	GCTTTACTGT	60
	AAAGGGGCTG	ATAATGTGAT	TTTGTGAGAGA	CTTTCAAAAG	ACTCAAATA	TATGGAGGAA	120
30	ACATTATGCC	ATCTGGAATA	CTTTGCCACG	GAAGGCTTGC	GGACTCTCTG	TGTGGCTTAT	180
	GCTGATCTCT	CTGAGAATGA	GTATGAGGAG	TGGCTGAAAG	TCTATCAGGA	AGCCAGCACC	240
	ATATTGAAGG	ACAGAGCTCA	ACGGTTGGAA	GAGTGTACG	AGATCATTTGA	GAAGAATTTG	300
	CTGCTACTTG	GAGCCACAGC	CATAGAAGAT	CGCCTTCAAG	CAGGAGTTCC	AGAAACCATC	360
	GCAACACTGT	TGAAGGCAGA	AATTAAAATA	TGGGTGTTGA	CAGGAGACAA	ACAAGAACT	420
35	GCGATTAATA	TAGGTATATC	CTGCCGATTG	GTATCGCAGA	ATATGGCCCT	TATCCTATTG	480
	AAGGAGGACT	CTTTGGATGC	CACAAGGGCA	GCCATTACTC	AGCACTGCAC	TGACCTTGGG	540
	AATTTGCTGG	GCAAGGAAAA	TGACGTGGCC	CTCATCATCG	ATGCCACAC	CCTGAAGTAC	600
	GCGCTCTCCT	TGGAAGTCCG	GAGGAGTTTC	CTGGATTTGG	CACCTCTCGT	CAAAGCGGTC	660
40	ATATGCTGCA	GAGTGTCTCC	TCTGCAGAA	TCTGAGATAG	TGGATGTGGT	GAAGAAGCGG	720
	GTGAAGGCCA	TCAACCTCGC	CATCGGAGAC	GGCGCCAAAG	ATGTCGGGAT	GATCCAGACA	780
	GCCCCAGTGG	GTGTGGGAAT	CAGTGGGAAT	GAAGGCATGC	AGGCCACCAA	CAACTCGGAT	840
	TACGCCATCG	CACAGTTTTT	CTACTTAGAG	AAGCTTCTGT	TGGTTCATGG	AGCCTGGAGC	900
	TACAACCGGG	TGACCAAGTG	CATCTGTGAC	TGCTTCTATA	AGAACGTGGT	CCTGTATATT	960
45	ATTGAGCTTT	GGTTCGCCTT	TGTTAATGGA	TTTTCTGGGC	AGATTTTATT	TGAACGTTGG	1020
	TGCATCGGCG	TGTACAAATG	GATTTTCACC	GCTTTGCCGC	CCCTCACTCT	GGGAATCTTT	1080
	GAGAGGTCTT	CCGACTATTT	GAGCATGCTC	AGGTTTCCCC	AGCTCTACAA	AATCACCAGG	1140
	AATGGGGAAG	GCTTCAACAC	AAAGGTTTTC	TGGGGTCACT	GCATCAACGC	CTTGGTCCAC	1200
	TCCTCATCC	TCTTCTGGTT	TCCCATGAAA	GCTCTGGAGC	ATGATACTGT	GTTTGACAGT	1260
50	GGTCATGCTA	CCGACTATTT	ATTGTTGGA	AATATTGTTT	ACACATATGT	TGTTGTTACT	1320
	GTTTGTCTGA	AAGCTGGTTT	GGAGACCACA	GCTTGGACTA	AATTCAGTCA	CTGGGCTGTC	1380
	TGGGGAAGCA	TGCTGACCTG	GCTGGTGT	TTTGGCATCT	ACTCGACCAT	CTGGCCCACC	1440
	ATTCCCATTG	CTCCAGATAT	GAGAGGACAG	GCAACTATGG	TCCTGAGCTC	CGCACACTTC	1500
	TGGTTGGGAT	TATTCTCGGT	TCCTACTGCC	TGTTTGATTG	AAGATGTGGC	ATGGAGAGCA	1560
55	GCCCAAGCACA	CCTGCAAAA	GACATTGCTG	GAGGAGGTGC	AGGAGCTGGA	AACCAAGTCT	1620
	CGAGTCTCTG	GAAGAAGCGG	GCTGCGGGAT	AGCAATGGAA	AGAGGCTGAA	CGAGCGCGAC	1680
	CGCTGATCA	AGAGGCTGGG	CCGGAAGACG	CCCCCGACGC	TGTTCCGGGG	CAGCTCCCTG	1740
	CAGCAGGGCG	TCCCGCATGG	GTATGCTTTT	TCTCAAGAAG	AACACGGAGC	TGTTAGTCAG	1800
	GAAGAAGTCA	TCCGTGCTTA	TGACACCACC	AAAAAGAAAT	CCAGGAAGAA	ATAAGACATG	1860
60	AATTTTCTTG	ACTGATCTTA	GGAAAGAGAT	TCAGTTTGT	GCACCCAGTG	TTAACACATC	1920
	TTTGTGAGAG	AAGACTGGCG	TCCAAGGCCA	AAACACCAGG	AAACACATTT	CTGTGGCCTT	1980
	AGTTAAGCAG	TTTGTAGTGT	ACATATTCCC	TCGAAACCT	GGAGTGCAGA	CCACAGGGGA	2040
	AGCTATCTTT	GCCCTCCCAA	CTCGTCTGCA	GTGCTTAGCC	TAACTTTTGT	TTATGTCTGT	2100
	ATGAAGCATT	CAACTGTGCT	CTGTGAGGTC	TCAAATTAAT	AACATTATGT	TTACCAATA	2160
65	AGAAAAAAA	AAAAAAA					

Seq ID NO: 222 Protein sequence:
Protein Accession #: NP_057613

	1	11	21	31	41	51	
	MSVIVRTPSG	RLRLYCKGAD	NVIFERLSKD	SKYMEETLCH	LEYFATEGLR	TLCVAYADLS	60
	ENEYEENLKV	QGEASTILKD	RAQRLEECYE	IEKNLLLLG	ATAIEDRLQA	GVPETIATLL	120
	KAEIKIWLVT	GDKQETAINI	GYSCLVSN	MALILLKEDS	LDATRAAITQ	HCTDLGNLLG	180
75	KENDVALIID	GHTLKYALSP	EVRRSFLDLA	LSCKAVICCR	VSPLOKSEIV	DVVKRVRKAI	240
	TLAIGDGAND	VGMIQTAVHG	VGISGNEGMQ	ATNNSDYAIA	QFSYLEKLLL	VHGAWSYNRV	300
	TKCILYCFYK	NVVLIIELW	PAFVNGFSQG	ILFERWCIGL	YNVIFTALPP	FTLGIFERS	360
	TQESMLRFPQ	LYKITQNGEG	FNTKVFNGHC	INALVHSLIL	PNFPMKALEH	DTVFDSGHAT	420
	DYLFVGNIVY	TYVVTVCLCK	AGLETTAWTK	FSHLAVWGS	LTWLVPFGIY	STIWPTIPIA	480
80	PDMRGQATMV	LSSAHFWLGL	FLVPTACLIE	DVAWRAAKHT	CKKTLLEEVQ	ELETCSRVLG	540
	KAVLRDSNGK	RLNERDLRIK	RLGRKTPPTL	FRGSSLQQGV	PHGYAFSQES	HGAVSQEEVI	600
	RAYDTTKKKS	RKK					

Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: BC017001
Coding sequence: 1-394

1 11 21 31 41 51

5 AACGCTGGGC AGGGCCGCGC CGGGTCGGGG GGC GCCCGAG GGGCCCGGGC CGAGCGGCGG 60
CGCGCAGGGC GGCAGCATCC ACTCGGGCCG CATCGCCGCG GTGCACAAAG TGCCGCTGAG 120
CGTGCTCATC CGCCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCTCGTGA 180
CACGATCCGG GAGGACCCAG ACAGCGTGCC CCCCATCGAT GTCCTCTGGA TCAAAGGGGC 240
CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGCTACGCGG CCTACCAGCA 300
ACTGCAGCGA GAGACCATCC CGGCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT 360
GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CTTGGCACC TGCTGCCACC 420
TTCAAGAGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCATGACAG AAGGGATAGC 480
AGGGGTGCAT TCTCTTTGCA CCTGGCGAGA GGGTCTGACT CTGGGCACCC CTCTCACC GG 540
CTACAAGGCC TTGGACTCAC TGTACAGTGT GGGAGCCCA GTTCCACCT CTGTGACAAT 600
AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCTTGAAGA 660
GCCACGTGCT GCGCGCTCCA AATCCCAAG GACAAGGATC CCTCTGCATT TTTGTCTATG 720
TAACCTCTTA TATGAGTAC ATTACGTGC AAGGAAAGGA AAACCTTGAT TGCAGTGGTT 780
15 TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTG TGGAGATGGG TGGCTAATGG 840
TATTGGTTCA ACAACTCCAC GGAGGTAGGG GTCACGTCTT GGATCCTTTT GCCTTAATCT 900
CAGTGCTGCT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAGAAT CATGCTGCG 960
TTCAAGGAAG GAGGGGTGGA GGAAGAGGAA GGGCCAACT AGCTGGACCC GTCACCTTCT 1020
20 ATCAGAAAGT AAAACCTCGT CAGAAGTCTG TTTCTGCTC TCTCCCTCTG CATATCTTCA 1080
CTTAGATGCC CTTGGCCCGA GCCAGCTACC ATTGCACCTC TAGCTGCAAA CAAAGCTAAG 1140
ACAGCAGGGA ACAGAATTGT CATGGCTGAA TAGACCAATC GTGTTCCATC TACTGAGACT 1200
GGCACACTGC CTCCTGCAAT AAAACTGGGA TCCCATTACC AAGAGAGAAA TGCAGAATTG 1260
TGTACCAAGT AGCTTTTGCT GTGTAACAAA CCATCCCCAA ACTTGGCAGC TAGAAACAAA 1320
25 CCCTGTATTT TCCCACAATC CTATGGGTTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT 1380
CTGCTGCTCA CACCTGGGAT CCCTCATGGA GCTAAGGTCA GCTGTTACCT CAGCTGGGCC 1440
TGGATGGTCT AGGATAGCCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT 1500
TGCTTGGTTC TCTCCATGT GGCCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG 1560
GCTTCAGGAT TCCAAAGAGA GTGAGAGTAG AAGCTGAAAG ACTTCTTGAG TCTTGGCCT 1620
30 GGAACCTGGG CTAGGACAGT GTCACTTCTG CTAAGTCTT TTTGGTCAAG CAAATCACAA 1680
GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGGAAACACA 1740
AAGAGCTTGT GGCCATTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTGGAT 1800
AAAGGTATTT CCCTCTTCCC CTTTTCTCTC TGTCTCATGG GGCCTCACTC TGCCAAAGTTG 1860
GAAGGCACTA AGACATTGTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA 1920
35 AGTGAGTCTC TCCATGGGCT GGAACCACTG TAGTAGGAGT GCCTCCTGT CTGCACTGCT 1980
GGTATGGGGT TAGGCCAGGT AGGACATTCC AGAGGGGCTT CTGAAAACCA AGAGTCCCTG 2040
GGGAAAGGGA ACAGAGTAAG GCAGGCCCTT TCTCACTGC CCTCTAAGGG AACTTGGTCA 2100
CTCGGCACCT TTAAGCCTCA GTTCTCCAG TTCAATAATA AGGACAAAG CTTTCCCAT 2160
GCATTCTCTT TCCC CGGAA AGTTGACTGA GGTGACCAAT AATAGAATTG AAAAGGAGGA 2220
40 GTGCTCTCAG TGCAATGTGG CATCCTGGAT TGGGTCTTGG AACAAAACA GGCATTAGT 2280
GGGAAATTG GAAATCTGAA AAAAGTCTGA ATTTAGTGA ATATACCAAT TTCAGTCTCT 2340
TGGTTTTGAC AGATGTACCA TGGTGATGTA AGATGTTGAC CTTGGGTAG GCTGGGTGAA 2400
GGGTATACAG GAACCTCTTG TACTATCTCT GCAACTTCTC TGTAAATCTA GTATCATTC 2460
AAAATAAAG TTTATTTAAT TTAATAAATA AAAAAAAAAA AA

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

50 1 11 21 31 41 51
TLGRAGAGRG APEGPGPSSG AQGSGSIHSGR IAAVHNVLPS VLIRPLPSVL DPAKVQSLVD 60
TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRETIPAKL VQSTLSDLRV 120
YLGASTPDLQ

55 Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

60 1 11 21 31 41 51
ATGCCTCGAG CTCCAAAGCG TCAGCGCTGC ATGCCTGAAG AAGATCTTCA ATCCCAAAGT 60
GAGACACAGG GCCTCGAGGG TGACAGGGCT CCCCTGGCTG TGGAGGAGGA TGCTTCATCA 120
65 TCCACTTCCA CCAGCTCTTC TTTTCCATCC TCTTTTCCCT CCTCTCTCTC TTCTTCTTCC 180
TCCCTCTGCT ATCCTCTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA 240
CCAAATCCTC CCCAGAGTGC TCAGATAGCC TGCTCCTCCC CCTCGGTGCT TGCTTCCCTT 300
CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCTTA 360
CAGGTCTGTC CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT 420
70 TTGGTGCATG TCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA 480
CTGGAGAGTG TCATAAAAAA TTATGAAGAC CACTTCCCTT TGTTGTTTAG TGAAGCCTCC 540
GAGTGATGTC TGCTGGTCTT TGGCATTGAT GTAAAGGAAG TGGATCCAC TGGCCACTCC 600
TTTGTCTTGG TCACCTCCCT GGGCCTCACC TATGATGGGA TGCTGAGTGA TGTCCAGAGC 660
ATGCCCAAGA CTGGCATTCT CATACTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC 720
75 ACCCTGAGG AGGTCTCTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG 780
CACCTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAAGTCTAC 840
CTGGAGTACC GGCAGGTGCC TGGCAGTGAT CCTGCACGGT ATGAGTTTCT GTGGGTCCA 900
AGGGCTCATG CTGAAATTAG GAAGATGAGT CTCTGAAAT TTTTGGCCAA GGTAAATGGG 960
AGTGATCCAA GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGAAGATGA GGAAGAGAGA 1020
80 GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTTCTAGC 1080
GCTACAGGTA GCTTCTCTTA CCCTGAATAA

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

85 1 11 21 31 41 51
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS 60

SSCYPLIPST PEEVSADDET PNPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
 QVLPDSBSLP RSEIDEKVTD LVQFLLPKYQ MKEPITKARI LESVIKNYED HFPLLFSEAS 180
 ECLMLVFGID VKEVDPTGHS FVLVTSGLTL YDGMLSDVQS MPKTGILILI LSIIFIEGYC 240
 TPBEVIWEAL NMGLYDGM EHLIYGEPRKL LTQDWMQENY LEYRQVPGSD PARYEFLWGP 300
 RAHAERIKMS LLKFLAKVNG SDPRSFLWY EEALKDEEER AQDRIATD TD TAMASASSS 360
 ATGSFSYPE

Seq ID NO: 227 DNA sequence
 Nucleic Acid Accession #: NM_005025.1
 Coding sequence: 82-1314

1 11 21 31 41 51
 | | | | |
 GCGGAGCACA GTCGCGCGAG CACAAGCTCC AGCATCCCGT CAGGGGTTGC AGTGTGTGTG 60
 GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTTGGACTCT TCTCTTTGCT GGTTCGTCAA 120
 AGTATGGCTA CAGGGGCCAC TTTCCTGAG GAAGCCATTG CTGACTTGTC AGTGAATATG 180
 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT 240
 GCTCTTGCAA TGGGAATGAT GGAACCTGGG GCCCAAGGAT CTACCCAGAA AGAAATCCGC 300
 CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT 360
 TCAACATGG TAACTGTCAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT 420
 GTGCAAAATG GATTTTCATGT CAATGAGGAG TTTTTCGAAA TGATGAAAAA ATATTTTAAT 480
 GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
 TGGGTGGAGA ATACACAAA CAATCTGGTG AAAGATTGGG TATCCCCAAG GGATTTTGAT 600
 GCTGCCACTT ATCTGGCCCT CATTAATGCT GTCTATTTC AAGGGAACTG GAAGTCGCGAG 660
 TTTAGCCCTG AAAATACTAG AACCTTTTCT TTCACTAAAG ATGATGAAAG TGAAGTCCAA 720
 ATTCCAATGA TGTATCAGCA AGGAGAAATTT TATTATGGGG AATTTAGTGA TGGCTCCAAT 780
 GAAGCTGGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
 ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTGTCTACTC TGGAGCCATT AGTCAAAGCA 900
 CAGCTGGTGA AAGAATGGGC AAACCTGTGT AAGAAGCAAA AAGTAGAAGT ATACCTGCCC 960
 AGGTTACAG TGATACAGGA AATTGATTTA AAAGATGTTT TGAAGGCTCT TGGAAATACT 1020
 GAAATTTTCA TCAAGATGC AAATTTGACA GGCCTCTCTG ATAATAAGGA GATTTTTCTT 1080
 TCCAAAGCAA TTCACAAGTC CTTCCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
 GTCTCAGGAA TGATGCAAT TAGTAGGATG GCTGTGCTGT ATCCTCAAGT TATTGTCGAC 1200
 CATCCATTTT TCTTCTTAT CAGAAACAGG AGAAGCTGTA CAATTTCTAT CATGGGACGA 1260
 GTCATGCATC CTGAACAAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
 TTATTTGAAT AACAAGGAAA ACAGTAACTA AGCACATTAT GTTTGCAACT GGTATATATT 1380
 TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAC 1440
 AATATATGTA AATTATAGT AACTTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC 1500
 TGTATGTCA TTGTGTTGT GTGCTGTTGT TTAATAATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:
 Protein Accession #: NP_005016.1

1 11 21 31 41 51
 | | | | |
 MAFGLFSL LVLQSMATGAT FPBEAIADLS VMYNNRLRAT GEDENILFSP LSIALAMGMM 60
 ELGAQGSTQK EIRHSMGYDS LKNGEEFSFL KEFSNMVTAK ESQYVMKIAN SLFVQNGFHV 120
 NEEFLQMMKK YFNAAVNHVD FSQNVAVANY INKWVENNTN NLVKDLVSPR DFDAATYAL 180
 INAVYFKGNW KQSPRPENTR TFSFTKDDDES EVQIPMMYQQ GEFYVGEFSD GSNEAGGIYQ 240
 VLEIPYEGDE ISMMLVLSRQ EVPLATLEPL VKAQLVEEWA NSVKKQKVEV YLPRFTVEQE 300
 IDLKVLKAL GITEIFIKDA NLTLSDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
 SRMAVLYPVQ IVDHPPFFLI RNRRTGTILF MGRVMHPETM NTSGHDFEEL

Seq ID NO: 229 DNA sequence
 Nucleic Acid Accession #: NM_003695
 Coding sequence: 12-398

1 11 21 31 41 51
 | | | | |
 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGACAGC CCTGGCTGTG GCTACAGGGC 60
 CAGCCCTTAC CCTGCGCTGC CAGGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120
 TCTGCCCGGC CAGCTCTGCG TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
 ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCTG CAAGGCCAGG 240
 TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
 ACAACGCTGC ACCCACCOCG ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
 TGAGCCTCCT GCGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
 TCATGCTTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CGGCAACGG 480
 GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
 ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
 GATTTTACAC TCCTTCTGTT TTGTTGCCGT TTATTTTGTG CTCAATCTC TACATGGAGA 720
 TAAATGATT AAAC

Seq ID NO: 230 Protein sequence:
 Protein Accession #: NP_003686

1 11 21 31 41 51
 | | | | |
 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTINT VEPLRGNLVK 60
 KDCAESCTPS YTLGQVSSG TSSTQCCQED LCNELKHNA PTRLALHSA LSLGLALSLL 120
 AVILAPSL

Seq ID NO: 231 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 126-752

1	11	21	31	41	51	
CCGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTCGGAGC	60
AGGGGCGCAG	GAATTCCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
AGAAGATGAA	GGATATCGAC	ATAGGAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
GTGTGAGGGA	GAGAACCCAGC	ACTTCTGGGA	CGCACAGAGA	CGTGAAGAT	TCCAAGTTCA	240
GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
TCTCTCTTGA	TGCTCTCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
ACCCAGTGA	CAATGCTGGG	CTTTTTCTCT	GTATGACTTT	TTCTGTGGCT	TCTTCTCTGG	480
CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
ACGAGTCTTC	TGACGTGAAC	TGCAGAAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCCAGG	660
TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAAAT	720
TTCAGGATGG	CTGTATTCTG	CGGTGAGAAT	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
CAAGAGTTCA	GCCTTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
TTCACTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
TGACTCAGTT	GACATTTTGG	GATTGCATAC	TGGAAAAGAA	GCCAACTCTC	TTGCTAGTAA	960
ACCAGCAACC	CGGCTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
TTATTTCTCG	GAGCTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
TCGTGTATTA	ATTTAATCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
GGAATTCAGC	GTAGCTACCT	CCAGACCGTG	GTGCTGGGCC	TCCATTTTGG	TCTGTCAATC	1260
AGCTCTGACT	TACAGCTGCA	GTCACTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
GGCTTCACAT	CAATTTTTTT	CTTCTTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGT	1380
GTGGTTTTTT	GTTTTATTTT	TGTCAAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
CAGAAGGATG	CCACCAGTTT	TTCTTGAGG	CCTAGGATTT	TTTATTCTGT	CCCAGCAGA	1500
GGTAATTCCT	CACAACTTAG	TGCACCAAGT	GCACCAAGCA	TTTTGAGCAG	AGTACCTCTT	1560
TGGGGAGCTT	TCTGTTTTTG	TTTGTTTTTA	ATTCTCTTTC	CTTAGCAGCA	AGGCTTTTTT	1620
TCCTAGAGAA	TCTACTCCGT	TGCAGAATCA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
TGCTGTGAGC	CTGATATACT	ACTTTGGACT	CTGGAACAG	ATATGGGTTT	TATTCTCTAT	1740
TTCTACTGTG	TGTGCTTAAA	CAACCGTCGG	AGACCAGATG	ACCTGTTAGA	TGGCTAGTCC	1800
TGTATAACTC	GACTCTGTAT	GTTCATATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
LDASMSQLR	ILDEEHPGK	YHEGLSALKP	IRTTSKHQHP	VDNAGLPSCM	TFSWLSLAR	120
VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLWQELNEV	GPDAASLRV	WVIFCRTRL	180
LSIVCLMITQ	LAGFSGNPNQ	DGCI LRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TTTAAATGGT	GCTCATATAT	ACTGTATTTT	TTGTTGTTTA	GTTTTACTTA	TTGAGAGTGT	60
CACAAACATG	ATCACATAAT	CATGATTTTT	TTTTTTTACT	TTTACTCCCC	AAATTATTCA	120
TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
TAGTAAACTT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TAACTCTGGA	TTTTAATTTT	240
TTTGTTTCCA	AGTCACAAAT	TGAATTATTC	TTAGATAACCT	TAAAGCCACTG	AATTCAGTTC	300
TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTTGATATT	360
TTGTTATGGT	ATATCTTTTT	ATTAAATATT	TATTTTGACT	AAGCTTTTCA	AAAATATTTG	420
AAGCTATTTT	AATCATCAAG	TATGGAAAAC	AAATTACTAT	TGCATTTTCC	TATATATGCA	480
TATATTATGG	ATTAAACAGA	ATTGTATCAT	TTTTGGCCTA	ATGCTCGGAT	ATAAAAGATA	540
ATTAGCCTAC	TATAGTATTA	ATAAAATTTT	CAGTTGGTTT	GGGCAAAATTT	AAACCTGAAA	600
AATAGGTTAA	AAAGTAGTTA	CAAAATTAAC	TTACTAAATTT	ATACCTGATT	TTTTTTCTTG	660
AATTAAAGTA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
TATGAAAGCT	CTGGCTATCA	TCCCTGGGATA	GTAATTTCTA	ATTATATAGT	ATTTCAAAC	780
TATATATTTT	TAGTTCCTT	TGAGATAAAT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
TATCTGTAT	TTTTTTTAA	AAATGTTTTA	TAAATAGTTC	ATAAGATACA	AGGTCTGCAT	900
TAGAAGACCC	ACTCTTACTA	GGTCCCTTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
TTTTTTTTTAG	GTAGTTTAAA	GCAAGCACTG	ATACCAGTGG	GAGTTGGTCT	TGATCTAGGA	1020
GATTCTGTGA	AGCATCCAAA	AACAATGCCT	AATTTCAAGT	CTTAGGTTAT	GGCTTGTGAC	1080
TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAATGAAT	TCTTAAATTT	1140
CTTAGGCTCT	CTCCATGTAT	CTTCTTAA	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
CCATAGTATC	AAGTGGAGGG	TAGTTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTATA	TAATTCAAAT	GATAAAAATG	1320
TATCAATGTT	ATCCAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCTAT	1380
TACATAAAAA	GTGCTCATGT	ATTTGAATTT	TAAATAATTT	ATTTAAATCA	AGACCACCAT	1440
AAGTCATTAA	TAATTTAATA	ATTGTTTTAA	ATCAGTGGTT	TCAACCCCTC	ACTTCATATT	1500
AGAATCATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
GGAAAGATGGA	GCCATGCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTTCTAA	TTTGTAGTCA	1620
GAGTTGAAGA	CAACTGCTCT	AAATTAGTGC	AGGAAAATGC	TTTTATTTCT	CCCATGTTAA	1680
CTTTTAAAC	TAGTAAATGA	CCCAGTTAAG	TTTTGATGTT	TTAAATTTCA	CTAAAGAACCA	1740
TATTTCTCTA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAAGT	CCATCAAAC	1800
AGCCCTTGTG	TAAGATTATT	ATTTCTTCTC	TATAACTTCA	AAATAGATAT	TTCATTCAAA	1860
CTGTTCAAGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	GCCTGTTTCA	1920
TGAGATGGAG	GAGGTGGGCA	CATTTAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
TTTTAATTTCT	CACTGTCTCA	AAAGAGAATC	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
CAATCCCAA	GGGCGAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAATTAA	2160
TTTCTGGAAT	TGCACTACA	TGTTTTCTTA	TTAACATTCA	GAATTTGGAA	TATTAATTTT	2220

TCCAGTGAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT 2280
CAATTTTGTG TTTGTTTACT TTTATGTAAA AATTGTGATAT GTGAATTACA CAGTTCTAAT 2340
AAAACTCAT GCCTTTTCAT TACATCTAAT TTGAACCTCTC AACTTCAGTG CCAGAAAGTGC 2400
TTTAAAGATG CTTTAATGAA AAGTATTAAG AAAATATATA GATTGTATG TCAGTTTATA 2460
CTTCAGAAAT CCATATATTT GTCATATTTA TTTTGTAGA AACCTCCTAA TTGGATAACT 2520
AGATGGTATT TAAATGAAT GCCCAAAAT ATCTGTGACC TTGTGCCAAA AGTTTATCTG 2580
TTGGAAGCCG CAGCCATTCT ATGTAGAGAG TTTATAAGAA AATAATTTAA AATTGTATGC 2640
ATTTTATATT ACTATGGTAT CTGTGTACCA TATTTCTAAG TATTCATTAT TAAATTGGTA 2700
CTTCTTAAAA CCATAACCTG GCTTGCCCTT TAGTGTAAAA CACAAAATCC AACATTGTAT 2760
ATAGAGATTG TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCAGTG CATCTGCACA 2820
AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAAACA 2880
CCACATTAAA CAACACGGC AACACTCAGA CTGGGCACTT TCCTACGAAT CCATCCTATA 2940
TGTGCTGTGT ATGCGCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTACGCT 3000
CCTTCATCAA GCACTTGCCA ACACATTAC CTCTAACTTG TACAACCTTA CCAACTCACC 3060
ACACATCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCAAC ACAACACAAC 3120
CCCAAAACAC AAAACCACTA AATCATTAACC ACCACACACG CCACACACCA CACACCCACC 3180
CACACAACA ACACACCAG ACCAAACACC CCACCACAAA CAAGCTAACA ACCACAAACA 3240
GACAACACAT CACATACACT CACTACCCCC CCATACTCCC ACCCACCA

Seq ID NO: 234 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 27-281

1 11 21 31 41 51
AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
GTCTACCGCG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
TTCTGCCCC GTGCTCATTT GGGGCTGACG CCAATTTTAGG CCTCAGCCCA TCTGCACCCA 180
GGCGCTCACT GAAACAGTGT GTTGCTCCAC ACCGCTTGT TTTGCTTGT GGCCTGCTCT 240
CAGGTTCCG ACCAATCCA GAGCCTTGCA GAAAGCATT ACCTGCTTT CTCTTTGGCA 300
GAGTTTTTCT TTGCTCTGAT CTGGAGACA TCCCTCTGCC TAGTGGAAAC ATAAGGAATA 360
CAGAAAGAAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCATGCACT CAAGAGAAAG 420
ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCCAGC 480
TTTTCTTCT CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAACA GGAAATGTTT 540
ATAAAACCTG TTCAGCGGTT CGCCAACAAG AAGTGGTAAA GTAGCAAAA TGGGGATGGA 600
GATGCCAGGA GGAAGATGTC CAGGGGTAAA GTGGGAAAAT GGGAACTGA AGCCAGGAGG 660
TCAAGCCAG CCAACAGGTG TTCTGTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
CTCAAAACCG GGAAGCCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
GGTCAGAAAC CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840
AGACAGCCTG TGACGTTTCA AAAGCAAAG TCCCTTACCA GCCAGTGAAG CTACCTGATT 900
TCTCAGTATC TTACGCCAG TGACACGATC TACCCTCAA ACTTAAAAA AAAAGGGAAA 960
CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAA 1020
GGAAAGGTCT CCTGTGACTG TTTTATTTT AGGGAAACAG AGAGGAAGAA GAATGATTTT 1080
TCTTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACCACA 1140
GCAAGAAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTCGAATTAA TGATTACTT 1200
TTTATTTTAA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
TTTGACCTTG AATAATCTT TACATGTAA ATTCTTATG ATCAAAACAA GGTCTCAGT 1320
GATTAAAAA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAATAC AACATTCTTA 1380
AAATCTCAAG GCTTTTAAAG CATTGTGACA AATGACTGGA CATTTTTTAA ATTTGAAAAA 1440
AAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTGAG TGCAACAACA AAAAAGGTAT 1500
GCACTTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
TCCCATCAA GCCAAAGAAA GAAAAGAAAA TTGTTCTGTA CAGATATATG ACATTAAAAA 1620
ATAATCCC

Seq ID NO: 235 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MHPLKTQREA VCLFRSSYIR LRHFLTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCV 60
PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
Nucleic Acid Accession #: NM_002075
Coding sequence: 406..1428

1 11 21 31 41 51
CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCCA 60
ACAGGATCAG ACCCAGAGGC AGCTGGTGG GGTGTGTCGA GAAGAAGGAT TATCCAGATC 120
AGTCCTTTCT AATCTCAGCT CTGCTGTGA CCTCCCATTA CTCACCAAC CCTCTTCCCC 180
ACCACTCTGA GCTGAGGAGC ACAGTTTGA GCCCCCCTAA CCCCCCGCCG GTCGGGGCCA 240
GGCCAGGCCA GGCCAGCTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
CGTCGAGCT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAACCC CGGCCGAGGT 360
CCAGCCAGAG CCCAAGAGCC AGAGTGACCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
CAACTGCGTC AGGAAGCGGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG 540
CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATTT ACGCCATGCA CTGGGCCACT 600
GATTCTAAGC TGCTGGTAAG TGCTCGCAA GATGGGAAGC TGAATCGTGT GGACAGCTAC 660
ACCACCAACA AGGTGCACGC CATCCCACTG CGCTCCTCCT GGGTCATGAC CTGTGCCTAT 720
GCCCATCAG GGAATCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTT CATCTACAAC 780
CTCAATCCC GTGAGGGCAA TGCTAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTTAT 840
CTCTCTGCT GCCCTCTCCT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACCCAG 900
TGTGCTTGT GGGACATTGA GACTGGGCG CAGAAGACTG TATTTGTGGG ACACACGGGT 960
GACTGCATGA GCCTGGCTGT GTCTCCTGAC TTCAATCTCT TCATTTCGGG GGCCTGTGAT 1020
GCCAGTGCCA AGCTCTGGGA TGTGCAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC 1080

GAGTGGGACA TCAACGCCAT CTGTTTCTTC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140
 GATGACGCTT CCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
 CACGAGAGCA TCATCTGCGG CATCAGCTCC GTGGCCTTCT CCCTCAGTGG CCGCTACTA 1260
 TTCGCTGGCT ACGACGACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
 GGCATCCTCT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
 GCTGTGGCCA CAGGTTCTGT GGACAGCTTC CTCAAAATCT GGAAGTGGAG AGGCTGGAGA 1440
 AAGGGAAGTG GAAGGCACTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTCA 1500
 GGTGTTCTCT TCTATATATC GGGTGCCATT CCCACTAAGC TTTCTCCTTT GAGGGCAGTG 1560
 GGGAGCATGG GACTGTGCCT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAAGTGCC 1620
 CCATCTCCTC CCATGGGCTT CCCTCCCCAC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
 GGACAAACCTG CCCCTCCCCA GCCCTTTGCA GGCCAGCAG ACTTGAGTCT GAGGCCCCAG 1740
 GCCCTAGGAT TCCTCCCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
 TTGGCCCTGT GACTATGGCT CTGGCACCACT TAGGGTCCTG GCCCTCTTCT TATTCTATGCT 1860
 TTCTCTCTTT TCTACCTTTT TTTCTCTCCT AAGACACCTG CAATAAAGTG TAGCACCTGT 1920
 GT

Seq ID NO: 237 Protein sequence:
Protein Accession #: NP_002066

1 11 21 31 41 51
 MGMEQLRQE AEQLKKQIAD ARKACADVTL AELVSGLEV V GRVQMRTRRT LRGLHLAKIYA 60
 MHWATDSKLL VSAQDQKLI VWDSTYTNKV HAIPLRSSWV MTCAYAPSGN FVACCGGLDNM 120
 CSYINLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGTTCALWD IETGQKQTVF 180
 VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFGHESDIN AICFPFNGEA 240
 ICTGSDDASC RLFPLRADQE LICFSHESII CGITSVAFSL SGRLLFAGVD DFNCNVWDSM 300
 KSERVGIISG HDNRVSLGV TADGMAVATG SWDSFLKIWN

Seq ID NO: 238 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCCCAATGTG TNGAACCTAC CATAAATCTT TTTCTTACNG GACAATCTTA TNCTAANCAA 60
 TACCATTTCG TTTTAAGGCA GATAATCCTC CAAGTTTCTT AATGATATCT GAAACTATTA 120
 ACTGATTCTG TGAATTATGA AATCTGAAAA GGAATTGGAA GTTGCTAAAA ATCTATCATT 180
 TGCATTGACC AGTGTAAGC ACAGTGGAAT GAGAAATGCGT GCCCTGACAC CAAAGAAAAA 240
 TAAGTGACTG GAAAGCTGAA GAATCACCAG CTTAGTGAC ATGGAACCCA GTGATTGAT 300
 TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
 CAAAAAGGGG AAAAAAAGA GCAACCAAAG AAAAAAATC CATAAAATTG CACAGAAGAA 420
 AAGAAAGAAA AATAAAATAC ACAATATGGA CGATGGAGAA AACACAGTAC ATTTCTTTAT 480
 GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540
 CAGAAAGTGA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCAGAT 600
 TAGAAAAGTT TTTCTGTAAA AGTCAGATAG TAAATATTTT AGGTTTGTGA GTGTCTTTTG 660
 CAACTACTCA ACTTTCCTAC TGTAGCAGAA GAGTAGCTGT GGTACTGTGC AAATAAATTG 720
 CTTGTGTTCC AATAAAGCTT CATTTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
 ACTGTTGTTT GCCAAGTCTT AATATAGTTG CTTAGCAAGT ATTGTAGCT ATTTGAGGAA 840
 GACATGAAAG TTCATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAATT 900
 TAGGCTAAGT TATAATACAC TGTTTAAACA ATTGTAATAT GTAAGAGAAA TTTACAATA 960
 AAAATCCCAA AAAAAA

Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_001786.1
Coding sequence: 130-1023

1 11 21 31 41 51
 GGGGGGGGGG GGCACCTGGC TTCAAAGCTG GCTCTTGGAA ATTGAGCGGA GAGCGACGCG 60
 GTTGTGTAG CTGCCGCTGC GGCGSCGCG GAATAATAAG CCGGATCTA CCATACCCAT 120
 TGAATACTA TGAAGATTA TACCAAAATA GAGAAAAATT GAGAAGGTAC CTATGGAGTT 180
 GTGTATAAGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240
 GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AAATTTCTCT ATTAAGGAA 300
 CTTGTCATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAGGATTC CAGGTTATAT 360
 CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCCTCCTGGT 420
 CAGTACATGG ATTCTTCACT TGTTAAGAGT TATTTATACC AAATCCTACA GGGGATTGTG 480
 TTTTGTCACT CTAGAAGAGT TCCTTACAGA GACTTAAAC CTCAAAATCT CTTGATTGAT 540
 GACAAAGGAA CAAATTAACCT GGCTGATTTT GGCCTTGCCA GAGCTTTTGG AATACCTATC 600
 AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAGT ATTGCTGGGG 660
 TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACTA 720
 GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATTG ATCAACTCTT CAGGATTTTC 780
 AGAGCTTTGG GCACTCCCAA TAATGAAGTG TGGCCAGAAG TGGAACTTTT ACAGGACTAT 840
 AAGAATACAT TTCCCAAATG GAAACCAAGG AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
 GAAAATGGCT TGGATTGTCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTCT 960
 GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTGG ACAATCAGAT TAAGAAGATG 1020
 TAGCTTTCTG ACAAAGAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATTGTT 1080
 AACTCTGTC TATTTTGTG TATATATAT TCTTTGTTA TCAAACTCA GCTGTACTTC 1140
 GTCCTCTAAT TTCAAATAA TAACATAAAA ATGTAAATAT TCTATATGAA TTTAAATATA 1200
 ATTCTGTAAA TGTGAAAAA AAAAAA

Seq ID NO: 240 Protein sequence:
Protein Accession #: NP_001777.1

1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EPLSMDLKKY LDSIPPQOYM DSSLVKSILY QILQGIVFCH 120

SRRLVLRDLK PQNLLIDDKG TIKLADFLGA RAFGIPIRVY THEVVTWLWYR SPEVLLGSAR 180
YSTPVDWISI GTIFAEIATK KPLPHGDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT 240
FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

Seq ID NO: 241 DNA sequence

Nucleic Acid Accession #: NM_033379.1

Coding sequence: 132-854

1 11 21 31 41 51
CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTGGGCAGAG CGCGCGGCCA 60
GCTTTGCAGA GAGCGCCCTC CAGGGAATAT GCGTGGCGGG ACACGGGATC TACCCATACC 120
ATTGACTAAC TATGGAAGAT TATACCAAAA TAGAGAAAAT TGGAGAAGGT ACCATGAGAG 180
TTGTGTATAA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
TAGAAAAGTA AGAGGAAGGG GTTCTAGTA CTGCAATTGC GGAAATTCT CTATTAAAGG 300
AACTTCGTCA TCCAAATATA GTCAGTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
ATCTCATCTT TGAGTTCTCT TCCATGGATC TGAAGAAATA CTGGATTCT ATCCCTCCTG 420
GTCAGTACAT GGATTCTTCA CTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
TATTGCTGGG GTCAGCTCGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT 540
TTGCTGAATC AGCAACTAAG AAACCACTTT TCCATGGGGA TTCAGAAATT GATCAACTCT 600
TCAGGATTTT GCGAATTTTG GGCACCTCCA ATAATGAAAT GTGGCCAGAA GTGGAATCTT 660
TACAGGACTA TAAGAAATACA TTTCCCAAAT GGAACCCAGG AAGCCTAGCA TCCCATGTCA 720
AAAACTTGGG TGAAGATGGC TTGGATTGTC TCTCGAAAAT GTTAATCTAT GATCCAGCCA 780
AACGAATTTT TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTG GACAATCAGA 840
TTAAGAGAT GTAGCTTTCT GACAAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
TTTTTATTGT TAACCTCTGT CTATTTTGT CTATATATA TTTCTTTGTT ATCAAACTTC 960
AGCTGTACTT CGTCTTCTAA TTTCAAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
ATTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAAAA AAAAAA

Seq ID NO: 242 Protein sequence:

Protein Accession #: NP_203698.1

1 11 21 31 41 51
MEDYTKIEKI GEGTYGVVYK GRHKTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
PNIVSLQDVL MQDSRLYLIF EPLSMDLKKY LDSIPPQYM DSSLVKVVTL WYRSPEVLLS 120
SARYSTPVDI WISGTFIAEL ATKPLPHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY 180
KNTFPKWKPG SLASHVKLND ENGLDLSKM LIYDPAKRIS GKMLNHPYP NDLDNQIKKM

Seq ID NO: 243 DNA sequence

Nucleic Acid Accession #: AF101051.1

Coding sequence: 221-856

1 11 21 31 41 51
GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CGGGCGCGGG ACCCAACCC 60
CGACCCAGAG CTTCTCCAGC GCGGGCGCAG CGAGCAGGGC TCCCCGCTT AACTTCTCC 120
CGCGGGGCCA GCCACCTTCG GGAGTCCGGG TTGCCACCT GCAAACTCTC CGCCTTCTGC 180
ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA 240
GCTGTTGGGC TTCACTCTCG CCTTCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
GCCCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
CGAGGGGCTG TGGATGTCTT GCGTGTGCGA GAGCACCCGG CAGATCCAGT GCAAACTCTT 420
TGACTCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCTTGA TGGTGGTTGG 480
CATCCTCTTG GGAGTGATAG CAATCTTTGT GGCACCGGTT GGCATGAAGT GTATGAAGTG 540
CTTGGAAAGC AATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
TCTTGCAAGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTAC 720
TGGCTGGGCT GCTGCTTCTC TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCTGTCTC 780
CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCAGCGG 840
GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAATCA TGTGAAACA AACCGAAAAT 900
GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GAAATCTGAA 960
GTATGGTATT ACAAAACAAA CAAACAAA AAAAAACCAT GTGTTAAAT ACTCAGTGCT 1020
AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
TTGTATTACT GCTTCCCATT GAGTAATCAT ACTCAATGG GGGAGGGGT GCTCCTTAAA 1140
TATATATAGA TATGATATATA TACATGTTTT TCTATTAATA ATAGACAGTA AAATACTATT 1200
CTCATTATGT TGATACTAGC ATACTTAAAA TATCTTAAAA ATAGGTAAAT GTATTTAATT 1260
CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCTTATAT ACATATGTAA 1320
CAGTCAAAATA TCATTACTC TTCTTCATTA GCTTTGGGTG CCTTTGCCAC AAGACCTAGC 1380
CTAATTTACC AAGGATGAAT TCTTCAATT CTTATGCGT GCCCTTTTCA TATACTTATT 1440
TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTTGTG 1500
TTTCTTGGT CTCTATCTCC TGAATCTAAC ACATTTTATA GCCTACATTT TAGTTTCTAA 1560
AGCCAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA 1620
GTGATAAATT CTTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCAT AGCACTCTTG 1680
TTTGCTTTGA AAATATTGTT CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740
CACAACTTAA TTGATTGAAT TTTTAAGCTA CTTATTCTA GTTTTATATC CCCCTAACT 1800
ACCTTTTGT TCCCATTTCC TTAATTGTAT TGTTTTCCCA AGTGTAAAT TCAATGCGTT 1860
TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTCTTACC 1980
TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAA AGGTAGTGTG 2040
AATATTAATT AGTTTATATT ACTCTATTCT TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
CTTCATGTGA TTCACCTGCT TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATT CCACTGAACA 2280
AAACCTAGCG ACATACCTTC ATGTGGCTCA GTGCCTTCT CTCTCTACCA GTCTATTTCC 2340
ATTCCTTCAG CTGTGTCTGA CATGTTTGTG CTCTGTCCA TTTTAAACAA TGCTCTTACT 2400
TTTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

GCACCTGGTGT CTGGAGACCT GGATTGTAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTTGT AATTGAAAAA GGGCTATACT AAGGGAAGA ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACCGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAAGCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAGTCAAGCC ACCGTGCTTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCCTTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT CTTCATGTAT TGTGAGTGTA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTTGTATA AAGCATTTACT CTTTTCATAT AAATTGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAA AAA

Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMY EGL WMSCVSQSTG 60
 QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIPVATV GMRCKMKLED DEVQKRMMAV 120
 IGGAIPLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FQQALETGWA AASLCLLGA 180
 LLCCSCPRKT TSYPTRPYP KPAPSSGKDY V

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TTTTCTTTT TTTTCTTTT TTTTCAAGG AGAGCACAAG GAACCTTATT AATGACTTTC 60
 TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTTGTG TCACTTAGT 180
 TTTTCTTCT GAGATTAGT TTCTTCATCG TTAACAATGA GGATATTAAAT ATGTTTCACA 240
 CAGTTGTTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGTACT CAGGAGGCTA 300
 AGGTGGGGAG GTGCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGCCA CTCACATTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
 GTCCTACGCC CACGAGTCT CGCTGATTGC TAGCACAGCA GTCTGAGATC AAATGCA

Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

1 11 21 31 41 51
 AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTCTT AATAGAAAAG GATTCAAAC 120
 GTGAAACCAT TTCTCTTTA ATGTTTCACA TTCTGTGTAC AGATTGTGTT TCTTGTGACT 180
 CTGTTATCCA TAATATGGAC AGTTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAGTATT GCCACTTTAG CACTGAAGAT 300
 TGGGATGAGA GGAGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCTC 360
 GATCATGTTT AAGAAAAGTC ATGAAAATGG TGAACATAGT TTCCAAGCA TATTGGAAGG 420
 GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCATTTC AGTCTCTAGA GAGGAACAAG 480
 ACTGGTAACC TGCTATCTG TATTTTAAAG AACCCAGGAG GAAAGCTTTA TAATAGAACA 540
 TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCAGGC CAGGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAAG TGATCTGCCT 660
 GCCTTTGCTT CCTGAGTAGC TGGGACTACA GGCATGAGCC CCAATGCCCT GCTAAGTTTG 720
 TTTTCTTGT TTGTTGTTG TTTGTTTTTG GGGGGGTTG TTTTGTTTT TGTAGAGACG 780
 TAGTCTTCT TTGTGTCAG GCTAGTCTCA AACTCCTGGC TTCAAGTGAT CCTCCTGCCT 840
 CAGCCTCCCA GAGTGTCTAG ATTACAGCAC TTGGATTGAG CTTCCTCATT TCCAACATGG 900
 AAGAACTTA CACCGACTCC CTGGACCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
 ACCATCAAAAT CAGGCTTGC AGGTTTCCTT ATCATCTTAT CAAGTGCGA AAGAATCATC 1020
 CTGATGTTGC AAGCAAAATG GCTACTTGTG CTTCAATGC TCGCCACCAG GTTCCTCGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAAGATGTTG 1140
 TCAACCAAA CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTG CAGTGCCCTC 1200
 CTTGGATGA AGACTGGAT AAAGATTTGT GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
 GCACAATCA CTAATCTGAC AACAACAGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 GTTGCTTCTT CTCTACCAAG TGGGTTCTCA TTTTCTCTCT AATCTAATTA TAGAATGGTA 1500
 AACTCCCTGT GACTTTCCAA ACTGACAAGC ACACCTTTTT CTCCCCCTCT TGAATCTCA 1560
 TTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAATAA ACCTTTTGATA CAGATTG

Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

1 11 21 31 41 51
 MEETYDSDL PEKLQCPYD KNEQIRACRF FYHLIKCRKN HPDVASKLAT CFPNARHQVP 60
 RAEISHISS CDDRSCIEQD VVNQTRSLRQ ETLAESTWQC PPCDEWDKD LWEQSTSPFV 120
 WGTTHYSNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW KNNNGNAQ

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
TTAAGGAAAT	CCGGGCTGCT	CTTCCCCATC	TGGAAGTGGC	TTTCCCCACA	TGGGCTCGTA	60
AACTGATTAT	GAACATACG	ATGTTAATTC	GGAGCTGCAT	TTCCAGCTG	GGCACTCTCG	120
CGCGCTGGTC	CCCGGGGCTT	CGCCCCCAC	CCCTGCCCT	TCCCTCCCG	GTCTGCCCC	180
CATCCTCCAC	CCCCCGCGCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
TCCACTCGCC	TCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTGTCTC	300
GGCCAGGTT	GGGAGAGGA	CGGAGGGTGG	CCGACGCGG	TTCTTGTAGT	AATTACCCAG	360
GAGGGACTGA	GCACAGCACC	AAC TAGAGAG	GGGTGAGGGG	GTGCGGACT	CGAGCGAGCA	420
GGAAAGGAGG	AGCGCCTGGC	ACCAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGTTTGTAA	480
TGCGTGGCGT	GCCCGCGCGA	CAGGATCCCA	GCGAAAATCA	GATTTCCTGG	TGAGGTTGCG	540
TGGGTGGATT	AATTTGAAAA	AAGAAACTGC	CTATATCTTG	CCATCAAAAA	ACTCAGGAG	600
GAGAAGCGCA	GTCAATCAAC	AGTAAACTTA	AGAGACCCCC	GATGCTCCCC	TGTTTAACT	660
TGTATGCTTG	AAAAATTATCT	GAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
GTCCATTGGA	ATATTAAGCC	CAGGAGTTGC	TTTGGGATG	GCTGGAAGTG	CAATGTCTTC	780
CAAGTTCTTC	CTAGTGGCTT	TGGCCATATT	TTTCTCTTC	GCCCAGGTTG	TAATTGAAGC	840
CAATTCTTGG	TGGTGGCTAG	GTATGAATAA	CCCTGTTCAG	ATGTCAGAA	TATATATTAT	900
AGGAGCAGAC	CCTCTCTGCA	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAACTGTG	960
CCACTTGTAT	CAGGACCAAC	TGCAGTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCAAAAG	1020
ATGCCAGTAT	CAATTCCGAC	ATCGACGGTG	GAACCTGCAG	ACTGTGGATA	ACACCTCTGT	1080
TTTTGGGAGG	GTGATGACAG	TAGGACGGCG	CGAGACGGCC	TTACATACG	CGGTGAGCGC	1140
AGCAGGGGTG	GTGAACGCCA	TGAGCCGGGC	GTGCCGCGAG	GGCGAGCTGT	CCACCTGCGG	1200
CTGCAGCGCG	GCCGCGCGCC	CCAAGSACCT	GCCGCGGGAC	TGGCTCTGGG	GCGGCTGCGG	1260
CGACAACATC	GACTATGGCT	ACCCTTTTGC	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGGA	1320
GCGCATCCAC	GCCCAAGGCT	CCTACGAGAG	TGCTGCGATC	CTCATGAACC	TGCACAACAA	1380
CGAGGCCGCG	CGCAGGACGG	TGTACAACCT	GGCTGATGTG	GCCTGCAAGT	GCCATGGGGT	1440
GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTGCAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
TGATGCCCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560
GTTGGTACAG	GTCAACAGCC	GCTTCAACTC	GCCCACCACA	CAAGACCTGG	TCTACATCGA	1620
CCCCAGCCCT	GACTACTGCG	TGCGCAATGA	GAGCACCGGC	TGCTGGGCA	CGCAGGGCGG	1680
CCTGTGCAAC	AAGACGTCGG	AGGGCATGGA	TGGCTGCGAG	CTCATGTGCT	GCGGCCGTGG	1740
GTACGACAGC	TTCAAGACCG	TGCAGACGGA	GCGCTGCCAC	TGCAAGTTCC	ACTGGTGCTG	1800
CTACGTCAAG	TGCAAGAAGT	GCAAGGAGAT	CGTGGACCGA	TTTGTGTGCA	AGTAGTGGGT	1860
GCCACCCAGC	ACTCAGCCCC	GCTCCAGGA	CCCGCTTATT	TATAGAAAGT	ACAGTGATTG	1920
TGGTTTTTGG	TTTTTAGAAA	TATTTTTTAT	TTTTCCCCAA	GAATTGCAAC	CGGAACCAAT	1980
TTTTTCTCTG	TTACATCTTA	AGAACTCTGT	GGTTTATTAT	TAATATTATA	ATTATTATTG	2040
GGCAATAATG	GGGGTGGGAA	CCACGAAAAA	TATTTATTTT	GTGGATCTTT	GAAAGGTAA	2100
TACAAGACTT	CTTTTGGATA	GTATAGAATG	AAGGGGAAAA	TAACACATAC	CCTAAGTTAG	2160
CTGTGTGGGA	CATGTGTACAC	ATCCAGAAGG	TAAAGAAATA	CATTTTCTTT	TTCTCAATA	2220
TGCCATCATA	TGGGATGGGT	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAAT	CTATTACAAA	2280
TTCAAGTTCT	ATGACCAAAA	TGAGTTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGTCTTGGG	2340
AAAAACAAAC	AAAAACAAAC	AAACCTCCCT	TCCCCAGCAG	GGCTGCTAGC	TTGCTTTCTG	2400
CATTTTCAAA	ATGATAATTT	ACAAATGGAAG	GACAAGAAATG	TCATATTCTC	AAGGAAAAAA	2460
GGTATATCAC	ATGTCTCATT	CTCCTCAAAAT	ATTCCATTTG	CAGACAGACC	GTCAATTCT	2520
AATAGCTCAT	GAATTTTGGG	CAGCAGGGAG	GAAGTCCCC	AGAAATTAAA	AAATTTAAAA	2580
CTCTATATGC	AAGATGTTGA	TTTGAAGCTG	TTATAAGAAAT	TGGGATTCCA	GATTTGTAAA	2640
AAGACCCCCA	ATGATTTCTG	ACACTAGATT	TTTTGTTTGG	GGAGGTTGGC	TTGAACATAA	2700
ATGAAATATC	CTGTATTTTC	TAGGGATAC	TTGGTTAGTA	AATTATAATA	GTAGAAATAA	2760
TACATGAATC	CCATTACAG	GTTTCTCAGC	CCAAGCAACA	AGGTAATTGC	GTGCCATTCA	2820
55	60	65	70	75	80	85
60	65	70	75	80	85	
65	70	75	80	85		
70	75	80	85			
75	80	85				
80	85					
85						

Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

1 11 21 31 41 51

MAGSAMSSKF FLVALAIFFS FAQVVIEANS WWSLGMNPFV QMSEVYIIGA QPLCSQLAGL 60
 SQGQKKLCHL YQDEMYYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET 120
 APTYAVSAAG VVNAMSRACR EGELSTOCGS RAARPDLPR DNLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYESAR ILMNLEHNEA GRRTVYNLAD VACKCHGVSG SCSLKTQWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRPNSTP TQDLVYIDPS BDYCVRNEST 300
 GSLGTQGRLC NRTSEGMDCG ELMCCGRGYD QFKTVQTERC HCKFWHCCYV KCKKCTEIVD 360
 QFVCK

Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

1 11 21 31 41 51
 15 TGACTTGGAT GTAGACCTCG ACCTTCACAG GACTCTTCAT TGCTGGTTGG CAATGATGTA 60
 TCGGCCAGAT GTGGTGAGGG CTAGGAAAAG AGTTTGTGTG GAACCCCTGGG TTATCGGCCT 120
 CGTCATCTTC ATATCCCTGA TTGTCCTGGC AGTGTGCATT GGACTCACTG TTCATTATGT 180
 GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACTGACAA 240
 20 ACTATATGCT GAGTTTGCCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 TGAATCAATG GTGAAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
 TCAGGTTATC AAGTTCAGTC AACAGAAGCA TGGAGTGTGG GCTCATATGC TGTGTGATTG 420
 TAGATTTTAC TCTACTGAGG ATCCTGAAAC TGTAGATAAA ATTGTTC AAC TGTGTTTACA 480
 TGAAGAGCTG CAAGATGCTG TAGGACCCCTC TAAAGTAGAT CCTCACTCAG TTAATAATTAA 540
 25 AAAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 TAAACTCTA GGTCAAGATC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCTCTGGCAG GCTAGCCTGC AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTTAATTAA 720
 TGCCACATAG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAACC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTCGAAAATG AAACGGGGTC TCCGGAGAAT 840
 30 AATTGTCCAT GAAAAATACA AACACCCATC ACATGACTAT GATATTTCTC TTGCAGAGCT 900
 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGTCTCCCTG ATGCATCTTA 960
 TGAGTTTCAA CCAGGTGATG TGATGTTTGT GACAGGATTT GGAGCACTGA AAAATGATGG 1020
 TTACAGTCAA AATCATCTTC GACAAGCACA GGTGACTCTC ATAGACGCTA CAACTTGCAA 1080
 TGAACCTCAA GCTTACAATG ACGCCATAAC TCCTAGAATG TTATGTGCTG GCTCCTTAGA 1140
 35 AGGAAAAACA GATGATGCC AGGGTGACTC TGGAGGACCA CTGGTTAGTT CAGATGCTAG 1200
 AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCCAACAA 1260
 GCCTGGTGTG TATAGTAGAG TTACGGCCTT GCGGGAGCTG ATTACTTCAA AAACCTGGTAT 1320
 CTAAGAGAGA AAAGCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG 1380
 40 CCATTTTTAG AGATACAGAA TTGAGAGAAG CTGCAAAAC AGCTAGATTT GACTGATCTC 1440
 AATAAACTGT TTGCTTGATG CAAAAAATAA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
 45 MYRPDVVRAR KRVCEPWWI GLVIFISLIV LAVCIGLTVH YVRYNQKRTY NYYSTLSFTT 60
 DKLYABFGRE ASNNTFEMSQ RLESMVKNFA YKSPLREEFV KSQVIKFSQQ KHGVLAMHLL 120
 50 ICRFHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGGSLR IYGGTEVEEG EWPQASLQW DGSHRGCGATL INATNLVSAA HCFPTYKNPA 240
 RWTASFVVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPVPVTN AVHRVCLPDA 300
 SYEFQPGDVM FVTGPGALKN DGYSQNHLRQ AQVTLLIDAT CNEPQAYNDA ITPRMLCAGS 360
 LEGKTDACQG DSGGPLVSSD ARDINWLAGI VSWGDECAKP NKPGVYTRVT ALRDWITSKT 420
 GI

Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
 60 GGCACGAGGC CTCGTGCCGC CGGGCTCTTG GTACCTCAGC GCGAGCGCCA GCGCTCCGGC 60
 CGCCGTGGCT ATGTTCTGTG CCGATTTCCG CAAAGAGTTC TACGAGGTGG TCCAGAGCCA 120
 65 GAGGGTCTCT CTCTTCGTGG CCTCGGACGT GSGATGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTTGTTT CAGTGTGACC ACGTGCAATA TACGCTGGTT CCACTTTCTG GGTGGCAAGA 240
 ACTTGAAACT GCATTCTTTG AGCATAAAGA ACAGTTTCAT TATTTTATTC TCATAAACTG 300
 TGGAGCTAAT GTAGACCTAT TGGATATTCT TCAACCTGAT GAAGACACTA TATTCTTTGT 360
 GTGTGACACC CATAGGCCAG TCAATGTCGT CAATGTATAC AACGATACCC AGATCAAATT 420
 70 ACTCATTAAG CAAGATGATG ACCTTGAAGT TCCCGCCTAT GAAGACATCT TCAGGGATGA 480
 AGAGGAGGAT GAAGAGCATT CAGGAAATGA CAGTGATGGG TCAGAGCCTT CTGAGAAGCG 540
 CACACGGTTA GAAGAGGAGA TAGTGGAGCA AACCATGCGG AGGAGGCAGC GGCAGAGAGT 600
 GGAGGCCCGG AGAAGAGACA TCCTCTTTGA CTACGAGCAG TATGAATATC ATGGGACATC 660
 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
 75 GTGGTGGGCC ATCGTTGGAC TAACAGACCA GTGGGTGCAA GACAAGATCA CTCAAAATGAA 780
 ATACGTGACT GATGTTGGTG TCCTGCAGCG CCACGTTTCC CGCCACAACC ACCGGAACGA 840
 GGATGAGGAG AACACACTCT CGGTGGAGTG CACACGGATC TCCTTTGAGT ATGACCTCG 900
 CCTGGTCTCT TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC 960
 80 AGCCAGTTTC AAGCTGTGGT CTGTGCATGG ACAGAAGCGG CTCAGGAGT TCCTTGAGA 1020
 CATGGGCTCT CCCCTGAAGC AGGTGAAGCA GAAGTTCCAG GCCATGGACA TCTCCTTGAA 1080
 GGAGAAATTT CGGAAATAGA TTGAAGATC TGCAAAATAA TTTGGGATGA AGGACATGCG 1140
 CGTGCAACTT TTAGCATTC ATTTGGGTT CAAGCACAAG TTTCTGGCCA GCGACGTGGT 1200
 CTTTGCCACC ATGCTCTTGA TGGAGAGCCC CGAGAAGGAT GGCTCAGGGA CAGATCACTT 1260
 CATCCAGGCT CTGGACAGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
 85 ACTCGCCAGG AAGCAGCTGC GAGCCACCCA GCAGACCATT GCCAGCTGCC TTTGCACCAA 1380
 CCTCGTCATC TCCAGGGGGC CTTTCTGTGA CTGCTCTCTC ATGGAGGGGA CTCAGATGT 1440
 CATGCTGTTC TCTAGGCCGG CATCCCTAAG CTTGCTCAGC AAACACCTGC TCAAGTCCCT 1500
 TGTGTGTTGC ACAAAGAACC GCGCTGCAAA ACTGCTGCCC CTGGTGATGG CTGCCCCCT 1560

GAGCATGGAG CATGGCCACAG TGACCGTGGT GGGCATCCCC CCAGAGACCG ACAGCTCGGA 1620
 CAGGAAGAAC TTTTITGGGA GGGCGTTTGA GAAGCAGCG GAAAGCACCA GCTCCCGGAT 1680
 GCTGCACAAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTATTITCCC TCTGTCCTA GGAATTTGAT TCTTCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTCA TTTAGATTGT AAGTTATGGA CATGATTGTA GATGTAGAAG 1860
 CCAATTTTAA TTAATAAAA TGCTTATTTT AGGCTCCGTC CCAAAAAAAA AAAAAAAA 1920
 AAAAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
 MFVSDFRKEF YEYVQSQRVL LFVADVDAL CACKILQALF QCDHVQYTLV PVSQWQLEET 60
 AFLEHKEQFH YFILINGAN VDILLILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDLEVPAY EDIPRDEED EEHSGNDS DG SEPSEKTRL EEEIVEQTM RRRREWEAR 180
 RRDILFDVEQ YEYHGTSSAM VMFELAWMLS KDLNDMLWVA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNEDEE NTLSVDCTRI SFYEYDLRLVL YQHWSLHDSL CNTSYTAARF 300
 KLWSVHGQKR LQEFPLADMGL PLKQVKQKFP AMDISLKENL REMIEESANK FGMKDMRVQT 360
 FSIHFQPKHK FLASDVVFAT MSLMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK 420
 KQLRATQQT I ASCLCTNLVI SQQPFYLCSL MEGTDPVMLF SRPASLSLLS KHLKSKFVCS 480
 TKNRRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
 HFDLSVIELK AEDRSKFLDA LISLLS

Seq ID NO: 254 DNA sequence
 Nucleic Acid Accession #: NM_022337
 Coding sequence: 48..683

1 11 21 31 41 51
 GGCTGCGCTT CCCTGGTCAG GCACGGCAGG TCTGGCCGGC CGCCAGGATG CAGGCCCGGC 60
 ACAAGGAGCA CCGTGTACAAG TTGCTGGTGA TTGGCGACCT GGGCGTGGGG AAGACCAGTA 120
 TCATCAAGCG CTACGTGCAC CAGAACTTCT CCTCGCACTA CCGGGCCACA ATCGCGCTGG 180
 ACTTCGCGCT CAAGGTGCTC CACTGGGACC CGGAGACTGT GGTGCGCCTG CAGCTCTGGG 240
 ATATCGCAGG TCAAGAAAGA TTTGGAAACA TGACGAGGGT CTATTACCGA GAAGCTATGG 300
 GTGCATTAT TGTCTTCGAT GTCACCAGGC CAGCCACATT TGAAGCAGTG GCAAAGTGGG 360
 AAAATGATT GGACTCCAAG TTAAGTCTCC CTAATGGCAA ACCGGTTTCA GTGGTTTTGT 420
 TGCCCAACAA ATGTGACCAAG GGAAGGATG TGCTCATGAA CAATGGCCTC AAGATGGACC 480
 AGTTCTGCAA GAGGACGGT TCGTAGGAT GGTTTGAAAC ATCAGCAAAG GAAATATATA 540
 ACATTGATGA AGCCTCCAGA TGCTGGTGA AACACATACT TGCAAATGAG TGTGACCTAA 600
 TGGAGTCTAT TGAGCCGGAC GTCGTGAAGC CCCATCTCAC ATCAACCAAG GTTGCCAGCT 660
 GCTCTGGCTG TGCCAAATCC TAGTAGGCAC CTTTGCTGGT GTCTGTAGG AATGACCTCA 720
 TTGTTCCACA AATTGTGCCT CTATTTTAC CATTTTGGGT AAACGTCAGG ATAGATATAC 780
 CACATGTGGC AAGCCAAAGA TCTATGCCTC TGTTTTTTCA ATGAGAGAGA AATAGCAAAT 840
 GTTCTTTCTA TGCTTTCTCT ACCATCATCA CAGTGTTTAC AAACCTTTGA AAATATTTAG 900
 TCTGTTACAA ACTTCTGTCA TGTAGCTGAC CAAATCCTG CAGGGCCACA GTCGGCACTG 960
 TTATTGCTT CTTTTAATCA GCAAAGCCCT CAAGTCTTAA AATAAAGGG GAGAAGAA 1020
 AACTAGCTGT CAAGTCAAGG ACTGGCTTTC ACCTTGCCCT GGTGTCTTTT TCCAGATTTC 1080
 AATATATTCT CTGATGGCCT GACAGGCCCTA TTAAGTAGAT GTGATATTTT CTTCAGAT 1140
 GACCTCCATT CTCGGCAGAC CTAAGAGTTG CCTCTGAGT AGCTCTTTGG AATCGTGAAC 1200
 ACAGGTGTGC TATATTGTCC TTGTCCTAAC TGTCACTTGC CATGGCCTGA ATGTTGGCTT 1260
 AACTGAATAT TGTATGAAA GACATGCCTC CATATGTGCC TTTCTGTTAG CTCTCTTTGA 1320
 CTCAAGCTGT GGGGCTCCTC TATACATGCT ATACATGTAA TATATATTAT ATATATTTT 1380
 GCAAGTGAAC AATAAACAT TAAAGATAA AA

Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
 MQAPHKEHLY KLLVIGDLGV GKTSIIKRYV HQNFSSHYRA TIGVDFALKV LHWDPETVVR 60
 LQLWDIAGQE RFGNMTRVY REAMGAFIV DVTRPATFEA VAKWKNLDS KLSLNGKPV 120
 SVVLLANKCD QGKDVLMNG LKMDQFCKEH GFVGWFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DVVKPHLTST KVASCSCAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
 Coding sequence: 25..1464

1 11 21 31 41 51
 GGAACCGCCC GCTGCCAGCC CGGCCAGGCA CCCCTGCAGC ATGGCCTGGA ACACCAACCT 60
 CGCTGGCGG CTGCCGCTCA CCGCTGCTGCT CCGCAGGTG ATTATGGTGA TTCTCTTCGG 120
 GGTGTTCTGT CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA 180
 GAACCTGAGC GACATGAGAG ACGAATTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
 CGTGATGTGT TCGTGGGCT TCGGCTTCCT CATGACTTTC CTGCAGCGCT ACGGCTTCAG 300
 CGCCGTGGGC TTCAACTTCC TGTGGCAGC CTTCCGCATC CAGTGGGCGC TGCTCATGCA 360
 GGGCTGGTTC CACTTCTTAC AAGACCGCTA CATCGTCTGT GGCCTGGAGA ACCTCATCAA 420
 CGCTGACTTC TCGTGGGCT CTGTCTGCGT GGCCTTTGGG GCAGTCTCTG GTAAAGTCAG 480
 CCCCATTCAG CTGCTCATCA TGACTTTCTT CCAAGTGACC CTCTCTGCTG TGAATGAGTT 540
 CATTTCTCCTT AACCTGTGAA AGGTGAAGGA TGCAGGAGGC TCCATGACCA TCCACACATT 600
 TGGCGCTTAC TTTGGGCTCA CAGTGAACCG GATCCTCTAC CGACGCAACC TAGAGCAGAG 660
 CAAGGAGAGA CAGAATTCTG TGTACCAATC GGACCTCTT GCCATGATTG GCACCTCTT 720
 CCTGTGGATG TACTGGCCCA GCTTCAACTC AGCCATATCC TACCATGGGG ACAGCCAGCA 780
 CCGAGCCGCC ATCAACACCT ACTGCTCCTT GGCAGCCTGC GTGCTTACCT CGGTGGCAAT 840

ATCCAGTGCC CTGCACAAGA AGGGCAAGCT GGACATGGTG CACATCCAGA ATGCCACGCT 900
CGCAGGAGGG GTGGCCGTGG GTACCGCTGC TGAGATGATG CTCATGCCTT ACGGTGCCCT 960
CATCATCGGG TCTGCTCTGG GCATCATCTC CACCTTGGGT TTTGTATACC TGACCCCAT 1020
CCTGGAGTCC CGGCTGCACA TCCAGGACAC ATGTGGCATT AACAACTGCG ATGGCATTCC 1080
5 TGGCATCATA GGCGGCATCG TGGGTGCTGT GACAGCGGCC TCGCCAGCC TTGAAGTCTA 1140
TGGAAAAGAA GGGCTTGTCC ATTCTTTGA CTTTCAAGGT TTCAACGGGG ACTGGACCGC 1200
AAGAACACAG GGAAGTTTCC AGATTATGG TCTCTTGGTG ACCCTGGCCA TGGCCCTGAT 1260
GGGTGGCATC ATTGTGGGGC TCATTTTGAG ATTACCATTG TGGGGACAAC CTTCAGATGA 1320
10 GAACTGCTTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGAACAGCA CTGTCTACAT 1380
CCCTGAGGAC CCCACCTTCA AGCCCTCAGG ACCCTCAGTA CCCTCAGTAC CCATGGTGTG 1440
CCCACTACCC ATGGCTTCCT CGGTACCCCT GGTACCCTAG GCTCCAGGG CAGGTGAGGA 1500
GCAGGCTCCA CAGACTSTCC TGGGGCCCG AGGAGCTGGT GCTGACCTAG CTAGGGATGC 1560
AAGAGTGAGC AAGCAGCACC CCCACTGCT GGCTTGGCCT CAAGGTGCTT CCACCCCTGC 1620
CCTCCCTTC ATCCAGGGG GTCTGCTGA GAAATGGAGG GAGAAAGCTA CAAAGTGGGG 1680
15 ATCCAAGCGG GGTCTGGCT GCAGAAAGTC TGCCCTGCTG TGGGTCTTG GCCACATTGG 1740
AGAAAAACAG GCTCAAAGTG GGGCTGGGAC CTGGTGGGTG AACCTGAGCT CTCCAGGAG 1800
ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCGTGCCTG CACCTCGGCC 1860
AGCATCTCCT ATGCTCCCTG GGTCCCCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC 1920
CAGGAATAAA CATTCTTGTG GTCCCTTGTG AAAAAAAAAA AAAAAAAA

Seq ID NO: 257 Protein sequence:
Protein Accession #: NP_057405

1 11 21 31 41 51
MAWNTNLRWR LPLTCLLLQV INVILFVGVF RYDFEADAHW WSEKTHKNLS DMENEFYRY 60
PSFQDVHVMV FVGFGLMTF LQRYGFSAVG FNFLAAFGI QWALLMQGFV HFLQDRYIVV 120
GVENLINADF CVASVCVAFG AVLGVSPQI LLIMTFQVT LFAVNEFILL NLLKVKDAGG 180
30 SMTIHTFGAY FGLTVTRILY RRNLBQSKER QNSVYQSDLF AMIGTLFLWM YWPSFNSAIS 240
YHGSQHRRAA INTYCSLAAC VLTSAISSA LHKKGKLDV HIQNTLAGG VAVGTAAEMM 300
LMPYCALIIG FVCGIISTLG FVYLTFFLES RLHIQDTGCI NNHIGIPGII GGIVGAVTAA 360
SASLEVYKGE GLVHSDFPQG FNGDWTARTQ GKPFQYGLLV TLMALMGGI IVGLILRLPF 420
WQPSDENCF EDAVYEMPE GNSTVIYIPED PTFKPSGSPV PSVPMVSPLP MASSVPLVP

Seq ID NO: 258 DNA sequence
Nucleic Acid Accession #: NM_002358.2
Coding sequence: 75..692

1 11 21 31 41 51
GGGAAGTGCT GTTGGAGCGG CTGTGGTTGC TGTCCGCGGA GTGGAAGCGC GTGCTTTTGT 60
TTGTGTCCCTT GGCATGCGG CTGCAGCTCT CCCGGGAGCA GGAATCACC CTGCGCGGGA 120
GCGCGGAAT CGTGGCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
45 GCATATATCC ATCTGAAACC TTTACTGAG TGCAGAAATA CGGACTCACC TTGCTTGTA 240
CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACTG AAAGATTGGT 300
TATACAAGTG TTCAGTTCAG AAACCTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
TCCTGGAAGG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGAC 420
50 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
CAGCTACCGT GACATTTCCT CCACTGTTGG AAGTTTCTTG TTCAATTGAT CTGCTGATTT 540
ATACAGACAA AGATTGGGTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
CCAATTCTGA GGAAGTCCGC CTTCGTTTCT TACTACTTAC AATCCACAAA GTAAATAGCA 660
TGGTGGCCTA CAAAATTCCT GTCAATGACT GAGGATGACA TGAGGAAAAT AATGTAATTG 720
55 TAATTTTGAA ATGTGGTTTT CTGAAATCA GGTCACTAT AGTTGATATG TTTTATTCA 780
TTGGTTAATT TTTACATGGA GAAAACCAA ATGATACTTA CTGAACGTG TGTAATTGTT 840
CCTTTATTTT TTTGGTACCT ATTGACTTA CCATGGAGTT AACATCATGA ATTTATTGCA 900
CATTGTTCAA AAGGAACCGG GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
60 GATAGTAAGT GTAGATGGAA AAACCTGTGC TATAAAGCTA GATGCTTCC TAAATCAGAT 1020
GTTTGTGCA AGTAGTTTGA CTCAGTATAG GTAGGAGAT ATTTAAGTAT AAAATACAAC 1080
AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGTGCCTG AAAGTAATCT ATAATCTATA 1140
TGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1200
75 ATATTGTAC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCAATGTTT 1320
TTATAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGT TTAATAAATA 1380
65 AAAAAAAAAA

Seq ID NO: 259 Protein sequence:
Protein Accession #: NP_002349.1

1 11 21 31 41 51
MALQLSREQG ITLRGSABIV AEFFSFGINS ILYQRGIYPS ETPTRVQKYG LTLVTTDLE 60
75 LIKILNNVVE QKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPREKS 120
QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLLIYTDKD LVVPEKWEES GPQFIINSEE 180
VRLRSFTTTI HKVNSMVAYK IPVND

Seq ID NO: 260 DNA sequence
Nucleic Acid Accession #: NM_001211
Coding sequence: 43..3195

1 11 21 31 41 51
AAAGGCTGCG AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
85 GAAGGGGGTG CTCTGAGTGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
GAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA 180
CAAGATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGGCATTGTA ATATGAAATT 240

CGATTTTACA	CTGGAATGA	CCCTCTGGAT	GTTTGGGATA	GGTATATCAG	CTGGACAGAG	300
CAGAACTATC	CTCAAGGTGG	GAAAGAGAGT	AATATGTCAA	CGTTATTAGA	AAGAGCTGTA	360
GAAGCACTAC	AAGGAGAAAA	ACGATATTAT	AGTGATCCCTC	GATTTCTCAA	TCTCTGGCTT	420
AAATTAGGGC	GTTTATGCAA	TGAGCCTTTG	GATATGTACA	GTTACTTGCA	CAACCAAGGG	480
ATTGGTGT	CACCTGCTCA	GTTCTATATC	TCATGGGCAG	AAGAATATGA	AGCTAGAGAA	540
AACTTTAGGA	AAGCAGATGC	GATATTTTCAG	GAAGGGATTTC	AACAGAAGGC	TGAACCACTA	600
GAAAGACTAC	AGTCCACAGC	CCGACAATTTC	CAAGCTCGAG	TGTCTCGGCA	AACCTCTGTTG	660
GCACTTGAGA	AAGAAGAAGA	GGAGGAAGTT	TTTGAGTCTT	CTGTACCACA	ACGAAGCACA	720
CTAGCTGAAC	TAAAGAGCAA	AGGGAAAAAG	ACAGCAAGAG	CTCCAATCAT	CCGTGTAGGA	780
GGTGCTCTCA	AGGCTCCAAG	CCAGAACAGA	GGACTCCAAA	ATCCATTTC	TCAACAGATG	840
CAAAATAATA	GTAGAATTAC	TGTTTTTGAT	GAAAAATGCTG	ATGAGGCTTC	TACAGCAGAG	900
TTGTCTAAGC	CTACAGTCCA	GCCATGGATA	GCACCCCCCA	TGCCCAGGGC	CAAGAGAAT	960
GAGCTGCAAG	CAGGCCCTTG	GAACACAGGC	AGGTCTCTGG	AACACAGGCC	TCGTGGCAAT	1020
ACAGCTTCAC	TGATAGCTGT	ACCCGCTGTG	CTTCCCAGTT	TCATCCATA	TGTGGAAGAG	1080
ACTGCACAAC	AGCCAGTTAT	GACACCATGT	AAAATTGAAC	CTAGTATAAA	CCACATCCTA	1140
AGCACCAAGAA	AGCTCGGAAA	GGAGAAGAGA	GATCCTCTAC	AAAGGGTTCA	GAGCCATCAG	1200
CAAGCGTCTG	AGGAGAAGAA	AGAGAAGATG	ATGTATTGTA	AGGAGAAGAT	TTATGCAGGA	1260
GTAGGGGAAT	TCTCCTTTGA	AGAAATTGGG	GCTGAAGTTT	TCCGGAAGAA	ATTAAAGAG	1320
CAAAGGGAAG	CCGAGCTATT	GACCAAGTGA	GAGAAGAGAG	CAGAAATGCA	GAAACAGATT	1380
GAAGAGATGG	AGAAGAAGCT	AAAAGAAATC	CAAACACTCTC	AGCAAGAAAG	AACAGGTGAT	1440
CAGCAAGAAG	AGACGATGCC	TACAAAGGAG	ACAACTAAAC	TGCAAAATTGC	TCCGAGTCT	1500
CAGAAAATAC	CAGGAATGAC	TCTATCCAGT	TCTGTTTGTG	AAGTAAACTG	TTGTGCCAGA	1560
GAAACTTCAC	TTGGGAGAAA	CATTGCGCAG	GAACAACCTC	ATTCTAAAGG	TCCAGTGTGA	1620
CCTTTCTCCA	TTTTTGATGA	GTTTCTTCTT	TCAGAAAAGA	AGAAATAAAG	TCCCTCTGCA	1680
GATCCCCCAG	GAGTTTTAGC	TCAACGAAGA	CCCCTTGCG	TTCTCAAAAC	CTCAGAAAGC	1740
ATCACCTCAA	ATGAAGATGT	GTCTCCAGAT	GTTTGTGATG	AATTTACAGG	AATTGAACCC	1800
TTGAGCGAGG	ATGCCATTAT	CACAGGCTTC	AGAAATGTAA	CAATTTGTCC	TAACCCAGAA	1860
GACACTTGTG	ACTTTGCCAG	AGCAGCTCGT	TTGTATCCA	CTCCTTTTCA	TGAGATAATG	1920
TCCTTGAAGG	ATCTCCCTTC	TGATCCTGAG	AGACTGTTAC	CGGAAGAAGA	TCTAGATGTA	1980
AAGACCTCTG	ATGAAGACGA	GACAGCTTGT	GGCACTATCT	ACAGTCAGAC	TCTCAGCATC	2040
AAGAAGCTGA	GCCCAATTAT	TGAAGACAGT	CGTGAAGCCA	CACACTCTCT	TGGCTTCTCT	2100
GGTTCTTCTG	CCTCGGTTGC	AAGCACCTCC	TCCATCAAAT	GTCTTCAAAT	TCCTGAGAAA	2160
CTAGAACCTTA	CTAATGAGAC	TTCAGAAAAC	CCTACTCAGT	CACCATGGTG	TTACAGTAT	2220
CGCAGACAGC	TACTGAAGTC	CCTACCAGAG	TTAAGTGCTT	CTGCAGAGTT	GTGTATAGAA	2280
GACAGACCAA	TGCCTAAGTT	GGAAATTGAG	AAGGAAATTG	AATTAGGTAA	TGAGGATTAC	2340
TGCATTAAAC	GAGAATACCT	AATATGTGAA	GATTACAAGT	TATTCTGGGT	GGCGCCAAGA	2400
AACCTCTCAG	AATTAACAGT	AATAAAGGTA	TCTTCTCAAC	CTGTCCCATG	GGACTTTTAT	2460
ATCAACCTCA	AGTTAAAGGA	ACGTTTAAAT	GAAGATTTTG	ATCATTTTTC	CAGCTGTTAT	2520
CAATATCAAG	ATGGCTGTAT	TGTTTGGCAC	CAATATATAA	ACTGCTTCAC	CCCTCAGGAT	2580
CTTCTCCAAC	ACAGTGAATC	TATTACCCAT	GAAATAACAG	TGTTGATTAT	TTATAACCTT	2640
TTGACAATAG	TGAGATGTCT	ACACAAAGCA	GAAATAGTCC	ATGGTGACTT	GAGTCCAAGG	2700
TGTCGTATTC	TCAGAAACAG	AATCCACGAT	CCCTATGATT	GTAACAAGAA	CAATCAAGCT	2760
TTGAAGATAG	TGGACTTTTC	CTACAGTGTT	GACCTTAGGG	TGCAGCTGGA	TGTTTTTACC	2820
CTCAGCGGCT	TTGGGACTGT	ACAGATCCTG	GAAGGACAAA	AGATCCTGGC	TAACGTGTTCT	2880
TCTCCCTACC	AGGTAGACCT	GTTTGGTATA	GCAGATTAG	CACATTACT	ATTGTTCAAG	2940
GAAACACCTAC	AGGTCTTCTG	GGATGGGTCC	TTCTGAAAC	TTAGCCAAA	TATTTCTGAG	3000
CTAAAAGATG	GTGAATTGTG	GAATAAATTC	TTTGTGCGGA	TTCTGAATGC	CAATGATGAG	3060
GCCACAGTGT	CTGTTCTTGG	GGAGCTTGCA	GCAGAAATGA	ATGGGGTTT	TGACACTACA	3120
TTCCAAAGTC	ACCTGAACAA	AGCCTTATGG	AAGGTAGGGA	AGTTAACTAG	TCTGGGGCT	3180
TTGCTCTTTC	ATTCAGCTAG	CGAATCAAGT	CTCAGAGATT	GCTGCCTCAG	AGCAATGGTT	3240
GTATTGTGGA	ACACTGAAAC	TGTATGTGCT	GTAATTTAAT	TTAGGACACA	TTTAGATGCA	3300
CTACCATTGC	TGTTCTACTT	TTTGGTACAG	GTATATTTTG	ACGTCACTGA	TATTTTAT	3360
ACAGTGATAT	ACTTACTCAT	GGCCTTGTCT	AACTTTGTG	AAGAATATT	TTATTCTAAA	3420
CAGACTCATT	ACAAATGGTT	ACCTTGTTAT	TTAACCCATT	TGCTCTACT	TTTCCCTGTA	3480
CTTTTCCCAT	TTGTAATTTG	TAAATGTTT	TCTTATGATC	ACCATGTATT	TTGTAATAA	3540
TAAATAGTA	TCTGTTAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA		

Seq ID NO: 261 Protein sequence:
Protein Accession #: NP_001202

60	1	11	21	31	41	51	
	MAAVKKEGGA	LSEAMSLGEGD	EWELSKENVQ	PLRQGRIMST	LQGALAQESA	CNNTLQQQKR	60
	APEYEIRFYT	GNDPLDVWDR	YISWTEQNYF	QGGKESNMST	LLERAVEALQ	GEKRYYS DPR	120
65	FLNLWLKLR	LCNEPLDMYS	YLHNQGIGVS	LAQPYISWAB	EYEARENFRK	ADAIFQEGIQ	180
	QKAEPLERLQ	SQHRQFQARV	SRQTLLEALEK	EEEEVEVFESS	VPQRSTLAE	KSKGKKKTARA	240
	PIIRVGGALK	APSQNRGLQN	PFPQMQNNNS	RITVFDENAD	EASTAELSKP	TVQPWIAPPM	300
	PRAKENELQA	GPWNTGRSLE	HRPRGNTASL	IAPPAVLPSF	TPYVEETAQQ	PVMTFCKIEP	360
70	SINHILSTRK	PGKEEGDPLQ	RVQSHQQA	EKKEKMMYCK	EKIYAGVGEF	SFEEIRAEVF	420
	RKKLKEQREA	ELLTSAEKRA	EMQKQIEEME	KKLKEIQTTQ	QERTGDQQUE	TMPTKETTKL	480
	QIASESQKIP	GMTLSSSSVCQ	VNCCARETSL	AENIWQEQPH	SKGPSVFFSI	FDEPLLSEKK	540
	NKSPPADPPR	VLAQRRPLAV	LKTSESITSN	EDVSPDVCDE	FTGIEPLSED	AIITGFRNVT	600
	ICPNPEDTCD	FARAARFVST	PFHEIMSLKD	LPSDPERLLP	EEDLDVKTSE	DQQTACGTIY	660
75	SQTLSEIKKLS	PIIEDSREAT	HSSGFSGSSA	SVASTSSIKC	LQIPEKLELT	NETSENPTQS	720
	PWCSQYRRQL	LKSLPELSAS	ABLCLIEDRPM	PKLEIEKEIE	LGNEDYCIKR	EYLICEDYKL	780
	PWVAPRNSAE	LTVIKVSSQP	PWDFYINLK	LKERLNEFD	HFCSCYQYQD	GCIVWHQYIN	840
	CFTLQDLQSH	SEYITHEITV	LIINYLLTIV	EMLHKAIEIVH	GDLSRCLIL	RNRHDPYDC	900
	NKQWQALQIV	DFSYSVDLRV	QLDVFTLSGF	RTVQILBQK	ILANCSPPYQ	VDLFGIADLA	960
80	HLLLFKEHLQ	VFDGDSFWKL	SONISELKDQ	ELWNKFFVRI	LNANDEATVS	VLGELAAEMN	1020
	GVFDITTFQSH	LNLKALWKVGK	LTSPGALLFO				

Seq ID NO: 262 DNA sequence
Nucleic Acid Accession #: NM_003784
Coding sequence: 365..1507

85	1	11	21	31	41	51
----	---	----	----	----	----	----

5
10
15
20
25
30
35
40

GTCTACTTAT	CAATAAGCAG	CTGCTGTGTC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
TAAAACTGAA	TTTCTCAGAAT	TTTAGAACAA	ATTTTGTGCT	AGAAATGCTG	ACTTTGGTTC	120
ATTAGGTAGT	GGTAAACACAG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAAT	ACCTAGGGCT	240
CAACAGTCTT	GAGAGTGTGT	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
AAGGAAACCA	GATTCCCATC	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACTCCATTT	360
TGCAATGGCC	TCCTTTGCTG	CAGCAAAATG	AGAGTTTTCG	TTCAACCTGT	TCAGAGAGAT	420
GGATGACAA	CAAGGAAATG	GAAATGTGTT	CTTTCTCTCT	CTGAGCCTCT	TCGCTGCCCT	480
GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
TGTTAAACAT	GCCTCAGGAT	ATGGAAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
ACTGAAAAGA	GTITTTTCTG	ATATAAATGC	ATCCCAACA	GATTATGATC	TCAGCATTGT	660
GAATGGGCTT	TTTGCTGAAA	AAAGTGTATG	CTTTCATAAG	GACTACATTG	AGTGTGCGGA	720
AAAATATATC	GATGCCAAAG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
ACGTAATATT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTGG	840
TGAAGGTGGC	ATAAGCTCAT	CTGCTGTAAT	GGTGTGGTGT	AATGCTGTGT	ACTTCAAAGG	900
CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
GTGCTCTGGG	AAGGCAGTCC	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGCTGTATT	1020
TGAGGACCCA	TCATATGAAGA	TTCTTGAGCT	CAGATACAAT	GGTGGCATAA	ACATGTACGT	1080
TCGTCTGCCT	GAGAAATGACC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
GGAATGGACC	AATCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCCTCAGTT	1200
CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTTGAGA	GCCCTAGGGC	TGAAAGATAT	1260
CTTTGATGAA	TCCAAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGGTGCTC	TGTATATATC	1320
AAGGATGATG	CACAAATCTT	ACATAGAGGT	CACGTAGGAG	GGCACCGAGG	CTACTGCTGC	1380
CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTTTA	GAGCTGACCA	1440
CCCATTCTTA	TTTGTTATCA	GGAAGGATGA	CATCATCTTA	TTCACTGGCA	AAGTTTCTTG	1500
CCCTTGAAAA	TCCAATTGGT	TTCTGTATA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
AAGTCAATAG	ATYTGRTGTT	AATTGGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
CTAACATTGG	TCAGCAGATG	ACACTGGTGA	CTTGACCTTC	CCTAGACACC	TGGTTGATTG	1680
TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGTCTC	ACCCATTTC	AATTTTATTG	1740
TCTTTCTTCC	CACGCTCATT	TCTATCATTC	TCCCCCATGA	CCGCTCTGGA	AATTATGGAG	1800
RGTGCTCAAC	TGTTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAAACTCTAC	1860
AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TTGTTGACCT	ATGAAGATT	TAGAGTTTAC	1980
CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAAAAAATG	TGAAATTGGG	2040
ATTAGGGACC	TACCAAAATA	TTTCAATTA	GCTTTCAATT	GACAAATTTT	GGCCTTTCTT	2100
TGATAGACAA	ATATGTACAT	GTTTTTTCAA	ATATTAAAGA	TCTTTTAACT	GTTGGCAGTT	2160
GTTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
AGAATAAAGA	AATACACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45
50
55

1	11	21	31	41	51	
MASLAAANAE	FCNFLFREMD	DNQNGNVFF	SSLSLFAALA	LVRLGAQDD	LSQIDKLLHV	60
NTASGYGNSS	NSQSGLSQL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYIECAEK	120
LYDAKVERVD	FTNHLEDRR	NINKWVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
WQSAFTKSET	INCHFKSPKC	SGKAVAMHQ	ERKFNLVIE	DPSMKILELR	YNGGINMYVL	240
LPENDLSBIE	NKLTQNLME	WTNPRRMTSK	YVEVFFPQFK	IEKNYEMKQY	LRALGLKDF	300
DESKADLSGI	ASGGRLYISR	MMHKS YIEVT	EEGTEATAAT	GSNIVEKQLP	QSTLFRAHP	360
FLFVIRKDDI	ILFSGKVS					

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60
65
70
75
80
85

1	11	21	31	41	51	
AAAACCTTGA	GGTGATTTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
GCTCCTGCTG	TCCGGCTGGT	CCCGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTT	AAGGCCAGGT	240
GGATGAAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
CCTGGGGAAG	AAACTAAATG	TCACAAACGC	CTGGAAAGCA	CAGAACCCAG	TACTGAGAGA	360
GGTGGTGGAC	ATACCTTACG	AGCAACTGCG	TGACATTTCAG	CTGGAGAAAT	ACACACCCAA	420
GGAAACCCCTC	ACCTTCGAGG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
TGGATCTTGG	CAGTTTCAGT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
AATGTGGACA	ACGGTTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
GGTTGTGGCC	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
CTTCTTGATG	GGCATGGACA	GCACCTTGGA	GCCAAAGTGA	GGAGCACCAC	TCGCCATGTC	720
CTCAGGCACA	ACCCAACCTCA	GGGCCACAGC	CACCACCTTC	ATCCTTTGCT	GCCTCCTCAT	780
CATCCTCCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
ACAGCTGCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
TGGACCCAA	AGCTCATTCA	CTGCCTTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
TTCTGGCTGA	CTAAACAAGA	TATATCAATT	TCTTCTTCT	CTTTTGTGTT	GGAAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTCTTGG	CAAAATGATAT	TGTGAGTAAA	ATAATCACGT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCGG	TGTCTGTAAA	GAGAAATTTT	AAATTATTTA	1260
ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAATAAA	A		

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
MAAAAAATKIL LCLPLLLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRNC AVQGGVDEKT 60
FLHYDCGNKT VTPVSPILGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTFKEPLT 120
5 LQARMSCBQK AEGHSSGSWQ PSFDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVM 180
SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLL LCCLLIILPC 240
FILPGI

Seq ID NO: 266 DNA sequence
Nucleic Acid Accession #: XM_084853.1
Coding sequence: 127-444

1 11 21 31 41 51
15 ATTGATGATA TATTTAACGA AATCAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
GACAAGATCA ACTTACCAGA TTTCCTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAAGGG 180
AAAAAGGCCA TTCGAAGAGA GGAATTCCTG AGACTGCTCG TTACTAAAGG TGAGCATATG 240
ACGGAGGAGG AGATGTTGGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
20 AAATCCGAGC CTGCAACCTG CTCCGTCAAA GGTTCAGAAA TTGCTTGA AGAAGAACTT 360
CCAGACGAAA TCACTGCAGA AATATTCGCG ACTGAAATTC TTGGCTTAAC CATTTCAGAA 420
GATTCGGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG 480
GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
25 CCCCCCTCTC ATCTTTAGAA CATTTAGACA TTAAGCAAG TTCTGTGTGA GCAATG

Seq ID NO: 267 Protein sequence:
Protein Accession #: XP_084853.1

1 11 21 31 41 51
30 MSGIHKSFEV LGYTSKGGK AIRREDFLRL LVTKEHMT EEMLDPCASL PGLNPEGWKS 60
EPATCSVKGS EICLEELPD EITAEIPATE ILGLTISEDS GQDQG

Seq ID NO: 268 DNA sequence
Nucleic Acid Accession #: NM_001898
Coding sequence: 57-482

1 11 21 31 41 51
40 GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG 60
CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120
GCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGAGAC CTCAATGATG 180
45 AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
ACTACTACAG ACGTCCGCTG CCGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
ATTACTTCTT CGACGTAGAG GTGGGCGCGA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAGAA ACAGTTGTGC TCTTTCGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
50 AGGGATCTGT GCCAGGCCAT TGCACCCAG CACCACCAC TCCACCCCC TGTAAGTGCTC 540
CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCTC CCCATGTGCC TCGGCCAAGA 600
GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGTCTCAG AGGGCGCTCT GCCCTCCCTC 660
CTTCCTCTCT GTCTTCAATA GCCCTGTGAT ATGGTACACA CCCCCCACC TCCTGCAATT 720
AAACAGTAGC ATCGCC

Seq ID NO: 269 Protein sequence:
Protein Accession #: NP_001889.1

1 11 21 31 41 51
60 MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
DDYYRRPLRV LRARQQTGVG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
EYIEVPWENR RSLVKSRCQE S

Seq ID NO: 270 DNA sequence
Nucleic Acid Accession #: XM_093210
Coding sequence: 13-1854

1 11 21 31 41 51
70 ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
GGCAGAGGGA ATGGGGAGGG GGCATCCTAC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCACGTGC 240
75 GCCTTCAAAA CGGTAAAGAGC TGCAACTGAA CGTGTGAGAC ATGGTGCAGA TAGGCTGAGA 300
GGCGGGCGGA GAGATGCCCA TGAATCAAG TACCCGGACA CGCCCTCCAC TTCTACCACC 360
ACGAGTAACA CCGCCCCAC GGGACCGCTC TCGAGGTCCC CCAAGCCAAG GACGCAAGGA 420
GGAACGCCCC GGCAGCGGCG CAGCAGCGGC GGGCACCAGG CCAATGGCCA CGGAATCAG 480
CACTGGCAGT CGGCCCTCCT CACACCGCAG GCGTGCACTG TGGCCGACGG AGCCTCCCGG 540
80 GCGAGGACCC CAGCTAGGCC GTCAACCCGG TTGCTCCAC GGAAGGGGG ACCAGGCAAA 600
CTGCCCCAAG CCGCAGCCCC AGGCTCCCTG GCGGAGGCCT CCGCTGTGTC CGCCAGATC 660
ATGCGCGCCA CCAGGCTCCC GAGCCATGCG TTCCTGTCCG GGAACGGCCC GCGCTCCTGG 720
CTGTCCAGCT AG

Seq ID NO: 271 Protein sequence:
Protein Accession #: XP_093210

1 11 21 31 41 51

MLRHGEQKRK RARKKWDPLP TCAFKTVRAA TERNRHGADR LRGGGRDAHE LKYPDTPSTS 60
TTTSNTAPTG PLRSRSPKPT QGGTPRRRPA AAGTRANGHG TQHWQSALLT PQACSVADGA 120
SRAEDPARPS PRLLPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVVISQALP 180
PNSSVGRKEE RPGAGQORRA PAPMATELST GSRPSSHRRR AVWPTEPPGP RTQLEPSPRL 240
LPREGAGPKL PKAPSPGSLA EASAGPAQIM AATRLPSRGP LSGNGPASWL SS

Seq ID NO: 272 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..732

1 11 21 31 41 51
GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT 60
TGAAAAAGCT TTTTTCCTCA CTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA 120
TAATGTGGAG GAAATTATTC TTCTCATTTG GAGATTACAG AATATATCTA TTCACTTTGA 180
ATACCCACTT GAAGCCTCTG TAGAAATGTC TCGTCTCTCG GTTGATTTTC TAAACCTTAC 240
ATGATTTTGT CTTGTTTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT 300
TAAATTATTT TTATTTATCT TTCATATAGT TCTTACAATT TCTAAAAAAT TAACACTCAT 360
TTAGTATCAC AATTATGTTG AGAGGGTTTT TTGTATTTT AAGCATATGT GGCCTATATA 420
AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCCTGAAAC 480
TTAAGCC

Seq ID NO: 273 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MGGRENREGR DAFEKAFFPT FNLL

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299-961

1 11 21 31 41 51
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAGAA GGGGATTAAA CCATTACCT 60
CATGGAGTTG TGAAAGAATA GCTGCAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCTCTG TTCTCTACCT GGAGAACTG 180
GGGTGGCAGG CCGGTCCCTCC ACAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
GGAACCTTGA CTGAGAGGCC TCTCCACGCT GTCCCACTGC CCTTGGCCTA GCGCGCAGCC 360
TGCCCTGTGG CCGCTCTGGG CCGCTCTGGG TCTGCTGAGC AGCGCTGCGC AGGCCTCCCT 420
GGGCTCCGCG CCGCGCAGCC CTGCCCCCGG CGAAGGCCCG CCGCTGTCTC TGGCGTCCCC 480
CGCCGGCCAC CTGCGGGGGG GACGCACGGC CCGCTGTGTC AGTGGAAGAG CCGCGCGGCC 540
GCGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCGCGCTGCA CCCCCTCTG CTCTTCCCCG 600
CGGGGGCGCG GCGCGCGGGG CTGGGGGGCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG 660
GGGTGCGCGC CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTGCGCCTGG GCCACCGCTC 720
CGACGAGCTG GTGCGTTCGC GCTTCTGCA GCGCTCTGTC CGCCGCGCGC GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CCGGGCCCTG CGACCGCCCC CGGGCTCCCC 840
GCCCCGTCAG CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGAGCT 900
CAACAGCACC TGAGAACCGG TGGACCGCCT CTCGCGCCAC GCCTGCGGCT GCCTGGGCTG 960
AGGGCTCGCT CAGGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCCCGAACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCTCACCCT TCGGATCCCT AGCCTAAAG ACACCAAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGCGCCAGG CCCTGTAGGG 1320
ACAGCATTTC AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCTGTG CTGGAACCTG 1380
CCTGTACTCA CTATGGGAG CTGGCCCC

Seq ID NO: 275 Protein sequence:
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
REVSPQCRPR TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 276 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783-1445

1 11 21 31 41 51
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
TCGCTCCCCG CCTCTACTCA CTTTCTCCCG CCTCGGCCCC GGCCTCCAG CTCTCTACTT 180
CGGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCTCTC CACGCTCGA GTTCTCTACT 240
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
CGGGGACGGG GCGCTCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
CACCAGACGG CTGCGGGGGC GGGCAGGAG CTGCTGAGGG ATGGAGTTGG GCCCGCCCCC 480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGGCCAGACC CTCGCTGCCA 540

CCGGGGCTG GAGCCCAACA CCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGGCT ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
 GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAGG GTGCAGGACC CGGTGCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGGCTCCTG GTGTTGATAG 780
 5 AGATGGAAGT TGGACTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTGG CCTAGGCGGC 840
 AGCTTGGCTT GTGGCCCACT CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC 900
 CCTTGGGCTC CGCGCCCGCG AGCCTGCGCC CCGCGAAGG CCCCCGCTC GTCTTGGCTG 960
 CCGCGCGCGG CCACCTGCGG GGGGAGCGCA CGGCCGCTG GTGCAGTGA AGAGCCCGGC 1020
 10 GGGCGCGCGG CAGCCCTTCT CGGCCGCGC CCGCGCGGCC TGCACCCCA TCTGCTCTTC 1080
 CCGCGCGGGG CCGCGCGGGG CGGGCTGGGG GCGCGGCGC CCGGCTCGG GCAGCGGGGG 1140
 CGCGGGGCTG CCGCTGCGC TGCAGCTGG TCGCGGTGCG CGGCTCGGC CTGGGCCACC 1200
 GCTCCGACGA GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG GCGCGCTCTC 1260
 CACACGACCT CAGCTGCGC AGCCTACTGG GCGCGGGGG CCTGCGACC CCGCGGGGCT 1320
 CCGCGCGGCT CAGCGAGCCC TGCTGCGGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 15 ACCTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCGC CACGCGCTG GGTGCTCTG 1440
 GCTGAGGGCT CGTCCAGGG CTTTGAGAC TGGACCTTA CCGGTGGCTC TTCTGCTCTG 1500
 GGACCTTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGAGCGAAG GCCTCAAGC 1560
 TGAGAGGCCC CTACCGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA 1620
 20 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
 CTATGGAGCC TCTCGGACCC ACTTCTCACA GACTCTGGCA CTGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCGC CAGGCGCTGT 1800
 AGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA 1860
 CTGGCTGTA CTACTCATG GGAGCTGGCC CC

Seq ID NO: 277 Protein sequence:

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 | | | | |
 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 30 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRRLRSQIV PVRLGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 278 DNA sequence

Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1-714

1 11 21 31 41 51
 | | | | |
 40 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCCTTC TCCCAAGCC 60
 CACTTGGGTG CCTCTTCTT CCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCACCCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCTC CTGGGCTCC 180
 GCGCCCGCGC GCGCTGCCCC CCGCGAAGGC CCGCGCGCTG TCCTGGCGTC CCGCGCCGGC 240
 45 CACTTGGCGG GGGGAGCGAC GCGCCGCTGG TGCACTGGAA GAGCCCGGCG GCGCGCGCGC 300
 CAGCCTTCTC GCGCCGCGCC CCGCGCGCTC GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGCGCG GGGCTGGGGG CCGGGGAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
 CGCTTGGCTC CGCAGCTGGT GCGGTGCGCG GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
 CTGGTGGCTT TCCGCTTCTG CAGCGGCTCC TGCGCGCGCG CGGCTCTTCC ACACGACCTC 540
 50 AGCCTGGGCA GCCTACTGGG CCGCGGGGCC CTGCGACCGC CCGCGGGCTC CCGCGCGCTC 600
 AGCCAGCCCT GCTGCCGACC CAGCGCTAC CAGCGGCTC CTTTCATGGA GCTCAACAGC 660
 ACCTGGAGAA CCGTGGACCG CCTCTCGGC ACCGCTCGG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTGCACTT GGACCTTAC CCGTGGCTCT TCCTGCTGG GACCTCCG 780
 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAGCT GAGAGGCCCC 840
 55 TACCGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
 AGAGCCCTCA CCTGCGGAT CCCAGCCTAA AAGACACAG AGACCTCAGC TATGGAGCCC 960
 TTCGACCCA CTTCTCAGC ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGCAGCAT 1080
 60 TTGAAGGACA CATATTGAG TTGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAC 1140
 TCACTCATGG GAGCTGGGCC C

Seq ID NO: 279 Protein sequence:

Protein Accession #: NP_476501.1

1 11 21 31 41 51
 | | | | |
 65 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PPPVLASAPG HLPGRRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGGPGS RARAAGARGC RLRSQVLPVR ALGLGHRSD E LVRFRFCGSGS CRRARSPHDL 180
 70 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 280 DNA sequence

Nucleic Acid Accession #: NM_057090.1

Coding sequence: 29-715

1 11 21 31 41 51
 | | | | |
 75 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTGAGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCTTGGCCTA GCGGCGAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
 80 GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCTTGGGCTC 180
 CGCGCCCGCG AGCCTTGCCC CCGCGAAGG CCCCCGCTC GTCTTGGCGT CCGCGCCGGC 240
 CCACCTGCGG GGGGAGCGCA CCGCCGCTG GTGCACTGGA AGAGCCCGGC GCGCGCGCGC 300
 GCAGCCTTCT CCGCCCGCGC CCGCGCGGCC TGACCCCA TCTGCTCTTC CCGCGGGGG 360
 CCGCGCGCGG CCGGCTGGGG GCGCGGCGC CCGCGCTCGG GCAGCGGGG CCGCGGGCTG 420
 85 CCGCTTGGC TCGCAGCTGG TCGCGGTGCG CCGCTCGGC CTGGGCCACC GCTCGACGA 480
 GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
 CAGCTGGGCC AGCCTACTGG GCGCGGCGC CTGCGACCG CCGCGCGGCT CCGCGCCGT 600
 CAGCCAGCCC TGCTGCGGAC CACGCGCTA CGAAGCGGTC TCCTTCATGG ACCTCAACAG 660

CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCCTTA CCGGTGGCTC TTCTGCCTG GGACCCCTCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCC 840
 CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGTGAAG GGACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGCGGA TCCACGCTTA AAAGACCCA GAGACCTCAG CTATGGAGCC 960
 CTTGGAACCC ACTTCTCACA GACTCTGSCA CTGGCCAGGC CTGAACTCG GGACCCCTCC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCC TGTGCTGGAA CTGGCTGTA 1140
 CTCACCTATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LNPILAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPPVLASPA GHLPGGRAR WSGRRARRPP PQPSRPAPPP PAPPSPALPRG GRAARAGGPG 120
 SRARAGARG CRLRSQLVFPV RALGLGHRSD ELVRFRFCSSG SCRARSPPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCTTTGGA AATCTCTTAC CTTTCATTAG GGTTCCTTC 60
 ATAGCAATTT CTTTGGTTT TTAAGACTTC TACATTGCTT TTCTTTTAT TATCTGTGCT 120
 CCGTGAAGCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTTAG CTGCCTACTC 180
 AGGTAAAGTT TTTCTTTGCT TCATCTTGG TTCCATATA CTATTTTGG TTTTGTGTA 240
 GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCCTGGCT AACAGTGATC ATGTTTATGT 300
 GCTAAAAATG AACTTGAAC ACAGGAAGTAG TGGTTGGTCC AGTTTGAAAG CTCTTATTAG 360
 TATTCTTCAT CTCGGCTGTA ATAATAGCCA TTATTTGTTA TGCCCTTGT ATGTAGCAGA 420
 CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TTCAATATAT ATGTATTTCCT TATT

Seq ID NO: 283 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAAC 120
 GAAGTGCTAC CAAACACGCG AATGACTGTC CTAAAAGTGC GTTCTGGGAT ACACCTGTAA 180
 ACTTGGATCA AGTTCCTCTC CCTCTCTCA AAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATTCT GACCTCGTAA TTATATAGGG GGTGGTTTTG GTTCTGCGT 300
 CTTTCCCTGA TTCAGTGGCA GGTAACATAT TTCATGTACA AAATGAACTG CAACACCACG 360
 GCAAAACAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAGTGGCGT 420
 GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCCTGCC ACTGAGGAGG 480
 AAGGGCTGGC TAAGGGAGGC CGGGCGGAG GAAGCCAAGC TCTGCAGGCC CTGACAAAGT 540
 CCTCCCGGCC TCCACGCGTC GCCATGGCAA CGCGGGGTCT GTGCTGGCCG GGATTGGCCG 600
 GCCTGGCGCG CGCAGGGCCC GCTGGGAAAG CGCGTCCCG CGCGCGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CCAGATGTGG GCGGCGGGC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGGCCCTC CTGGGACTCC TGCTCAGTCC 780
 CTATGACGGG CGCACGTGGG CAGGGGCTGG AGGTGGTGG CTGCGCGTCG CCGCGCTGC 840
 CGCTGAGCTG CAGCAATTC ACCAGGTGCG TGTGTCTCC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGACG 960
 TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCAGA AAGCCGCTG ACACCATGGG AGGTGTGGTT TATTGGCAAA GAAAAAGAA 1140
 AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAA TCAACAACTA GAAAAAGAA 1200
 AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGTGTA AGAAAAAGCA AAGGAATGG 1260
 TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGAACA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAAAGGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT 1380
 ATCAAGAATG GTTAAAGAAA AAAAATGCTG AAGAAATGTA GAGGAAGAAG AAAGAAAAAG 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAAA AGTTTCAAGA 1500
 ATGGTTGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACCGAGCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTCG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGGAATCT GTGCAGAATA CAAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTGTT TTTTACTGCT 1860
 CAGTCAATAA CTCACACTT AATGTGATTA TTGACAAATA GCAATTTTGG CATTTGTATA 1920
 TGGAGTCTCT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTTATAA ACTTTTAAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGAAATA AGTGGCTGAA TATGTAAGAA TGTGTTTGT 2040
 ATTTAGCTTG TATTAAGT ACCTGTAAT ACCAATAAAA CTACAAATT TTCTTG

Seq ID NO: 284 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCWPG LAGLARAGPA GKARPRRGSA SLNLAGQWNA AGRWGPFPSP SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARGQ GLEVVRSPSP PLPLSCSNST RSLLSPLGHQ SFQFDEDDGD 120
 GEDEEDVDDE EDVDEDAHDS EAKVASLRGM ELQGCSTQV ESENNQEEQK QVRLPESRLT 180
 PWEVWFIGKE KEERDRQLQK ALEELNQOLE KRKEMEEREK RKI IAEKHK ENVQKIQEOK 240
 RKEREQKINK EMEKAAKEL EKEYLQEKAK SKYQEWLKKK NAECEERKKK EKKNNSKLY 300

RRKRX

Seq ID NO: 285 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1746

5

	1	11	21	31	41	51	
10	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCACC	120
	GGGGCAGCGA	TTGTGGCGGT	GGCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GGCCTGAGGA	TTGAGAAGAA	TGAGCTGTGC	CGCATCACGC	CTGGGGCCTT	CGGAAACCTG	300
15	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCCTC	360
	TTCCAGGGCC	TGACAGCCTT	TGAGTCTCTC	CTTCTGTCCA	GTAACAGCT	GTTCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACTGGG	CAATCTCCAG	600
	GTCTTCCGGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
20	GTAACTCTGC	AGGAACCTGC	TCTACAGCAG	AACCAGATTG	GACTGTCTCT	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACACAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGGCGGA	GCTTTGGCTC	900
25	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TTAGCCGCAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCATGT	TGGCCAAACCT	CGAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGGAGAACT	TGCCCTCTCG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
30	TATGACAATC	CCTGAGAGTG	GAGTCCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAGCCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCACGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGCTGTTTC	CAAGCGTCCA	TGTCCTTGAG	1440
	GTGCTAGTTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
35	ATTCAAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCACAG	CGGGCTGGCC	1620
	ATTGCCGCCA	TTGTAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTCGGC	1680
	TGTTGCTGCT	GCAGAAAGAG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
40	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCTCTG	CTTGCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGAC	CTTCTTCAAA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTCATACCCC	TGGGCTTCTC	TCGAGAGGGC	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAGAAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTC	CTGTAGACTC	2100
45	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCTCTCG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTGTTTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAAAGAA	CAGTTCAAAC	CATTAACTGC	GTGTTCTAAG	AGCCGTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
50	AGACAGAAGA	GGCTTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAAAGAAAC	2460
	CCCCAGCACA	GCAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
	TGAAAAGTTT	AGCCCTTAA	GGAAAGAAAT	CATGTAGAAT	TTTGGACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTGTTGTTTA	AAATTTTAA	TGAAGCATG	TGAAGTGTAC	GTGCAGAAAA	2700
55	GTGGGAACAT	GATAGTGAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCAAG	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCACA	GTCAAGCTGT	GCAGAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCCTG	3000
60	AGAGACCTCG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCTC	3120
	TCCGCTCGGA	GCCTTCTATG	GAGTGATAT	GCCTGTATCT	GTGTTTAATT	TTCACTTCTC	3180
	ACTTAGGGGA	AGTGAATACG	CTCAGAGATG	AGATCCTTTA	ATTGAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCCTTCTAAT	TGTGTAATA	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
65	TGAACCTCAG	AATCTCACT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTACTG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCTCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATTACCA	TGGCGCTCAA	GAAAGTTAGG	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGGCCCACT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCC	3600
70	AGGAAGAAGC	TTCAAGCTGAC	TCCACGGGGA	TCTGGAAATC	CAGGACCAAT	CCCGATCGGC	3660
	TCCTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
	CCCGATCGGC	TCCTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCA	TTTTCCCTTC	CAGTTCTGTC	ACAAAAAGTG	TCCAGAGGGC	3900
75	TGTTTGCAAA	CAGTGTGCA	CTTTGTAGCT	TTTCAACCTC	TGTTCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAAGTAGC	4080
	CCAGAGCATG	GCAATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTC	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTGTCGCCAC	AGACCTGTGC	4200
80	GGTGCTCTCT	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCAATCCGGT	GGCCCTGCCA	ATCTTAACCC	AGAAACCTTA	4320
	GGTATTCTCT	TCGATAGCCA	TGACATTGGA	GCACCTTCTC	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTTCAGAT	GACACCAACC	AGGAGCACC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTC	TCCCATCAGA	GTGGTGGAT	GGAGCCATTG	4500
85	GCCTCCTTTT	CTCCAGGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTGTC	TCAATTCTCA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AGCTGGAGT	GGGGTACAGA	GTTCAGTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740

GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCCTA TTTTAAAAA GTGCTTACTG 4800
 TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
 GGTAGGAGTG CCGCTCTAC CCACTTGTGA TGGGTACAG AGGCACTTGC TCTTCTGCAT 4920
 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAC TTTGTACAAG AGCTCATGGC 4980
 TTGTCTTGGG CTTTCTGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCTT GTTGTCTCTCC 5040
 TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100
 GGAAAAAATA AACTCTTCCA TCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160
 TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTTAGA GATACAAGAG TTCTACTTAG 5220
 AACTTTTCAT GGACACAATT TCACAACCTT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
 GAACCTTCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340
 AGTTGGTCGA CAGATGTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
 GCCCCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCTTG 5460
 GGAAGGAAGC ACTGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
 CTCCTTCCGC CCCAGGTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
 CTTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCCTTGTG TAGAGAATTA CTGCAAATCA 5640
 GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCC TCAGGGTTT GTAGAGGTG 5700
 AGCCCTGGTG GGCAGGGTGG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 286 Protein sequence:
 Protein Accession #: NP_570843.1

1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPGL 120
 FGGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFL HVLGLTKLNL 180
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRRLWL 300
 YDNHISLEPD NVFNSNLRQL VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
 FRMLANLQNI SLQNNRRLQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420
 YDNPWRCDS ILPLRNWLL NQPRLTGTDV PVCFSANVR GQSLIINVN VAVPSVHVPE 480
 VPSYPETPWY PDPSPYDPT SVSSTTELS PVEDYDLTT IQVTDERSV GMTOAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCKRSQA VLMQMKAPNE C

Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 1..954

1 11 21 31 41 51
 ATGTCTTCTG AGCAGAAGAG TCAGCACTGC AAGCCTGAGG AAGGCGTTGA GGCCCAAGAA 60
 GAGGCCCTGG GCCTGGTGGG TGCACAGGCT CCTACTACTG AGGAGCAGGA GGCTGCTGTC 120
 TCCTCTCTCT CTCCTCTGGT CCTGGCACC CTGGAGGAAG TGCCTGCTGC TGAGTCAGCA 180
 GGTCTCTCCC AGAGTCTCTCA GGGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACTTGC 240
 TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTCGCCT 300
 GACGCAGAGT CCTGTGTTCC AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
 CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
 ATCAAAAATT ACAAGCGCTG CTTTCTCTGT ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
 ATGATCTTTG GCATTGACGT GAAGGAAGTG GACCCCGCCA GCAACACCTA CACCTTGTC 540
 ACCTGCCTGG GCCTTTCTTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
 GGCCTTCTGA TAATCGTCTT GGGCACAAAT GCAATGGAGG GCGACAGCGC CTCTGAGGAG 660
 GAAATCTGGG AGGAGCTGGG TGTGATGGGG GTGTATGATG GGAGGGAGCA CACTGTCTAT 720
 GGGGAGCCCA GGAACCTGCT CACCCAAAGT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
 CAGGTACCCG GCAGTAATCC TGCAGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
 GAAACCAAGT ATGTGAAGT CCTGGAGCAT GTGGTCAGGG TCAATGCAAG AGTTGCGATT 900
 GCTACCCAT CCCTGCGTGA AGCAGCTTGT TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 288 Protein sequence:
 Protein Accession #: NP_002353.1

1 11 21 31 41 51
 MSSEQKSQHC KPEEGVEAQE EALGLVGAQA PTTEEQEAHV SSSSPLVFGT LEEVPAESA 60
 GPPQSPQAS ALPTTISFTC WRQPNEGSSS QEEEGPSTSP DAESLFREAL SNKVDELAHF 120
 LLRKYRAKEL VTKAEMLERV IKNYKRCFPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
 TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
 GEPRKLLTDQ WVQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNAVRI 300
 AYPRLREAA LEEEEGV

Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 46..1344

1 11 21 31 41 51
 CGGCGGCCGC GCCCTGGTTG GGTCCCCACT GCTCTCGGGG GCGCCATGGA CGAGGCCGTG 60
 GGCGACCTGA AGCAGGGCGCT TCCTCTGTGT GCGAGTGCAG CAACGGTCCA CGTGGAGGTG 120
 CATCAGCGCG GCAGCAGCAC TGCAGAGAAA GAAGACATAA ACCTGAGTGT TAGAAGGCTA 180
 CTCAACAGAC ATAATATTGT GTTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
 TTGACCAAGAA ATGTGCGAGT TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
 CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACCTTACA TTTTCCAGCT GAATGAAGAT 360
 GGCCCCAGCA GTGAAAATCT GGAGGAAGAG ACAGAAAACA TAATTCAGC AAATCACTGG 420
 GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC 480
 AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTACAGCAA GAACGTCAAC 540

AGCAACCTCA TCACCTGGAA CCGGGTGGTG CTGCTCCACG GTCCTCCTGG CACTGGAAAA 600
 ACATCCCTGT GTAAAGCGTT AGCCAGAGAA TTGACAATTA GACTTTCAAG CAGGTACCGA 660
 TATGGCCAAAT TAATTGAAAT AAACAGCCAC AGCCTCTTTT CTAAGTGGTT TTCGGAAAGT 720
 GGCAAGCTGG TAAACCAAGAT GTTTCAGAGG ATTACAGGAT TGATTGATGA TAAAGACGCC 780
 CTGGTGTGCG TGCTGATTGA TGAGGTGGAG AGTCTCAGAG CCGCCCGAAA TGCTGCAGG 840
 GCGGGCACCG AGCCATCAGA TGCCATCCGC GTGGTCAATG CTGTCTTGAC CCAAATTGAT 900
 CAGATTAAAA GGCAATCCAA TGTGTGATT CTGACCACTT CTAACATCAC CGAGAAGATC 960
 GACGTGGCCT TCGTGGACAG GGCTGACATC AAGCAGTACA TTGGGCCACC CTCTGCAGCA 1020
 GCCATCTTCA AAATCTACCT CTCTTGTGTT GAAGAATGA TGAAGTGTCA GATCATATAC 1080
 CCTCGCCAGC AGCTGCTGAC CCTCCGAGAG CTAGAGATGA TTGGCTTCAT TGAAAAACAC 1140
 GTGTCAAAAT TGAGCCTTCT TTTGAATGAC ATTTCAAGGA AGAGCGAGGG CCTCAGCGGC 1200
 CCGGTCCTGA GAAAACTCCC CTCTCTGGCT CATGCGCTGT ATGTCCAGGC CCCCACCGTC 1260
 ACCATAGAGG GGTTCCTCCA GGCCCTGTCT CTGGCAGTGG ACAAGCAGTT TGAAGAGAGA 1320
 AAGAAGCTTG CAGCTTACAT CTGATCCTGG GCTTCCCCAT CTGGTGCTTT TCCCATGGAG 1380
 AACACACAAC CAGTAAGTGA GGTGCCCCA CACAGCGTC TCCAGGGAA TCCCTTCTGC 1440
 AAACCAACG TTACTTAGAC TGCAAGCTAG AAAGCCACCA AGGCCAGGCT TTGTTAAAA 1500
 AAGTGTATT TATTATGTT GTTTTAAAT GCATACTGAG AGACAAACAT CTGTGCATT 1560
 TCACTGTTTG TAAAGATAA TTCAGATTGT TTGTCTCCTT GTGAAGAAC ATCGAAACCT 1620
 GTTTGTTCCC AGCCACCCCC CAGTGGATGG GATGCATAAT GCCAGCAAGT TTTGTTAAC 1680
 AGCAAAAAAG GAAGATTAAT GCAGGTGTTA TAGAAGCCAG AAGAGAAACT GTGTCAACCT 1740
 AAAGAAGCAT ATAATCATAG CATTAATAAT GCACACATTA CTCCAGGTGG AAGGTGGCAA 1800
 TTGCTTTCTG ATATCAGCTC GTTTGATTGA GTGCAAAAT GTTTTCAAGA CTATTAAATG 1860
 GATGTAAAAA AGCCTATTTC TACATTATAC CAACTGAGAA AAAAAAGTGC GGTAAAGTGT 1920
 TCTTTCTATA TAAATAATCA AGACATGGTC CCATTGTCAG GAAAAAGTGA GACTCTGAGT 1980
 GTTCCAGGGA AACACATGCT GGACATCCCT TGTAACCCGG TATGGGCGCC CTGCTATTGC 2040
 TGGGATGTT CTGCCCACGG TTTTGTGTT GCAATAACGT TATCACAATT CTAATGAGGA 2100
 TTCACATTAA TATAATATAA AATAAATAGG TCAGTTACTG GTCTCTTTCT GCCGAATGTT 2160
 ATGTTTGTCT TTTATCTCAC AGTAAATAA ATATAATTAA AAA

Seq ID NO: 290 Protein sequence:
 Protein Accession #: NP_004228

1 11 21 31 41 51
 MDEAVGDLKQ ALPCVAESPT VHVEVHQRGS STAKKEDINL SVRKLNNRHN IVFGDYTWTE 60
 FDEPFLTRNV QSVSIIDTEL KVHDSQPIDL SACTVALHIF QLNEDGPSSE NLEETENII 120
 AANHWWLPAA EFHGLWDSLV YDVEVKSLLH DYVMTLLFS DKNVNSNLIT WNRVLLHGP 180
 PGTKTSLCK ALAQKLIRL SSRYRYQLI EINSLSLFSK WFSSEGLVIT KMFQIQDLI 240
 DDKDALVFLV IDEVESLTA RNACRAGTEP SDAIRVVNAV LTQIDQIKRH SNVILITSN 300
 ITEKIDVAFV DRADIKYIG PPSAAAIKFI YLSCLSELMK CQIIYPRQL LTLRELEMIG 360
 FIENNVSKLS LLLNDISRKS EGLSGRVLRL LPFLAHLAYV QAPTVTIEGF LQALSIAVDK 420
 QFERKKLAA YI

Seq ID NO: 291 DNA sequence
 Nucleic Acid Accession #: NM_002658.1
 Coding sequence: 77-1372

1 11 21 31 41 51
 GTCCCCGAG CGCCGTCGCG CCTCCTGCCC GCAGGCCACC GAGGCCGCG CCGTCTAGCG 60
 CCCCGACCTC GCCACCATGA GAGCCCTGCT GCGCGGCTG CTCTCTGCG TCGTGGTGGT 120
 GAGCGACTCC AAAGGCAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCACATT CACTGGTGCA ACTGCCAAA 240
 GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
 TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
 CTCTGCCACT GTCTCTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420
 CCTGGGGAAA CATATTTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
 GCAGGTGGGC CTAAGCCGCG TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
 AAAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCAAGT GTGCCAAAAG CTCTGAGGCC 600
 CCGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACAGCCCTT GGTTTGCGGC 660
 CATCTACAGG AGGCACCGGG GGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
 CCCTTGCTGG GTGATCAGCG CCACACACTG CTTTATTGAT TACCCAAAGA AGGAGGACTA 780
 CATCGTCTAC CTGGGTGCTC CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTTGA 840
 GGTGAAAAAC CTCATCCTAC ACAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
 CATTGCCCTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
 ACAGACCATC TGCCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACA GCTGTGAGAT 1020
 CACTGGCTTT GGAAGAAGGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAATGAC 1080
 TGTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
 CACCACAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGAGA 1200
 CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGCTG ACTTTGACTG GAATTGTGAG 1260
 CTGGGGCGGT GGTATGTCCT TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACAATT 1320
 CTTACCCCTG ATCCGAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CCGGCAACAC CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
 TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCTGTGG 1500
 CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCCTGGT GCTGGCTGCC 1560
 CAGACCTCTT GGCCAGGATG GAGGGGTGGT CTTGACTCAA CATGTTACTG ACCAGCAACT 1620
 TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAATAAGGG CAGGGCATCT CTTGTGCATG 1680
 GGCTCGAAGG GAGAGCCAGC TCCCCGACC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
 AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGA CTTGAGGGA GGGCTCTGAT 1860
 ATTCCATGAA TGTATCAGA AATATATATG TGTGTGATG TTTGCACAT TGTGTGTGG 1920
 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATT TTAAGTCTAA ATATTCTCT 1980
 AAAGTGTGCT GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040
 CTGGGGCTC CTGCTGCCCC CACGTGACAG TGCCCTGGGA TGTACTTATT CTCGACATG 2100
 ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
 ATCCCTTCTT TTAGCCTTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
 AACTGAATA TTTATTTTCT ACTATTTTAA TTTATATTTT TGTAAATTTA AATAAAGTG 2280

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #: NP_002649.1

5

1	11	21	31	41	51	
MRALLARLLL	CVLVVSQSKG	SNELHQVPSN	CDCLNGGTCV	SNKYFSNIHW	CNCPKKGFGQ	60
HCEIDKSKTC	YEGNGHFYRG	KASTDTMGRP	CLPWN SATVL	QQTYHAHRSD	ALQLGLGKHN	120
YCRNPDNRRR	PWCYVQVGLK	PLVQECMVHD	CADGKKPSSP	PEELKFQCGQ	KTLLRPRFKII	180
GGFEFTIENQ	PWFAAIYRRH	RGGSVTVYCG	GSLISPCVI	SATHCIDYF	KKEDYIVVLG	240
RSRLNSNTQG	EMKFEVENLI	LHKDYSADTL	AHNDIALLLK	IRSKEGRCQA	PSRTIQITICL	300
PSMYNDPQFG	TSCITGFGK	ENSTDYLYPE	QLKMTVVKLI	SHRECOQPHY	YGSEVTTKML	360
CAADPQWKTD	SCQGDSSGGL	VCSLQGRMTL	TGIVSWGRGC	ALKDKPGVYT	RVSHFLPWIR	420
SHTKEENGLA	L					

Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

20

1	11	21	31	41	51	
GGCAGGAGGC	TGAGTGTCCG	TCTCGCGCCC	GGAAGCGGGC	GACCGCCGTC	AGCCCGGAGG	60
AGGAGGAGGA	GGAGGAGGAG	GAGGGGGCGG	CCATGGGGCT	GCTGTCCCAG	GGCTCGCCGC	120
TGAGCTGGGA	GGAAACCAAG	CGCCATGCCG	ACCACGTGCG	GCGGCACGGG	ATCCTCCAGT	180
TCCGTGCACAT	CTACCAAGCC	GTCAAGGACC	GGCACAAGGA	CGTTCTCAAG	TGGGGCGATG	240
AGGTGGAATA	CATGTTGGTA	TCTTTTGATC	ATGAAATAAA	AAAAGTCGGG	TTGGTCTGT	300
CTGGGGAGAA	AGTCTCTGAA	ACTCTGCAAG	AGAAGGGGGA	AAGGACAAAC	CCAAACCATC	360
CTACCCCTTG	GAGACCAAGG	TATGGGAGTT	ACATGATTGA	AGGGACACCA	GGACAGCCCT	420
ACGGAGGAAC	AATGTCGAG	TTCAATACAG	TTGAGGCCAA	CATGCGAAAA	CGCCGGAAGG	480
AGGCTACTTC	TATATTAGAA	GAATAATCAG	CTCTTTGCAC	AATAACTTCA	TTTCCAGAT	540
TAGGCTGTCC	TGGGTTTACA	CTGCCGAGG	TCAAACCCAA	CCCAGTGGAA	GGAGGAGCTT	600
CCAAGTCCCT	CTTCTTTCCA	GATGAAGCAA	TAAACAAGCA	CCCTCGCTTC	AGTACCTTAA	660
CAAGAAATAT	CCGACATAGG	AGAGGAGAAA	AGGTTGTGAT	CAATGTACCA	ATATTAAAGG	720
ACAAGAATAC	ACCATCTCCA	TTTATAGAAA	CATTTACTGA	GGATGATGAA	GCTTCAAGGG	780
CTTCTAAGCC	GGATCATATT	TACATGGATG	CCATGGGATT	TGGAATGGGC	AATTGCTGTC	840
TCCAGGTGAC	ATCCAAGCC	TGCAGTATAT	CTGAGGCCAG	ATACCTTTAT	GATCAGTTGG	900
CTACTATCTG	TCCAATTGTT	ATGGCTTTGA	GTGCTGCATC	TCCCTTTTAC	CGAGGCTATG	960
TGTGAGACAT	TGATTGTGCG	TGGGGAGTGA	TTTCTGCATC	TGTAGATGAT	AGAACTCGGG	1020
AGGAGCGAGG	ACTGGAGCCA	TTGAAGAACA	ATAACTATAG	GATCAGTAAA	TCCCGATATG	1080
ACTCAATAGA	CAGCTATTTA	TCTAAGTGTG	GTGAGAAATA	TAATGACATC	GACTTGACGA	1140
TAGATAAAGA	GATCTAGCAA	CAGCTGTGTC	AGGAAGGCAT	TGATCATCTC	CTGGCCCAGC	1200
ATGTTGCTCA	TCTCTTTATT	AGAGACCCAC	TGACACTGTT	TGAAGAGAAA	ATACACCTGG	1260
ATGATGCTAA	TGAGTCTGAC	CATTTTGAGA	ATATTCAATC	CACAAATTGG	CAGACAATGA	1320
GATTTAAGCC	CCCTCCTCCA	AACTCAGACA	TTGGATGGAG	AGTAGAATTT	CGACCCATGG	1380
AGGTGCAATT	AACAGACTTT	GAGAACTCTG	CCTATGTGGT	GTTTGTGGTA	CTGCTCACA	1440
GAGTGATCCT	TTCTACAAA	TTGGATTTTC	TCATTCCACT	GTCAAAGGTT	GATGAGAAAC	1500
TGAAGGTAGC	ACAGAAAAGA	GATGCTGTCT	TGCAGGGAAT	GTTTTATTTC	AGGAAAGATA	1560
TTTGCAAGG	TGGCAATGCA	GTGGTGGATG	GTTGTGGCAA	GGCCAGAAAC	AGCACGGAGC	1620
TGCTGTCAGA	GGAGTACACC	CTCATGAGCA	TAGACACCAT	CATCAATGGG	AAGGAAGGTG	1680
TGTTTCTCTG	ACTGATCCCA	ATTCTGAACT	CTTACCTTGA	AAACATGGAA	GTGGATGTGG	1740
ACACAGATG	TAGTATTCTG	AACTACCTAA	AGCTAATTAA	GAAGAGAGCA	TCTGGAGAAC	1800
TAATGACAGT	TGCCAGATGG	ATGAGGGAGT	TTATCGCAAA	CCATCCTGAC	TACAAGCAAG	1860
ACAGTGTGAT	AACGTGATGA	ATGAATTATA	GCCTTATTTC	GAAGTGTAAC	CAAAATTGCAA	1920
ATGAATTATG	TGAATGCCCA	GAGTTACTTG	GATCAGCATT	TAGGAAAGTA	AAATATAGTG	1980
GAAGTAAAC	TGACTCATCC	AACTAGACAT	TCTACAGAAA	GAAAAATGCA	TTATTGACGA	2040
ACTGGCTACA	GTACCATGCC	TCTCAGCCCG	TGTGTATAAT	ATGAAGACCA	AATGATAGAA	2100
CTGTACTGTT	TTCTGGGCCA	GTGAGCCAGA	AATTGATTAA	GGCTTTCTTT	GGTAGGTAAG	2160
TCTAGAGTTT	ATACAGTGTA	CATGTACATA	GTAAAGTATT	TTTGATTAAAC	AATGTATTTT	2220
AATAACATAT	CTAAGTCTAT	CATGAACCTG	CTTGACATTT	TTTAAATCTT	TACTCTGGAG	2280
CAACCTACTG	TCTAAGCAGT	TTTGTAATG	TACTGGTAAT	TGTACAATAC	TTGCATTCCA	2340
GAGTTAAAT	GTTTACTGTA	AATTTTGTIT	CTTTTAAAGA	CTACCTGGGA	CCTGATTTAT	2400
TGAAATTTT	CTCTTTAAAA	ACATTTTCTC	TCGTTAATTT	TCCTTTGTCA	TTTCTTTTGT	2460
TGTCTACATT	AAATCACTTG	AATCCATTGA	AAGTGCTTCA	AGGGTAATCT	TGGGTTTCTA	2520
GCACCTTATC	TATGATGTTT	CTTTTGCAAT	TGGAATAATC	ACTTGGTCAC	CTTGCCCCAA	2580
GCITTTCCCT	CTGAATAAAT	ACCCATTGAA	CTCTGAAAAA	AAAAAATAAA	AAAA	

Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

70

1	11	21	31	41	51	
MGLLSQGSPL	SWEETKRHAD	HVRRHGILQF	LHIYHAVKDR	HKDVLKNGDE	VEYMLVSFDH	60
ENKVKRLVLS	GEKULETLQE	KGERTNPNHP	TLWRPEYGSY	MIEGTPGPQY	GGTMSFNTV	120
ENMRKRREK	ATSIILEENQA	LCTITSPRL	GCPGFTLPEV	KPNPVEGGAS	KSLFFPDEAI	180
NKHPRFSTLT	RNIRHRRGEK	VVINVPFKD	KNTSPFFIET	FTEDDEASRA	SKPDHIYMDA	240
MGFGMGNCC	QVTFQACIS	EARYLYDQLA	TICPIVMALS	AASPFYRGYV	SDIDCRWGI	300
SASVDDRTRE	ERGLEPLKNN	NYRISKSRYP	SIDSYSKCG	EKYNDIDLTI	DKEIYEQLLQ	360
EGIDHLLAQH	VAHLFIRDPL	TLFEKIHLD	DANESDHPEN	IQSTNWQTM	FKPPFPNSDI	420
GWRVEFRPME	VQLTDFENSA	YGVFVLLTR	VILSYKLDPL	IPLSKVDENM	KVAQKRDAVL	480
QGMFYFRKDI	CKGNAVVDG	CGKAQNSTEL	AABEYTLMSI	DTIINGKEGV	FPGLIPILNS	540
YLENMEVDVD	TRCSILNLYK	LIKKRASGEL	MTVARWMREF	IANHPDYKQD	SVITDEMNY	600
LILKCNQIAN	ELCECPPELLG	SAFRKVKYSG	SKTDDSN			

Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

```
5 1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
10 CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGCAAGG 360
AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
ATGACAGGAC ATGCTATTCC ACCAGCCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
15 TTCAGCAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC 600
CAACAGAGAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
20 AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
CACACCCCAA ATGCATAATC TCATTAAATG TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAATATGC 960
CTTCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTCCCAA AGCATTTTAT 1020
25 TTGAAAGGAT AACTTGTGTT TTGGTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
```

Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

```
30 1 11 21 31 41 51
| | | | |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVT SPSGDDLECR ETASSPKSQR 120
35 EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDFVKH 180
LKKKLKRLMI
```

Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```
40 1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
45 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGCAAGG 360
50 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
ATGACAGGAC ATGCTATTCC ACCAGCCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
TTCAGCAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAAGC 600
CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
55 CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
AAACGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
CACACCCCAA ATGCATAATC TCATTAAATG TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960
60 CTTCAGAGG CTAAGAAATT TCTGTTAGTA AAAGATGTTC TTTTCCCAA AGCGTTTAT 1020
TTGAAAGGAT AACTTGTGTT TTGGTTATT TGTATTCCCA CCTGTGCTGG TAGATATTAT 1080
TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A
```

Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

```
65 1 11 21 31 41 51
| | | | |
MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
70 GHAIPPSQLD SQIDDFTGFS KDRMMQKPGS NAPVGGNVT SPSGDDLECR ETASSPKSQQ 120
EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDFVKH 180
LKKKLKRLMI
```

Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```
75 1 11 21 31 41 51
| | | | |
AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
80 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
CCTAGGGGGC ACATTTCCCA CAACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGCAAGG 360
85 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
```


TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGGCC 600
 AACCAAGAAAT TAATGCTGAT ATAAAAACGTA AATTAGTGAA GGAACCTCGA TGGTTGGAC 660
 AAAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACCTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CATTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTATT 1020
 TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKAKKLMT 60
 GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQ 120
 EINADIKRKL VKELRCVQKG YEKIFEMLEG VQPTAVRKR FPESIIKEAA RCMRRDFVKH 180
 LKKLKRMI

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-812

1 11 21 31 41 51
 AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
 GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCAGGTGC 120
 CCTAGGGGGC ACATTTCCCA CACTCCCGAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
 GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
 TCAGCAAAGA TGGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
 CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAGGCC 600
 AACCAAGAAAT TAATGCTGAT ATAAATGTC AAGTAGTGAA GGAAATCCGA TGCCTTGGAC 660
 AATATGAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
 GATTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAG TTTGTTAAGC 780
 ACCTTAAGAA GAAACTGAAA CGTATGATTT GAGAATACTT GTCCCTGGAG GATTATCACA 840
 CCCCAATGC ATATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTCT 900
 ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
 CAGAGGCTAA GAAATTTCTG TTAGTAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTGA 1020
 AAGGATAACT TGTGTTTGG TTATTTTGTA TTCCACCTG TGCTGTTAGA TATTATTAA 1080
 CCATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
 MTDKTEKVV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
 GHAIPPSQLD SQIDDFTFGS KDGMMQKPGS NAPVGGNVTS NFSGDDLECR GIASSPKSQ 120
 EINADIKQV VKELRCVQGY EKIFEMLEGV QGPTAVRKR FPESIIKEAAR CMRRDFVKHL 180
 KKKLKRMI

Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

1 11 21 31 41 51
 AGTGTTCGGC TGGGACAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
 GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCCA TGCACATCAC TCCAGATGC 120
 CCTAGGGGGC ACATTTCCCA CACTCCCGAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
 GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCGG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
 TCAGCAAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAGGCC 600
 AACCAAGAAAT TAATGCTGAT ATAAACGTA AATTAGTGAA GGAACCTCGA TGGTTGGAC 660
 AAAAAATATGA AAAAATCTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA AGGATAACTG AAACGTATGA TTTGAGAATA CTTGTCCCTG GAGGATTATC 840
 ACACCCCAAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTATT 1020
 TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MTDKTEKVAV	DPETVFKRPR	ECDSPSYQKR	QRMALLARKQ	GAGDSLIIAGS	AMSKAKKLMT	60
GHAIPPSQLD	SQIDDFTFGS	KDRMMQKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQQ	120
5 EINADIKRKL	VKELRCVQK	YEKIFEMLEG	VQGPTAVRKR	FFESIIEKAA	RCMRDFVKH	180
LKKKLRMI						

Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

1	11	21	31	41	51	
CGTGGAGGCA	GCTAGCCGCA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
15 CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAGGTTGA	CCCCAAGAAA	CCAAAGGGCA	120
AGATGTCGCG	TTATGCTTTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	AAGAAAAACC	180
CAGAGGTCCC	TGTCAAATTTT	GCGGAATTTT	CCAAGAAGTG	CTCTGAGAGG	TGGAAGACGA	240
TGTCGCGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	GTGCGCTATG	300
20 ATCGGGAAAT	GAAGGATAT	GGACCAAGTA	AGGGAGGCAA	GAAGAAGAAG	GATCCTAATG	360
CTCCCAAAG	GCCACCGTCT	GGATCTTCC	TGTTCTGTTC	AGAATTCGCG	CCCAAGATCA	420
AATCCACAAA	CCCCCGCATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480
ATAATTAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	CTGAAGGAGA	540
AGTATGAGAA	GGATGTTGCT	GACTATAAGT	CGAAAGGAAA	GTTTGTATGGT	GCAAAGGGTC	600
25 CTGCTAAAGT	TGCCCGGAAA	AAGGTGGAAG	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG	660
AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTTT	ATCTGTCTCC	TTGTGAATAC	720
TTAGAGTAGG	GGAGCGCCGT	AATTGACACA	TCTCTTATTT	GAGAAGTGTC	TGTTGCCCTC	780
ATTAGGTTTA	ATTACAAAT	TTGATCACGA	TCATATTGTA	GTCTCTCAA	GTGCTCTAGA	840
AATTGTCAGT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCTGA	AACTGTATCA	900
30 AAGTTGTACA	TATTTCCAAA	CATTTTTTAA	ATGAAAAGGC	ACTCTCGTGT	TCTCCTCACT	960
CTGTGCACCT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	TTTTCTTTTT	1020
ATTTGTAAGG	TGGTGGTAAC	TATGGTTATT	GGCTAGAAAT	CCTGAGTTTT	CAACTGTATA	1080
TATCTATAGT	TTGTAAAAG	AACAAAACAA	CGAGACAAA	CCCTTGATGC	TCCTTGCTCG	1140
GGGTTGAGGC	TGTGGGGAAG	ATGCCCTTTG	GGAGAGGCTG	TAGCTCAGGG	CGTGCACTGT	1200
35 GAGGCTGGAC	CTGTTGACTC	TGCAGGGGGC	ATCCATTTAG	CTTCAGGTTG	TCTTGTCTCT	1260
GTATATAGTG	ACATAGCATT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	GCTCAGCTGG	1320
CATGAGAATA	TTTTTTTTTT	TAAAGTCCGT	AGTTTTTAAA	CTGTTTGT	TTAAACAAAC	1380
TATAGAACTC	TTCATTGTCA	GCAAAGCAAA	GAGTCACTGC	ATCAATGAAA	GTTCAAGAAC	1440
CTCCTGTACT	TAAACACGAT	TCGCAACGTT	CTGTTATTTT	TTTTGTATGT	TTAGAATGCT	1500
40 GAAATGTTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTTA	AAACTCTTCT	CTAATTATAAC	1560
AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCACTC	CATTGTATTT	GGAGACTGGC	1620
CTCCCTATAA	ATGTGTAGC	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	AGGGCTGAGA	1680
TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGT	TGTGTCTGAG	TGGCATTTCAG	1740
ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1800
45 AGGAAGGTGG	GTGTTTAGGA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	ACCTCCACCC	1860
CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
AAATTAAGGC	CTTATTTT	TTCTCTTTCA	CCCCACCCCC	CCGTGCTCCT	GGCAGATATC	1980
CAATTTATTG	TGTTGGCCAA	CATTTGGGGT	CTTGAGCCTG	CTGCTGGTCT	CCTGGATGCC	2040
AGTGAGGGTA	TGTGGGATGC	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	TTGCTCCTAC	2100
50 TTGGAACAC	CAAAACACCC	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	CCTGAGCTAT	2160
AGGGCAGGCT	AATGGAATCA	ACCATTCTG	AGCACTAAAT	GTATCATGAA	AAGTTGAATG	2220
GCCTGCTCAT	AAGTTTAGCT	CATTCACTGG	AAATGTAGAT	TGATGTTCAA	TGTTAAACTG	2280
GAAGGAGCTT	GGTTTGTGTG	TCACTGGTTA	TATTAGTGGG	TAGTGAACA	TTTTATCCAG	2340
GTGAGGTTGA	GGGAGATGG	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	ATTTTGAAGG	2400
55 CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	TGTGTTGTGG	2460
GTGAGTGTG	CTATTGCCCA	GCATTAAATAT	TTGGGTGTGT	ATGTTTGAGG	CTATGAACA	2520
CGCAGGAGTG	TTTTTGTGCT	ATTAAATTTA	AGAGAAAGCA	GCTTTTCT	AAAATTCCT	2580
GTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCGCG	CCTGTGCGGT	CCTGGATGAG	2640
TACGAGTTAT	GGTCACGGTC	ACAGCCTGAT	CTCTTATGTG	TTCATAGCCA	TTGCTCTCC	2700
60 CATCAGAACT	GTTTGTCTCT	AATGTGTTC	TCTAGTTCTA	GAAAAAGACC	ACTAATTTAA	2760
AAAACTCGGT	TGTGAGGTTT	GCCCAGAGGC	ACTTGTTC	GAATTTCCCC	TCCTGCTTCA	2820
GCCATGTCTT	TGTCACCTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	TCGTGATGTG	2880
CTAGGCCAAG	ATTCCGGGAGC	TGTTGCCAGC	CTCGTCAAA	ATGGAAGAGA	AACAACCTGC	2940
GGTCAAAAGG	GAGTGATTG	TTAAGTGGT	CGCGTCTATC	TCATAACTAG	ATGTACCAAC	3000
65 CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAAGTAG	CTAAGCAGAA	3060
GTGGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCAA	ACATTGAGTT	TTAAGAGGC	3120
TGTCAAGTTG	AGGCCACTTG	GTCATTAGC	TGGGGCAGCA	AGATCACTAC	TCAACGTTTT	3180
CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	AATAATGCCC	TAGTTTCTCT	GAGATGATGT	3240
AAGTGGCATG	ATGTTACCTA	AGGCTTAGGC	TTAGCTTGAT	TTCTGGGCCC	ACTGTCTGTG	3300
70 TTCTTAAGAT	GCCAACCTGT	TGCTTTTTTT	TTTTTTTCC	CCCATTAAAA	AGGATAGTAC	3360
CTACTCCCTC	TAACCACTCT	ACCCATTCT	TGAATGACAT	TTTATCTCT	GGAAAGAACA	3420
AGGCTGTGAT	GTAGTGACTA	TTGTCTGTGT	CTCCTGTGTG	TGTCTGTCT	TGTCACAAAT	3480
GTATTTGGGG	ACGTTGGATG	CATTCAATTT	CTGTAATAAA	G		

Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

1	11	21	31	41	51	
MAKGDPPKPK	GKMSAYAFFV	QTCREEHKKK	NPEVPVNFAB	FSKKCSERWK	TMSGKEKSKP	60
80 DEMAKADKVR	YDREMKDYG	AKGGKKKKDP	NAPKRPSPGF	FLPCSEFRPK	IKSTNPGISI	120
GDVAKLKGEM	WNLNLDSEKQ	PYITKAAALK	EKYEKDVADY	KSKGKFDGAK	GPAKVARKKV	180
EEEEEEEEEE	EEEEEEEEEE					

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

	1	11	21	31	41	51	
	ATGGGTACTA	GGAAAAAAGT	TCATGCATT	GTCCGTGTCA	AACCCACOGA	TGACTTTGCT	60
5	CATGAAATGA	TCAGATACGG	AGATGACAAA	AGAAGCATTG	ATATTCACCT	AAAAAAGAC	120
	ATTCGGAGAG	GAGTTGTCAA	TAAACCAACAG	ACAGACTGGT	CGTTTAAGT	GGATGGAGTT	180
	TTCAACGATG	CCTCCACGGA	CTTGGTTTAT	GAGACAGTTG	CAAAGGATGT	GGTTTCTCAG	240
	CCCTCGATG	GCTATAATGG	CACCATCATG	TGTTATGGGC	AGACGGGAGC	TGGCAAGACA	300
10	ACACCATGA	TGGGGGCAAC	TGAGAATTAC	AAGCACCGGG	GGATCCTCCC	TCGTGCCCTG	360
	AGCAGGTTT	TTAGGATGAT	CGAAGAACGC	CCCACACATG	CCATCACTGT	GGGTGTTTCC	420
	ACTTGGAAA	TCTATAATGA	GAGCCTGTTT	GATCTCCTGT	CCACTCTGCC	CTATGTTGGA	480
	CCTCAGTCA	CACCAATGAC	CATCGTGGAA	AACCTCAAG	GAGTCTTCAT	TAAGGGCTTG	540
	CAGTTCAAC	TCACAAGTCA	GGAGGAGGAT	GCATTCAAGC	TCCTTTTGA	GGGTGAGACC	600
15	ACAGGATTA	TAGCCTCCCA	CATATGAAC	AAAACTCTT	CCAGATCACA	CTGCATTTTC	660
	CCATCTACT	TAGAGGCCCA	TTCCCGGACC	TTATCAGAGG	AAAAGTACAT	CACCTCCAAA	720
	TTAACTTGG	TGGATCTGGC	AGGCTCAGAG	AGGCTGGGGA	AGTCTGGGTC	TGAGGGCCAA	780
	TCCTGAAGG	AAGCCACCTA	CATCAACAAA	TCGCTCTCAT	TCCTGGAGCA	GGCCATCATT	840
	CCCTTGGGG	ACCAGAAGCG	GGACCACATC	CCCTTTCGGC	AGTGCAAGCT	CACCCACGCT	900
20	TGAAGGACT	CGTTAGGGGG	AACTGCAAT	ATGGTCTCG	TGACAAACAT	CTATGGAGAA	960
	CTGCCAGT	TAGAAGAAC	GCTATCTTCA	CTGAGATTG	CCAGCAGGAT	GAAGCTAGTC	1020
	CCACTGAGC	CTGCCATCAA	TGAAAAGTAT	GATGCTGAGA	GAATGGTCAA	GAACCTGGAG	1080
	AGGAAGTAG	CACCTACTCA	GCAGGAGCTG	GCTATCCATG	ACAGCCTGAC	CAACCGCACC	1140
	TTGTGACCT	ATGACCCCAT	GGATGAAATC	CAGATTGCTG	AGATCAACTC	CCAGGTGCGG	1200
25	GGTACCTGG	AGGGGACACT	GGACGAGATC	GACATAATCA	GCCTTAGACA	GATCAAGGAG	1260
	TGTTCAACC	AGTTCCGGGT	GGTCTGAGC	CAACAGGAAC	AGGAAGTGGG	GTCCACTTTG	1320
	GCAGGAAGT	ACACCTCAT	TGACAGGAAT	GACTTTGCAG	CCATTCTGCG	TATCCAGAAG	1380
	CGGGGCTTG	TGGATGTTGA	TGGCCACCTA	GTGGGTGAGC	CTGAAGGACA	AAACTTTGGA	1440
	TCGGAGTCG	CCCCTTTCTC	TACCAACCT	GGGAAGAAAG	CCAAGTCCAA	GAAGACATTC	1500
30	AAGAGCCAC	TGAGGCCCGA	CACCCACCCC	TCCAAACCCG	TGGCCTTTGA	GGAGTTTAAG	1560
	ATGAGCAAG	GTAGTGAGAT	CAACCGAATT	TTCAAAGAAA	ACAATCCCAT	CTTGAATGAA	1620
	GGAGGAAAA	GGGCCAGCGA	GACCACACAG	CACATCAATG	CCATCAAGCG	GGAGATTGAT	1680
	TGACCAAGG	AGGCCCTGAA	TTTCCAGAAAG	TCACTACGGG	AGAAGCAAGG	CAAGTACGAA	1740
	ACAAGGGGC	TGATGATCAT	CGATGAGGAA	GAATTCTCTG	TGATCCTCAA	GCTCAAAGAC	1800
35	TCAAGAAGC	AGTACCGCAG	CGAGTACCAG	GACCTGCGTG	ACCTCAGGGC	TGAGATCCAG	1860
	ATTGCCAGC	ACCTAGTGGG	TCAGTGTGCG	CACCGCCTGC	TCATGGAATT	TGACATCTGG	1920
	ACAATGAGT	CCTTTGTGAT	CCCTGAGGAC	ATGCAGATGG	CACTGAAGCC	AGGCGGCAGC	1980
	TCCGGCCAG	GCATGGTCCC	TGTGAACAGG	ATTGTGTCTC	TGGGAGAAGA	TGACCAAGGAC	2040
	AATTCAGCC	AGCTGCAGCA	GAGGGTGCTT	CCTGAGGGCC	CTGATTCAT	CTCCTTCTAC	2100
40	ATGCCAAAG	TCAAGATAGA	GCAGAAGCAT	AATTACTTGA	AAACCATGAT	GGGCTCCAG	2160
	AGGCACATA	GAAAAATG					

Seq ID NO: 308 Protein sequence:
Protein Accession #: NP_071737

	1	11	21	31	41	51	
	MGTRKKVHAF	VRVPTDDFA	HEMIRYDDK	RSIDIHLKID	IRRGVVNNQ	TDWSFKLDGV	60
	LHDASQDLVY	ETVAKDVVSQ	ALDGYNGTIM	CYQGTGAGKT	YTMGATENY	KHRGILPRAL	120
50	QQVFRMIEER	PTHAITVRVS	YLEIYNESLF	DLLSTLPYVG	PSVTPMTIVE	NPQGVFIKGL	180
	SVHLTSQEDD	AFSLFPEGET	NRIIASHTMN	KNSSRSHCIF	TIYLEAHSRT	LSEEEKYITSK	240
	INLVDLAGE	RLKSGSEGG	VLKEATYINK	SLSFLEQAI	ALGDQKRDHI	PFRQCKLTHA	300
	LKDSLGNLGN	MVLVTNIYGE	AAQLEETLSS	LRFASRMKLV	TTEPAINEKY	DAERMVKNLE	360
	KELALLKQEL	AIHDSLNTNR	FVTYDPMDEI	QIAEINSQVR	RYLEGLTDEI	DIISLRQIKE	420
55	VFNQFVRVLS	QQEQVESTL	RRKYTLIDRN	DFAAISAIQK	AGLVDVDGHL	VGEPEGQNFQ	480
	LGVAPFSTKP	GKKAKSKKTP	KEPLRPDTPP	SKPVAFEEFK	NEQGSSEINRI	FKENKSILNE	540
	RRKRASETQ	HINAIKREID	VTKEALNFQK	SLREKQGYE	NKGLMIIDEE	EPLILKLKD	600
	LKKQYRSEYQ	DLRLDRAEQ	YQCHLVQDQR	HRLLMEFDIW	YNESFVIPED	MQMALKPGGS	660
	IRPGMVPVNR	IVSLGEDDDQ	KFSQLQQRVL	PEGPDSISFY	NAKVKIEQKH	NYLKTMMGLQ	720
60	QAHRK						

Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
65	TTTTTTTTT	TTTTTTTAA	TGCTGCTGT	CATGCTCTGT	CTACCAGGCT	GAATTTCCAA	60
	AAATTTCTGC	ATAGCAATTT	TAGCCAAAAC	TATATATGTT	CTGGGGAGGA	TAGGCATAGG	120
	CACATTGAAG	ACCAAAGGAA	AGAGTGAAGA	AGTGTAGTTG	GGTCATTGTG	AATGGATGTT	180
70	TAGATTGTCA	AGAAAAGTGG	GCCAGAGGCC	CCACCTCACA	CTAGGACGGC	AATTGCCTCT	240
	CATTAGTATC	TCAGGCACCA	TGGGTCTTAT	TTGGTGTGAT	AAGAAACACC	CTCAACAAAG	300
	TAATGAACCC	TCAGCCTCCA	GCTTCTCTTC	TTGGGGATTC	TTCTTAGGGC	CTCCTTTTTC	360
	CTTTTATGTT	TCCAGTACCC	TGAATTTCTT	ATTCCCATCC	CCCATTAATA	TCTGCTTCAA	420
75	AGAAAAACA	AGAAGGACAC	ATTCATTTA	AGATCCAAAT	GAATGATAAG	AGCTTAAAC	480
	ATTATACTTA	TCAGTATTAT	TTGCATTTTT	ATAGAAACCA	AAACCATATT	TCAACCAAC	

Seq ID NO: 310 DNA sequence
Nucleic Acid Accession #: NM_018622.2
Coding sequence: 1-1140

	1	11	21	31	41	51	
80	ATGGCGTGGC	GAGGCTGGGC	GCAGAGAGGC	TGGGGCTGCG	GCCAGGCGTG	GGGTGCGTGG	60
	GTGGGCGGGC	CGACTCTGGA	GGAGCTCACT	GCGGTCTTAA	CCCCGCGGCA	GCTCCTCGGA	120
85	CGCAGGTTTA	ACTCTTTTAT	TCAACAAAAA	TGCGGATTCA	GAAAAGCACC	CAGGAAGGTT	180
	GAACCTCGAA	GATCAGACCC	AGGGACAAGT	GGTGAAGCAT	ACAAGAGAAG	TGCTTTGATT	240
	CCTCCTGTGG	AAGAAACAGT	CTTTTATCCT	TCTCCCTATC	CTATAAGGAG	TCTCATAAAA	300
	CCTTATTTT	TTACTGTGGG	GTTTACAGGC	TGTGCATTTG	GATCAGCTGC	TATTTGGCAA	360

TATGAATCAC TGAAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTTG 420
 GATAGCATAA GACCACAAAA AGAAGGAGAC TTCAGAAAGG AGATTAAACA GTGGTGAAT 480
 AACCTAAGTG ATGGCCAGCG GACTGTGACA GGTATTATAG CTGCAATGT CCTGTATTTC 540
 5 TGTTTATGGA GAGTACCTTC TCTGCAGCG ACAATGATCA GATATTTTAC ATCGAATCCA 600
 GCCTCAAGAGG TCCTTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCCTTATTT 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTTCATGC AGTGTACCTA TCTGCAGGTG TTATTTCCAA TTTTGTCACT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGCCATC 840
 10 ATGACAGTCC TCGCAGCTGT CTGCACTAAG ATCCCAGAAAG GGAGGCTTGC CATTATTTTC 900
 CTTCOGATGT TCACGTTTCA AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA 960
 GCAGGAATGA TCCTGGGATG GAAATTTTTT GATCATGCGG CACATCTTGG GGGAGCTCTT 1020
 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACCTGATT GGAAGAACAG GGAGCCGCTA 1080
 GTGAAATCT GGCATGAAAT AAGGACTAAT GGCCCCAAAA AAGGAGGTGG CTCTAAGTAA

Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

1 11 21 31 41 51
 MAWRGWAQRG WCGCQWANGS VGGRSCEELT AVLTPPQLLG RRFNFFIQK CGFRKAPRKV 60
 EPRRSDPGTS GEAYKRSALI PPVBETVFYP SPYPIRSLIK PLFFTGVFTG CAFGSAAIWQ 120
 YESLKSRLVQS YFDGIKADWL DSIKRPQKEGD FRKEINKWNW NLSDGQRTVT GILAAINVLF 180
 20 CLWRVPSLQR TMIRYFTSNP ASKVLCSPLM LSTFHFSLF HMAANMYVLW SFSSSIVNLI 240
 25 GQEQFMAYVL SAGVISNFVS YLGKVATGRY GPSLGASGAI MTVLAAVCTK IPEGRILAIIF 300
 LPMFTTFTAGN ALKAIIMADT AGMILGWKFF DHAHLGGAL FGIWYVYGH ELIWKNNREPL 360
 VKIWEHIRTN GPKKGGGSK

Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

1 11 21 31 41 51
 CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG 60
 CACAGGTCTC TTCTGTGTTT GACTGTCTT ACCCGGGGGA GGCAGTGACG CCAGCTGCAA 120
 GCCCCACAGT GAAGAATCAT TGAGTCAAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 40 GTAAAGCCAT AGAGATGGCC TGTCTTGGG AATTTCTGTT CAAGACCAA TTCCACCAAGT 240
 ATGCAATGAA TGGGGAAGAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CCACTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCCGAGCC CCTCGTGGAG ACGGGAAGA AGTCTCCAGA ATCTCTGGTC AAGCTGGATG 420
 CAACCCCAT TTCTCCCCA CGCATGTGA GGATCAAAA CTGGGCGAGC GGGATGACTT 480
 45 TCCAGACAC ACTTCACCAT AAGGCCAAAG GGATTTTAACT TTGCAGGTCC AAATCTTGCC 540
 TGGGGTCCAT TATGACTCCC AAAAGTTTGA CCAGAGGACC CAGGGACAAG CCTACCCCTC 600
 CAGATGAGCT TCTACCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG 660
 AGGCAAAAT AGAGGAACAT CTGGCCAGGG TGGAAAGCGT AACAAAGGAG ATAGAAACAA 720
 CAGTAACCTA CCAACTGACG GGAGATGAGC TCATCTTCGC CACCAAGCAG GCCTGGCGCA 780
 50 ATGCCCCAGC CTGCATTGGG AGGATCCAGT GGTCCAACT GCAGGTCTTC GATGCCCGCA 840
 GCTGTTCCAC TGCCCGGGAA ATGTTTGAAC ACATCTGCAG ACACGTGCGT TACTCCACCA 900
 ACAATGGCAA CATCAGGTGC GCCATCACCG TGTTCCCCA GCGAGTGAT GGCAAGCAG 960
 ACTTCGGGT GTGGAAATGCT CAGCTCATCC GCTATGCTGG CTACCAGATG CCAGATGGCA 1020
 GCATCAGAGG GGACCTGGCC AAGCTGGAAT TCACTCAGCT GTGCATCGAC CTGGGCTGGA 1080
 AGCCCAAGTA CGGCCGCTTC GATGTGGTCC CCTGGTCTCT GCAGGCCAAT GGCCGTGACC 1140
 55 CTGAGCTCTT CGAAATCCCA CTGACCTTG TGCTTGAGGT GGCCATGGAA CATCCCAAAT 1200
 AGAGTGGTT TCGGGAACAT GAGCTAAAGT GGTACGCCCT GCCTGCAGT GCCAACATGC 1260
 TGCTTGAGGT GGGCGGCTGC GAGTTCCAG GGTGCCCTT CAATGGCTGG TACATGGGCA 1320
 CAGAGATCGG AGTCCGGGAC TTCTGTGATG TCCAGCGCTA CAACATCCTG GAGGAAGTGG 1380
 60 GCAGGAGAAAT GGGCCTGGAA ACGCACAAGC TGGCCTCGCT CTGGAAGAC CAGGCTGTGC 1440
 TTGAGATCAA CATGTCTGTG TCCATAGATT TCCAGAAACA GAATGTGACC ATCATGGACC 1500
 ACCACTCGGC TGCAGAACTC TTCTGAAAT ACATGCAGAA TGAATACCGG TCCCGTGGGG 1560
 GCTGCCCGGC AGACTGGATT TGGCTGGTCC CTCCCATGTC TGGGAGCATC ACCCCCGTGT 1620
 TTCACCAAGA GATGCTGAAC TACGTCTGT CCCCTTTCTA CTACTATCAG GTAGAGGCCT 1680
 65 GGAAACCCCA TGTCTGGCAG GACGAGAAGC GGAGACCCAA GAGAAGAGAG ATTCCATTGA 1740
 AAGTCTTGGT CAAAGCTGTG CTCTTTGGCT GTATGCTGAT GCGCAAGACA ATGGCGTCCC 1800
 GAGTCAGAGT CACCATCTCT TTTGCGACAG AGACAGGAAA ATCAGAGGCG CTGGCTGGG 1860
 ACCTGGGGGC CTTATTTCAGC TGTGCCCTTA ACCCAAGGT TGTCTGCATG GATAAGTACA 1920
 GGCTGAGCTG CCTGGAGGAG GAACGCTGTC TGTGGTGGT GACCAGTACG TTTGGCAATG 1980
 70 GAGACTGCCC TGGCAATGGA GAGAACTGA AGAARTCGCT CTTATGCTG AAAGAGCTCA 2040
 ACAACAAATT CAGGTACGCT GTGTTTGGCC TGGCTCCAG CATGTACCTC CGGTTCTGCG 2100
 CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACCTGGG GGCTCTCAG CTCACCCCGA 2160
 TGGGAGAAGG GGATGAGCTC AGTGGGCGAG AGGACGCTT CCGCAGCTGG GCGGTGCAAA 2220
 CCTTCAAGGC AGCCTGTGAG ACCTTTGATG TCCGAGGCAA ACAGCACATT CAGATCCCCA 2280
 75 AGCTCTACAC CTCCAATGTG ACCTGGGACC CGCACCACTA CAGGCTCGTG CAGGACTCAC 2340
 AGCCTTTGGA CCTCAGCAA GCCCTCAGCA GCATGCATGC CAAGAACGTG TTCACCATGA 2400
 GGCTCAATTC TGGCAGAAAT CTACAAAGTC CGATGCCAGC CCGTGCCACC ATCCTGGTGG 2460
 AACTCTCTG TGGAGATGGC CAGGCGCTGA ACTACCTGCC GGGGAGCAC CTGGGGTTT 2520
 GCCCAGGCAA CCAGCCGGCC CTGGTCCAAG GCATCTGGA GCGAGTGGTG GATGGCCCA 2580
 80 CACCCACCA GGCAGTGGC TGGAGGCCCC TGGATGAGAG TGGCAGTAC TGGGTCACTG 2640
 ACAAGAGGCT GCCCCCTGCT TCACTCAGCC AGGCCCTCAC CTACTTCTG GACATCACA 2700
 CACCCCAAC CCAGCTGCTG CTCCAAAAGC TGGCCAGGT GGCCACAGAA GAGCCTGAGA 2760
 GACAGAGGCT GGAGGCCCTG TGCCAGCCCT CAGAGTACAG CAAGTGAAG TTCACCAACA 2820
 GCCCCACATT CCTGGAGGTG CTAGAGGAGT TCCGTCCTCT GCGGGTGTCT GCTGGCTTCC 2880
 85 TGCTTTCCCA CTGCCCCATT CTGAAGCCCA GGTTCCTACT CATCAGCTCC CCGGGGATC 2940
 ACACGCCAC GGAGATCCAC CTGACTGTGG CCGTGGTCACT CTACCACACC CGAGATGGCC 3000
 AGGGTCCCCT GCACACCGGC GTCTGCAGCA CATGGCTCAA CAGCCTGAAG CCCCAAGACC 3060
 CAGTGCCCTG CTTTGTGCGG AATGCCAGCG GCTTCCACCT CCGGAGGAT CCTCCCATC 3120

CTGTCATCCT CATCGGGCCT GGCACAGGCA TCGCGCCCTT CCGCAGTTTC TGGCAGCAAC 3180
 GGCTCCATGA CTCACAGCAC AAGGGAGTGC GGGGAGGCGG CATGACCTTG GTGTTTGGGT 3240
 GCGCGCGCCC AGATGAGGAC CACATCTACC AGGAGGAGAT GCTGGAGATG GCCCAGAAGG 3300
 GGGTGGCTGA TCGGGTGAC ACAGCCTATT CCGGCTGCTC TGGCAAGCCC AAGGTCTATG 3360
 5 TTGAGGACAT CCTGCGGCAG CAGCTGGCCA GCGAGGTGCT CCGTGTGCTC CACAAGGAGC 3420
 CAGGCCACCT CTATGTTTGC GGGGATGTGC GCATGGCCCG GGACGTGGCC CACACCTTGA 3480
 AGCAGCTGCT GGTGTCACAG CTGAAATTGA ATGAGGAGCA GGTGAGGAC TATTTCTTTC 3540
 AGCTCAAGAG CCAGAAGGCG TATCAGGAAG ATATCTTTGG TGCTGTATTT CCTTACGAGG 3600
 CGAAGAAGGA CAGGGTGGCG GTGCAGCCCA GCAGCCTGGA GATGTGAGCG CTCTGAGGGC 3660
 10 CTACAGGAGG GGTAAAGCT GCCGGCACAG AACTTAAGGA TGGAGCCAGC TCTGCATTAT 3720
 CTGAGGTAC AGGGCCTGGG GAGATGGAGG AAAGTGATAT CCCCCAGCCT CAAGTCTTAT 3780
 TTCTCTCAAG TTGCTCCCCA TCAAGCCCTT TACTTGACCT CCTAACAGT AGCACCTTGG 3840
 ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
 Protein Accession #: NP_000616

1 11 21 31 41 51
 MACPWKFLPK TKFHQYAMNG EKGINNVEK APCATSSPVT QDDLQYHNLS KQONESPQPL 60
 VETGKKSPES LVKLDATPLS SPRHVRINKW GSGMTFQDTL HHKAKGILTC RSKSCLGSIM 120
 TPKSLTRGPR DKPTPPDELL PQAIEFVNQY YGSLKEAKIE EHLARVEAVT KEIETTVTYQ 180
 25 LTGDELIFAT KQAWRNAPRC IGRQWSNLQ VFDARSCSTA REMFEHICRH VRYSTNNNGNI 240
 RSAITVFPQR SDGKHDFRNV NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWPKPYG 300
 RFDVVLVLQ ANGRDPELFE IPPDLVLEVA MEHPKYENFR EELKMYALP AVANMLLEVIG 360
 GLEFPGCPFN GWYMTGIGV RDCDVQORYN ILEEVGRRMG LETHKLASLW KDQAVVEINI 420
 AVLHSPQKQN VTIMDHSAE ESFPMKYMONE YRSRGGCPAD WIWLVPPMSG SITPVFHQEM 480
 30 LNVVLSPPFY YQVEAWKTHV WQDEKRRPKR REIPLKVLVK AVLFACMLMR KTMASRVVVT 540
 ILFATETGKS EALAWDLGAL FSCAFNPKVV CMDKYRLSCL EEERLLLVVT STFGNGDCPG 600
 NGEKLLKSLF MLKELNNKFR YAVFGLGSSM YPRFCAFAHD IDQKLSHLGA SQLTPMGEED 660
 ELSGGQDAFR SWAVQTFKAA CETFDVVRGKQ HIQIPKLYTS NVTWDPHHYR LVQDSQPLDL 720
 SKALSSMHAK NVFTMRLLKSR NQLQSPSSR ATILVELSCS DGQGLNYLPG EHLGVCPCGN 780
 35 PALVQGILER VVDGPTPHQA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
 LLLQKLAQVA TEEPERQRL EALQSPSEYSK WKFTNSPTFL EVLEEFPSLR VSAGFLLSQL 900
 PILKPRFYSI SSPRDHTPTE IHLTVAVVTY HTRDQGGPLH HGVCSTWLSN LKPDQDPVPCF 960
 VRNAGSFHLP EDPSPHCILI GPGTGIAPFR SFWQQRLLHDS QHKGVRGGRM TLVFGCRRPD 1020
 EDHIYQEML EMAQKGLVHA VHTAYSRLPG KFKVYVQDIL RQQLASEVLR VHLKEFGHLY 1080
 40 VCGDVARMARD VAHTLKQLVA AKLLKLNEEQV EDYFFQLKSQ KRYHEDIFGA VFPYEAKKDR 1140
 VAVQPSSELM SAL

Seq ID NO: 314 DNA sequence
 Nucleic Acid Accession #: XM_087254
 Coding sequence: 47..2332

1 11 21 31 41 51
 AGAGTACGTG TTTACAGATA AAAGTGGTAC ACTGACAGAA AATGAGATGC AGTTTCGGGA 60
 50 ATGTTCAATT AATGGCATGA AATACCAAGA AATTAATGGT AGACTGTGAC CCGAAGGACC 120
 AACACCAGAC TCTTCAGAA GAAACTTATC TTATCTTAGT AGTTTATCCC ATCTTAACAA 180
 CTTATCCCAT CTTACAACCA GTTCTCTTTC CAGAACCACT CCTGAAATAT AACTGAACT 240
 AATTAAGAAA CATGATCTCT TCTTTAAAGC AGTCAGTCTC TGTCACACTG TACAGATTAG 300
 55 CAATGTTCAA ACTGACTGCA CTGGTGATGG TCCCTGGCAA TCCAACCTGG CACCATCGCA 360
 GTTGGAGTAC TATGCATCTT CACCAGATGA AAAGGCTCTA GTAGAAGCTG CTGCAAGGAT 420
 TGGTATTGTG TTTATTGGCA ATTCTGAAGA AACTATGGAG GTTAAAACTC TTGAAAACT 480
 GGAACGGTAC AAAGTGTCTC ATATTCTGGA ATTTGATTCA GATCGTAGGA GAATGAGTGT 540
 AATGTGTCAG GCACCTTCAG GTGAGAAGTT ATTATTGCTT AAAGGAGCTG AGTCATCAAT 600
 60 TCTCCCTAAA TGTATAGGTG GAGAAATAGA AAAAACCAGA ATTCATGTAG ATGAATTTGC 660
 TTTGAAAGGG CTAAGAAGTC TGTGTATAGC ATATAGAAAA TTTACATCAA AAGAGTATGA 720
 GGAATATAGT AAAGCATAT TTTGAAGCCG GACTGCCCTG CAGCAGCGGG AAGAGAAATT 780
 GGCAGCTGTT TTCCAGTTCA TAGAGAAAGA CCTGATATTA CTTGGAGCCA CAGCAGTAGA 840
 AGACAGACTA CAAGATAAAG TTCGAGAAAC TATTGAAACA TTGAGAAATG CTGGTATCAA 900
 65 AGTATGGGTA CTTACTGGGG ATAAACATGA AACAGCTGTT AGTGTGAGTT TATCATGTGG 960
 CCATTTTCAT AGAACCATGA ACATCCTTGA ACTTATAAAC CAGAAATCAG ACAGCGAGTG 1020
 TGCTGAACAA TTGAGGCAGC TTGCCAGAG AATTACAGAG GATCATGTGA TTCAGCATGG 1080
 GCTGGTAGTG GATGGGACCA GCCTATCTCT TGCACTCAGG GAGCATGAAA AACTATTTAT 1140
 70 GGAAGTTTGC AGAATTTGTT CAGCTGTATT ATGCTGTCTG ATGGCTCCAC TGCAAGAAAGC 1200
 AAAAGTAATA AGACTAATAA AAATATCACC TGAGAAACCT ATAACATTGG CTGTTGGTGA 1260
 TGGTGCTAAT GACGTAAGCA TGATACAAGA AGCCCATGTT GGCATAGGAA TCATGGGTAA 1320
 AGAAGGAAGA CAGGCTGCAA GAAACAGTGA CTATGCAATA GCCAGATTGA AGTTCCTCTC 1380
 CAAATGCTTT TTTGTTTCATG GTCAATTTTA TTATATTAGA ATAGCTACCC TTGTACAGTA 1440
 75 TTTTTTATAT AAGAATGTGT GCTTTATCAC ACCCCAGTTT TTATATCAGT TCTACTGTTT 1500
 GTTTTCTCAG CAAACATGTT ATGACAGCGT GTACCTGACT TTATACAATA TTTGTTTATC 1560
 TTCCCTACCT ATTCTGATAT ATAGTCTTTT GGAACAGCAT GTAGACCTTC ATGTGTTACA 1620
 AAATAAGCCC ACCCTTTATC GAGACATTAG TAAAAACCGC CTCTTAAGTA TTTAAACATT 1680
 TCTTTATTGG ACCATCTCTG GCTTCAGTCA TGCCCTTATT TTCTTTTGTG GATCCTATT 1740
 ACTAATAGGG AAGATACAT CTCTGCTTGG AAATGGCCAG ATGTTTGGAA ACTGGACATT 1800
 80 TGGCATTCTG GTCTTCACAG TCATGGTTAT TACAGTCACA GTAAAGATGG CTCTGGAAC 1860
 TCATTTTGTG ACTTGGATCA ACCATCTCGT TACCTGGGGA TCTATTATAT TTTATTTTGT 1920
 ATTTTCTCTG TTTATCTGAG GGAATCTCTG GCCATTTTGG GGCTCCCGA ATATGTATT 1980
 TGTGTTTATT CAGCTCTCTG CAAGTGGTTC TGCTTGGTTT GCCATAATCC TCATGTTTGT 2040
 TACATGTCTA TTTCTGTGTA TCATAAGAA GGTCTTTGAC CGACACCTCC ACCCTACAAG 2100
 85 TACTGAAAG GCACAGCTTA CTGAAACAAA TGCAGGTATC AAGTGTCTGG ACTCCATGTT 2160
 CTGTTTCCCG GAAGGAGAAG CAGCGTGTGC ATCTGTTGGA AGAATCTGCG AACGAGTTAT 2220
 AGGAAGATGT AGTCCAACCC ACATCAGCAG ATCATGGAGT GCATCCGATC CTTTCTATAC 2280
 CAACGACAGG AGCATCTTGA CTCTCTCCAC AATGGACTCA TCTACTTGT AAAGGGGCG 2340

Seq ID NO: 315 Protein sequence:
Protein Accession #: XP_087254

Seq ID NO: 316 DNA sequence
Nucleic Acid Accession #: NM_004473
Coding sequence: 661..1791

303

CCGGCTGGG CCGGCGCCCC GACCTCGCTG CCCCCGCTC GCCTCTCTGC CGGTGGCGCT 120
 TACCGCCACC TTGGCTCTGG GGGCAGGGCA TGGGCGGCCC CGCCAGATC GCCCAGCGCC 180
 AGTACTAACT GCCCTCGCTC TGGCCTTCGA GCCCGAAGCC TCTTCTGCGC GCACAACTTA 240
 GGCACTAATC CTTAACTAGC GGGCACCACA GACCAGCTGC AGCCACCCCA ACCCAGGGAT 300
 5 CACTTCCGGA CCCCTCGACC GCGCGGCACC AGCGCGCAAG GGACCTTCA GCCCGAGACC 360
 AGAGTCCAGT CCGGGTCCGG AGGCCACCGC CGCTGCCCGC CTCGAGAAGC ACAACGCGGG 420
 CTGAGCCGTC GGCTAGCGGG TCACTCCCGA GCCTCTGTCT GCACGCGGCC AGCCCCAGAC 480
 CACGGACGCT GAGCTCCAG CGCGCGCCAG CCTGGGCGCG TGGGCTCTCC GGGCCAGCCC 540
 10 GCGACGATCC CCTGAGCTCT CCGCAGAAAG GCGGAGCGTC CGTTCGCGGG AGCCCAGGCC 600
 CGCCCCCGCC CCGCGACAG CGCGGGGATC CAGAGCCCGG GGGTGCGGGA CGCCCGCGCC 660
 ATGACTGCGG AGAGCGGGCC GCGCGCGCGC CAGCCGAGGG TGCTGGCTAC CGTGAAGGAA 720
 GAGCGCGGCG AGACGGGAGC AGGGGCGCGG GTCCAGGGG AGGCCACGGG CGCGGGGGCG 780
 GCGGGGCGGC GCGGCAAGCG CCCCTGCGAG CGCGGGAAGC GCCCTACAGC CTACATCGCG 840
 CTATCGCCCA TGGCCATCGC GCACGCGCCC GAGCGCGGCC TCACGCTGGG CGGCATCTAC 900
 15 AAGTTCATCA CCGAGCGCTT CCCCTTCTAC CGCGACAACC CCAAAAAGTG GCAGAACAGC 960
 ATCGGCCACA ACCTCACACT CAACGACTGC TTCCTCAAGA TCCGCGCGGA GGCCGGCCGC 1020
 CCGGGTAAGG GCAACTACTG GGGCTCGAC CCCAACGCGG AGGACATGTT CGAGAGCGGC 1080
 AGCTTCTGCG CCGCGCCCAA GCGCTTCAAG CGCTCGGACC TCTCCACCTA CCGGCTTAC 1140
 20 ATGCAAGAGC CGCGCGCTGC CGCAGCGGCC GCTGCGCGAG CCGCGCGCGC CGCCCGCGCC 1200
 GCGCCATCTT TCCAGGCGCG GGTGCGCGCC GCGCGCGCCC CCTACCCGGG CGCCGCTCTAT 1260
 GCAGGCTACG CGCGCGCGTC GCTGGCGCGG CGGCTCCAG TCTACTACCC CGCGGCGTCG 1320
 CCGGGCCCTT GCGGCTCTT CGGCTTGGT CCTGAGCGGC CGCTCAGCCC AGAGCTGGGG 1380
 CCGCGACCGT CCGGGCCCGG CGGCTCTTGC GCCTTTCGCT CCGCGCGCGC CCGCGCTACC 1440
 25 ACCACCGGCT ACCAGCCCGC AGGCTGCACC GGGGCGCGGC CGGCCAACCC CTCTGCCTAT 1500
 GCGGCTGCGT ACAGCGGGCC CGACGCGCGG TACCGCGCAG GCGCGGCGAG TGCGATCTTT 1560
 GCGGCTGCTG GCGGCGCTGC GGGACCGCGT TCGCCCCCAG CGGGCGGCGAG CAGTGGCGGC 1620
 GTGGAGACCA CGGTGACCTT CTACGGGCGC ACGTCGCGCG CCGAGTTCGG AGCGCTGGGA 1680
 GCCTGCTACA ACCCTGCGCG GCAGCTCGGA GGGGCGCAGT CAGGCGCCTA CCATGCTCGC 1740
 CATGCTGCGC CTTATCCCGG TGGGATAGAT CGGTTCTGTT CCGCCATGTG AGCCAGCGTA 1800
 30 GGGACGAAAA CTCATAGAC CAATCGGCTGT TCACACGTTT CCGCGAACCT GAGAACGAA 1860
 AGGAATGGAG AGAGGACTCA ACTGGGACCC ACGTGGAAAA GACCGAGCAG GCCACAGAGG 1920
 CTCGGTCTCC CCGCGCACAG CGTAGGCACC CTGTGTACTC TGTAAACGGG AGGAGGTGGG 1980
 GCGAGGCGAG CAGAGCCCTT GGAATGCGAC AGGGACCCCT GATGGAGCGA AGCCCTCAAA 2040
 CGGGATGCTT TCTGCGATTC TATCGGGGAG GGTCTTGGC GGTAAACAGA GGGCAGCGTA 2100
 35 GTGTCAACAC CAGAGACGAG GATCCAAATT GTGGGGAATC AGTTTCAGCC TTCCATGTGC 2160
 TGCGGGAATC CGGGCCCTTT TAGCGGTTT GTCCCTTAGT GCCTTTAACT GCGTTACTAC 2220
 AATAAAAGGC TGCGGCGAGC CTTTCTTCT TAAAGTGAGG AGGACAAATT TGCAAAAGAA 2280
 ATAGGCTTTT CTTCTTTTTT AAATTGGAGA AATCTCTGCT CTGGTTGACC TGGGCTGGTT 2340
 40 TTCCCTGTCT CTGAGAACTT GAGACCTAGC TCCGAGTTGA ACTGTGCGTC AGCACTCCAG 2400
 TCCCATCACC TGAACCTTCA GTCTCCCCCA TCTGTTACAC TAGAGGCGTG CAGGACTCTA 2460
 TCCACGCGCC CCGGGTTATC ATTCAAGGCC CCATCATCTT GGAATGCTGC CTGCGTATTT 2520
 GGCAGCAATG GTGGGCCACC CAGGGCCTCT GAGTAGCCAC CCAAGCCTA GCCGCTGTTT 2580
 TAGGGAACGG AAAAGAGTTC ATGGCCAAGC GTCTAACCTA AAGTCCAGG ATTGGCTCCA 2640
 45 GGCAGCAATT ATATCATAAC TTATTGAACT TTTGAGCAGG ACGTGTGTTT AATTTTCATG 2700
 CTGTTACTGC CCAATCATAA ATCTGCTTTT CCATTATAAG GCAGAGAGAA GTACATTCTG 2760
 TCATTGTGCC ACTGTTTCTT GTCATCACGC AGCCCTGGAC CCAAGGGGTG AACTAAAGTT 2820
 TAAGGAGATG AGAGGATTC AAGAGCCCGT TGGTGACGCC TTTCACTAGC TGGGAGGGCC 2880
 TCTTCCATCC CCAGCACCCC CTGCTACACC TCAGCAGCCT CCCCATGCA AAAAGGAAAG 2940
 50 AGAAAAATTA AGTTAGGSCA GTCAGTAAAG TGAGCTTTAG AAAGAACTG GAATTTTAA 3000
 TTCAATTTGT ATCTTGCTTA AGTAGCAGGC TCACTAAAT TAGAGAAAGT CCAATAA 3060
 TCCCCCTTTC CTTTGAGAAA TCTTTAAGTT TCGATTCTGG AGCAAAACTT TTCAGCATTA 3120
 AATATTTTCA AGGCTCCATT CACAGCTTTC AGATAAACTG GAGTGTTCAG ATGGACTGTT 3180
 TTAATAAAAA TCTTTGAGCA AGTGAGTTAT GGCAAGAGAA ACTCAGCCTC TTTCTGTATA 3240
 55 AACTTAACAG GGAAGGGCTG GGGTGTGAAA AAGAAGATTG TATGAAACC ATTGGTAATT 3300
 TTTATTTTTT ATTTTGGGA CTGCACTATC CTGTTACGGA AGACATGTGA ACTTGGTTCA 3360
 GTCCAAATGG GGATTGTAT AAACCACTGC TCTCCATTAG AATATGGTG CAAGCCACAT 3420
 ATGTAATTTT AATATTCTA GTAGCCACAT TAATAAAGTN AAAAGAAACA AAAAAA 3480
 AA

Seq ID NO: 317 Protein sequence:
Protein Accession #: NP_004464

1 11 21 31 41 51
 | | | | |
 65 FKHLTHYROI DTRANSCRIP TIONFACTOR TTFMTAESGP PPPQPEVLAT VKEERGETAA 60
 GAGVPGEATG RGAGRRRRKR PLQRKPPYS YIALIAMAIA HAPERRLTG GIYKFITERP 120
 PFYRDNPKKW QNSIRHNLTL NDCFLKIPRE AGRPGKGNWY ALDPNAEDMF ESGSPLRRRK 180
 RFRKSDLSTY PAYMHDAAAA AAAAAA AAAAIFPGA VPAARPPYPG AVYAGYAPPS 240
 70 LAAPPVPVYP AASPGPCRFV GLVPERPLSP ELGPAPSGPG GSCAFASAGA PATTTGYQPA 300
 GCTGARFANP SAYAAAYAGP DGAYPQGAGS AIFAAAGRLA GPASPPAGGS SGGVETTVDF 360
 YGRTSPGQFG ALGACYNPGG QLGGASAGAY HARHAAAYPG GIDRFVMSAM

Seq ID NO: 318 DNA sequence
Nucleic Acid Accession #: NM_005688
Coding sequence: 126..4439

1 11 21 31 41 51
 | | | | |
 80 CCGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC 60
 AGGGGCGCAG GAATCTGAT GTGAACTAA CAGTCTGTGA GCCCTGGAAC CTCGCTCAG 120
 AGAAGATGAA GGATATCGAC ATAGGAAAAG AGTATATCAT CCCCAGTCCT GGGTATAGAA 180
 GTGTGAGGGA GAGAACCCAG ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240
 85 GGAGAACTCG ACCGTTGAAA TGGCAAGATG CCTTGGAAAC AGCAGCCCGA GCGGAGGGCC 300
 TCTCTCTTGA TGCCCTCCATG CATCTCAGC TCAGAACTCT GGATGAGGAG CATCCCAAGG 360
 GAAAGTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC 420
 ACCCAGTGGG CAATGCTGGG CTTTCTTCTT GTATGACTTT TTCGTGGCTT TCTTCTCTGG 480

	CCCGTGTGGC	CCACAAGAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTGTGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTGT	GATCTTCTGC	CGCACCAGGC	660
5	TCATCTGTCT	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCCAGCT	720
	TCATGTGTAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTGTAGT	GCTGGGCTCT	CTCCTGACGG	AAATCGTGGC	GTCTTGGTGG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGGGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
10	TTTGCTCCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TGTTGCCATC	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
15	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCT	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTC	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCTTGGGC	TTGATCTGTA	CAGCAGCACA	GGCTTTTACA	GTGGTGACAG	1440
	TCTTCAATTCT	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
	AAGCCTCAGT	GGCTGTGAC	AGATTTAAGA	GTTTGTTCCT	AATGGAAGAG	GTTCACATGA	1560
20	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCTCT	CCACTCCAGT	ATCCGAAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GSCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCACGTC	1800
	CCGAAGAGGA	AGAAGGCCAG	CACATCCACC	TGGGCCACCT	CGCCTTACAG	AGGACACTGC	1860
25	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGAAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGTACTCT	2040
	TGAGAGACAA	CATCTGTGTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGTCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
30	GAGAGCGAGG	AGCCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTG	CAGTGCCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTCTCTG	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
35	CCATTTTTAA	TAACTCTGTT	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCACTGG	TTACAGAAG	AAGTCACAAG	ACAAGGCTCC	TAAACAGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGCTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCCTGGTTAT	TATGGCCCTT	TTATGCTGTA	ATGTAGGCAG	CACCGCCTTC	AGCACTCGGT	2760
40	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAACACCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCATG	CTGATCCTGA	AAGCCATTGG	AGGAGTTGTC	TTTGTCAGGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	CTATGAAGTT	TTTTGACAGG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAGAGCA	3060
45	TGGATGAAGT	TGACGTGCGG	TGCGGTTCC	AGGCCGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCTCTGT	CATCTCTTTT	TCAGTCTGTC	ACATTGTCTC	CAGGCTCCTG	ATTCCGGAGC	3240
	TGAAGCGTCT	GGACAAATATC	ACGAGTCAC	CTTCTCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACATAA	AAGGGCAGGA	GTTTCTGCAC	AGATAACAGG	3360
50	AGCTGCTGGA	TGACAACCAA	GCTCCTTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGACCGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACGGGGCT	GTTCAGGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAAGCACT	GCCAGAATTA	3660
55	AGAAACAAGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGA	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAAC	3780
	CTAAAGAGAA	GATTGGGATT	GTTGGGGCGA	CAGGATCAGG	GAGTCTCTCG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGCAGAC	CTCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
60	TGTTCACTGG	CAGTGTGAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGTAGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTG	AAGAGACCAT	CCGAGAAGCA	TTTGCAAGCT	4260
65	GTACCATGCT	GACCATGTCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCCGCTG	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
	CCCTCATCGC	CGTCTCTCTA	CCGAAACCTT	GCCTTCTCTG	ATTTTATCTT	TCGCACAGCA	4560
70	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTTTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAATA	AGCACTGTGC	TAATAACAGT	GCATATTCTT	TTCTATCATT	TTGTACAGT	4860
75	TTGCTGTACT	AGAGATCTGG	TTTGTCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTTCT	4920
	CTTAGCTGG	TGGTTTCAAG	GTGCCAGGTT	TTCTGGGTGT	CCAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCC	GCCTCCCCAC	AGCGCTTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCGA	AGCGCGGTGA	GTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTGGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTC	5160
80	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCGAGGCC	GGGGAGTTTC	5220
	TTTCTCTGCT	TCTTCTTTTT	GCTGTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCACTGCC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTTGGTTCCA	AGCCCTGGAG	CCAAGTCTGT	CTTTTGTAGG	TGGCACTTTT	TCAATTGCTC	5400
	ATTCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TGTTGGGTCT	GTTTTCCTTT	5460
85	CTCACCGCAG	TGCTCGCACA	GTCCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
	GGGGCTGGTA	GCTCAGGTGG	CGGTGGTCAC	TGCTGTCAAT	AGTTGAATGG	TCAGCGTTGC	5700

ATGTCGTGAC CAAC TAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTGTGTGGAAG 5760
CAAAAATCTG AAAATGTGAA TAAAAATTATT TTGGATTITG TAAAAAATAA AAAAAAATAA 5820
AAAAAATAA AAAAAA

5

Seq ID NO: 319 Protein sequence:
Protein Accession #: NP_005679

10 1 11 21 31 41 51
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRP TRPLECQDAL ETAARAEGLS 60
LDASMHSQRL ILDEEHPKPK YHHGLSALKP IRTTSKHQHP VDNAGLFSCL TFSWLSSLAR 120
VAHKKRGLSM EDVWSLSKHE SSDVNCRRLE RLWQEEELNEV GPDAASLRV VWIFCRTRLI 180
LSIVCLMITQ LAGFSGPAPM VKHLLLEYTQA TESNLQYSL LVLGLLLTEI VRSWSLALTW 240
15 ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300
PVVAILGMIY NVIILGPTGF LGSAPFILFY PAMMFASRLT AYFRRCVAA TDERVQKMNE 360
VLTYYIKFIK YAMVKAPSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV 420
HMTLGFDLTA AQAPTUVTVF NSMTFALKVT PFSVKSLSEA SVAVDRPKSL FLMEEVHMIK 480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKDK RASRGKKEV RQLQRTEHQA 540
20 VLAEQKHLL LDSDERPSE EEEGKHIHLG HRLQRTLHS IDLEIQEGL VIGCGSVGSG 600
KTSLSAILG QMTLLEGSIA ISGTFAVVAQ QAWILNATLR DNILPGKEYD EERYNSVLNS 660
CCLRPDLAIL PSSDLTIGE RGANLGGQR QRI SLARALY SDRSIYLLD PLSALDAHVG 720
NHIFNSAIRK HLKSKTYLVF TQQLQYLVD DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
FNNLLGSETP PVEINSKKE SSGSKKSQDK GPKTGSVKKE KAVKPEGQL VQLEEKGGQS 840
25 VPWSVYGVYI QAAGGPLAPL VIMALFMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
VSDSMKDNPH MQYVASYAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRIRLRSFM 960
KFFDTPTGR ILNRFSDMD EVDVRLPFQA EMFIQNVILV PFCVGMIAV FFWFLVAVGP 1020
LVILFSLVHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
LDDNQAPFFL FTCAMRLAV RDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
30 GLFQPTVRLA SETEARTSV ERINHVIKT SLEAPARIKN KAPSPDWQPE GEVTFENAEM 1200
RYRENLPVLV KKVSPFIKPK EKIGIVGRG SGKSSLMGAL FRLVELSGGC IKIDGVRISD 1260
IGLADLRSLK SIIPQEPVLF SGTVRNSLDP FNQYTEDQIW DALERTHMEK CIAQLPLKLE 1320
SEVMENGDNF SVGERQGLLCI ARALLRHCKI LILDEATAAM DTETDLIQE TIREAFADCT 1380
MLTIAHLRHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

35

Seq ID NO: 320 DNA sequence
Nucleic Acid Accession #: AK022089.1
Coding sequence: 181-1488

40

1 11 21 31 41 51
AGCAGTTGCA CAACTTCCAG CAACTTTCTC AGCCGGCTAC TAATGAGCTG AAAGCCAGGA 60
ACATCCGAGG AGAAGAGAAA GCTTCCAGCC CTCCTCCCTT CACCCTGGAA ATCCAGACAC 120
45 CCCCACCCCC ACCCTCAGAT CACTTTAAGA TAATTTCTTT ATTCGTTTGC CCGACAGACC 180
ATGGCTCCCT TTGGAAGAAA CTGTCTAAAG ACTCGGCATA AAAACAGATC TCCAACTAAA 240
GACATGGATT CAGAAGAGAA GGAATTTGTG GTTTGGGTTT GCCAAGAAGA GAAGCTTGTC 300
TGTGGGCTGA CTAAACGCAC CACCTCTGCT GATGTCATCC AGGCTTTGCT TGAGGAACAT 360
GAGGCTACGT TTGGAGAGAA ACGATTCTCT CTGGGGAAGC CAGTGATTA CTGCATCATA 420
50 GAGAAGTGGA GAGGCTCCGA AAGGGTTCTT CCTCCACTAA CTAGARTCCT GAAGCTTTGG 480
AAAGCGTGGG GAGATGAGCA GCCCAATATG CAATTTGTTT TGGTTAAAGC AGATGCTTTT 540
CTTCCAGTTC CTTTGTGGCG GACAGCTGAA GCCAAATTAG TGCAAAACAC AGAAAAATTG 600
TGGAGACTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAGAATA 660
55 GTCAGGAAAA CTTTCCGGAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
GATAATATGG AGACATTAGT TCATCTGATC ATTTCCAGG ACCATACTAT TCATCAGCAA 780
GTCAAGAGAA TGAAGAGCT GGAATCTGAA ATTGAAAGT GTGAAGCTAA GTTCCATCTT 840
GATCGAGTAG AAAATGATGG AGAAACTAT GTTCAGGATG CATATTTAAT GCCCAGTTTC 900
AGTGAAGTTG AGCAAAATCT AGACTTGCAG TATGAGGAAA ACCAGACTCT GGAGGACCTG 960
60 AGCGAAAGTG ATGGAAATTGA ACAGCTGGAA GAACGACTGA AATATTACCG AATACTCATT 1020
GATAAGCTCT CTGCTGAAAT AGAAAAAGAG GTAAAAAGTG TTTGCATTGA TATAAATGAA 1080
GATGCGGAAG GGAAGCTGC AAGTGAAGT GAAAGCTCTA ATTTAGAGAG TGTAAAGTGT 1140
GATTTGGAGA AAAGCATGAA AGCTGGTTTG AAAATTCAT CTCAATTTGAG TGGCATCCAG 1200
AAAGAGATTA AATACATGTA CTCAATGCTT CAGATGAAAG CAAAAGAATA TGAACCTCTG 1260
65 GCCAAGGAAT TCAATTCAT TCACATTAGC AACAAAGATG GGTGCCAGTT AAAGGAAAAAC 1320
AGAGCGAAGG AATCTGAGGT TCCCAGTAGC AATGGGGAGA TTCTCCCTT TACTCAAAGA 1380
GTATTTAGCA ATTACACAAA TGACACAGAC TCGGACACTG GTATCAGTTC TAACACAGT 1440
CAGGACTCCG AACCAACAGT AGGAGATGTG GTGCTGTTGT CAACATAGTT CCAATGGCTC 1500
CTTTCGACC TGCTTTTCATG TTTTAATGTT TGTTTAATTT AATAGGAAAC CTCATTTTAA 1560
70 ATATAACACT CAAAAAATG TAAATCATAT TGTAGTATTC AATAGTTAAT AAAAATCTGA 1620
GAAATGTGTT GTTCTG

70

Seq ID NO: 321 Protein sequence:
Protein Accession #: NP_005438.1

75

1 11 21 31 41 51
MAPFGRNLLK TRHKNSRPTK DMDSEEBIV VWVCQEEKLV CGLTKRTTSA DVIQALLEEH 60
EATFGEKRF LKGPSDYCI EKWRGSEVL PPLTRILKLW KAWGDEQPM QFVLVKADAF 120
80 LPVPLWRTAE AKLVQNTKEL WELSPANMYK TLPPDKQKRI VRKTPFKLAK IKQDVTSHDR 180
DNMETLVHLI ISQDHTIHQQ VKRMKELDLE IEKCEAKFHL DRVENDGENY VQDAYLMPSP 240
SEVEQNLDLQ YEENQTLLEDL SEDSGIEQLE ERLKYRILI DKLSAEIERE VKSVCDIDINE 300
DAEGEAASEL ESSNLESVKC DLEKSMKAGL KIHSHLSGIQ KEIKYSDSL QMKAKEYELL 360
AKEFNSLHIS NKDGCQLKEN RAKESEVPSS NGEIPPFTQR VFSNYTNDTD SDTGISSNHS 420
85 QDSETVGDV VLLST

85

Seq ID NO: 322 DNA sequence
Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

	1	11	21	31	41	51	
5	AGCATTTGAAG	GGGAAGGAAC	TGCGGGTGTG	GTGTGTGTAT	GTGTGTGTGT	ATGTGTGTGC	60
	GGCGCGTGGC	TGCGTGTGTG	TGCGCGCGCT	AGTGTGTGGA	CAAGGAGGTG	GGGGCAGCTG	120
	AGTTAGAGTC	CCAACTCTTG	GACTCCATTT	GCTATTCTCT	TCTTTCTCCC	CCACACCTAT	180
	CTGGTGGTGG	TAGTGGGCGT	TTATATTTCG	GTTCCTTTTC	ATTCATTCTT	AAATCTCTTA	240
	AAAATTTTGG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
10	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAAC	CTGGAGTTAA	GGAAACAGATC	360
	CCCGAGAGAG	GTGACAGAGT	TAGTCCTTGA	TAATTGCCTG	TGTGTCAATG	GGGAAATTGA	420
	AGGCGCTGAAT	GATACTTTCA	AAGAACTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAACTAAG	480
	TTGCGTGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TTGGAGCTTA	GTGATAATAT	540
	AATTTCTGGA	GGCTTGAAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
15	GAGTGGAAAC	AAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAAGTCTT	GACTGTGTTA	ACTGTGAGAT	CACAAACCTG	GAAGATTATA	GAGAAAGTAT	720
	TTTGAACATA	CTGCAGCAAA	TCACATACCT	AGATGGATTT	GATCAGGAGG	ATAATGAAGC	780
	GCCGGACTCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
20	AAATGAAGCT	GGTCCACCGG	AAGGATATGA	GGAAGAGGAG	GAGGAAGAGG	AAGAGGAGGA	900
	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTGAGAG	TTGGGAGAGG	GAGAAGAGGA	960
	AGTGGGCTCT	TCATACTTAA	TGAAAGAAGA	AATTGAGGAT	GAAGAAGATG	ATGATGACTA	1020
	TGTTGAAGAA	GGGAAGAAG	AGGAAGAAGA	GGAAGAAGGA	GGTCTTCGAG	GGGAGAAGAG	1080
	GAAACGAGAT	GCTGAAGACG	ATGGAGAGGA	AGAAGATGAC	TAGATCATTG	TAAGACCAGA	1140
	TTCTCTAATG	TTTCTGGGTG	TGCAATAGAG	TGATCACATC	TTTGTTCCTT	CATGTACGAT	1200
25	AGCTATCCCT	ACAGAAGATA	ATGTGTAAC	TTTTATAGGA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCCCTTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTTCATTG	ACTCCCATTT	TGGAATTCCT	TAGCAATTTA	TTTAGACTTA	ATTTTTTAAA	1380
	TTCAAGCTTA	CTGTATTAGT	CATTTTATAG	CCATAATTAA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGCAATTC	ATTCCTTAT	TATAGATTAA	CTGAAATTAC	AGTTTGCTAT	1500
30	AAATATAAAT	GACAATAGTC	TCTTGAGTGG	TAAGTTGGTT	ATTTTTCATG	AGGTGATCCA	1560
	GGAAATCTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTT	ACTAAGAGTG	1620
	TTTGGTTGCT	TTTTTGTGAC	AAGTAACCTG	GAAAAATAGAA	GCAGAATAGT	AAAGGTTCTA	1680
	TTCAAGCAAC	TAGTTCATGG	ATTTTGTGGA	GGTTCATATC	AGTAATATGG	TTTCATGATT	1740
	TAGTGGTGAC	TGATAAGATT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
35	CATGCAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
	GTTTTTAGGT	GTGCATTCTT	TTTCTTCTTA	GCAATTCCTT	TATGATCACC	TTCCCTTCTT	1920
	GTTTCACTCC	CTCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAAC	CCAGGAAATC	1980
	CTTTAGTCTT	ATACCTCAAC	TACGTTTCAG	TCCGTCTGCG	GTTTAAATAA	AGTGAAGTAG	2040
	AAGAAATGGA	GTATTTTCTG	ACATAAGAAT	ATATTATCAA	TACAGTTTAA	TGCAGTAAGC	2100
40	TCTCCTTACC	ATAAATGTTT	CTTGGTTGAC	AACATCTAAG	ACAATATTAG	TGGGATGAAG	2160
	AAAGAAAAGC	AGGGGTGCTT	TTGGAAGCAG	TGTTAGTGTT	CCTCAAAAGT	CGGAACAATT	2220
	GCCGTGTTAT	GTATATAATA	GACATTAAAG	TCAAAATTTA	ATGTTGGCCT	CTCAATATGAT	2280
	TTGGATACCA	CTCTGCAAG	TATTTCTAAC	CTTTAATTC	CAGTTTAAAT	ACAGATATAA	2340
	TAATAGCATT	TAATTGGAAT	ATACTAGGCA	GCTGGAAAAG	TATTTGAAAC	TAAATTGACA	2400
45	TTAAATATAA	GATTTGTTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTTGGGATA	2460
	AGTGAGTGTG	TGTTTCCTTA	CATGGCTACT	AAATAAAATA	TAATGAGTAT	ACAAGTATAT	2520
	CTCCTCTTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTAAAT	CTTGGCTATC	2580
	TAAAAATTTT	TCCCTTTGTT	TTGAATATTT	GTAAGTTTTT	AAGAAGTTAG	TGTCAGCAAA	2640
	TTAATTGAAG	TTATGCTTCT	ATACTGGGAC	ATATTAAAT	ACTGAGTATA	GTACTGCTGC	2700
50	TACTGCTTCT	ACAATGTAAA	ATGTATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTTGTGGAGA	AACTAAAAAT	GTTGTACAAC	TGACCGAAAG	AAAACCCCTG	GGGATAAGTT	2820
	TAGTGAGGGG	ATTGGAATCC	CCAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAACTGAA	2880
	ATTCCTCTGT	CTAGTTCCTA	ACAATCTCTA	TTACATACTA	TGCCAGATTA	CAAAATACIT	2940
	ATTTTAAAAA	TGAAATCTAT	ATATTGACTT	TCTTATCAAT	CATCTTACTG	TGCAATCAAA	3000
55	ATTAGAGTAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAGACTTAT	3060
	TTAGCTTTGT	GGGTGGTATT	TTCATGCAAA	TAAGTAAGGG	TGGGTTTTAT	ATTTTGTAGA	3120
	AGTTTTTCGT	CCTATTTTAA	TGCTCTTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
	CTCAAGAATC	TCCTTAAAAA	CTTTGAAGTT	AATACTTTGT	TGCAACTGTG	TTTGAATATA	3240
60	AGCCATGACA	GTGTTAAAAA	CAAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

	1	11	21	31	41	51	
65	MEMKKKINLE	LRNRSPEEVT	ELVLDNCLCV	NGEIEGLNDT	FKELEFLSMA	NVELSSLARL	60
	PSLNKLRKLE	LSDNIISGGL	EVLAEKCPNL	TYLNLSGNKI	KDLSTVEALQ	NLKNLKSLLD	120
	FNCEITNLED	YRESIFELLQ	QITYLDGFDQ	EDNEAPDSEB	EDDEDGDEDD	EEEEENEAGP	180
70	PEGYEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEFVGLSY	LMKEEIQDEE	DDDDVVEEGE	240
	EEEEEEBGL	RGEKKRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

	1	11	21	31	41	51	
75	TCCTCTGCGT	CCCGCCCGGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
	GCCCGGCCCC	GAGCCCGCGG	CCCGGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
80	CCATGCGCGC	CGAGCCGCGG	TGACCGGCTC	CGCCCGCGGC	CGCCCGCGAG	CTAGCCCGGC	180
	GCTCTCGCGG	GCCACACGGA	GCGCGGCGCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCGG	240
	CAGCTCGCGG	CAGCGGCGCC	TGCGGGCTGC	CAGCCTTGCC	GCGCTTCTCT	GCGGCCCCCA	300
	ACGCGGCCCC	GCGGCTCGG	TGCTTCCGAG	CGCCCGGCGC	CGCAGCGCGC	CCTGCGGCGT	360
	GCTTCTCGCT	CTTCTCTTGC	TGCTTCCGCT	CGCCGCGCTG	TCCCGGCCCC	GCGCTTGGGG	420
85	GGCTGCTGCG	CCGAGCGGCT	CGCATTGGAA	TGAACTGCA	GAAAAAATTT	TGGGAGTCTT	480
	GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

WO 02/086443									
5	ACAGCCCTTAC	CACGTCCTGT	ACACAAGGCG	AAGACACACG	CAAAACATCA	ATAAGGCTGT	660		
	CCATCTGGCC	CAGGCAAGCT	TCAGATTGGA	AGCCCTTCGG	TCCAAAATCA	TCCTTGACCT	720		
	CATACCTGAAC	AATGGTTTGT	TGTCCTCTGA	TTATGTGGAG	ATTCACCTACG	AAAATGGGAA	780		
	ACCACAGTAC	GTCTAAGGCTG	GAGACGACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840		
	AGACTCCAAG	TGCGCTCTGT	CAACCTGCGA	TGGACTTCAT	GGCATGTTTG	AAGGTGATAC	900		
10	CTTCGTGTAT	ATGATAGAGC	CACCTAGAGCT	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960		
	ACATATAATC	CAGAAAACCT	TGGCAGGACT	GTATTCTAAG	CAAAATGAAGA	ATCTCACTAT	1020		
	GGAAAGGAGG	GACCAAGTGC	CTCTTCTCTC	GGAAATACAG	TGTTTGA AAA	GAAAGGAAGAG	1080		
	AGCAGTAAT	CCATCAGGTG	GTATATTGGA	AGAAATGAAA	TATTTGAACAT	TTATGATTGT	1140		
	TAATGATCAT	AAAAAGCTATA	AGAAGCATCG	CTCTTCTCAT	GCATACACCA	ACAACTTTGC	1200		
15	AAGTCCGCTG	GTCAACCTTG	TGAATTCAT	TTCAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260		
	CCGTGCTGGCT	GTAGAGAGCT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAAACCTGT	1320		
	CGAGATGTCT	CATAGATTCT	CAAAAATCCG	CGACGGCATT	AAGCAGCATG	CTGATGTCTG	1380		
	GCACCTCATC	TGCGGGGTGA	CATTCTACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440		
	TGTCCTTTCT	CGCACAAGAG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500		
20	ACAAGTATTA	TGCGAGAGCC	TGCTCAAAA	CTCTGGAATC	CATGGAAGCA	CTTCTAGCAG	1560		
	AAAGCCAAAA	TGTGACTGCA	CAGAATCCTG	GGGTGCTGTC	ATCATGGAGG	AAACAGGGGT	1620		
	GTCCCATCT	CGAAAAATTTT	CAAAAGTCGAC	CATTTTGGAG	TATAGAGACT	TTTTACAGAG	1680		
	AGAGAGTTGA	CGCTGCGTTT	TCAACGAGCC	AACAAAGCTA	TTTGAAGCCA	CGGAATGTGG	1740		
	AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCACTGTTG	AATGCTATGG	1800		
25	ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGCAT	GGCCCTCTGT	1860		
	TAACATAACC	TCATGTCTTT	TTCAGGCCAG	GGGCTATGAA	TGCGGGGATG	CTGTGAACGA	1920		
	GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTTGGCTCAG	TGCCCCACAA	ATCTTCAATA	1980		
	CGAAGACGGA	TATGCATGCA	ATCAAAATCA	CGCGCGCTGC	TACAATTGGC	AGTGAACAGC	2040		
	CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTCTCT	2100		
30	CTATGAAAGC	CTGAATACAG	AGAAGCATGA	GAAAGGAAAC	TGCGGGAAGG	ATGGAAGCCG	2160		
	TGGATTTCAG	TGCGAGCAAC	ATGATGTGTT	CTGTGGATTC	TTACTCTGTA	CGCATCTTAC	2220		
	TGCGAGCTCCA	CGTATTGGTC	AACTTCAGGG	TGAGATCATT	CCAATCTCCT	TCTACCATCA	2280		
	AGGCGGGGTG	ATTGACTGCA	TGGGTGCCCC	TGTAGTTTTA	GCATGATGTA	CGGATGTGGG	2340		
	CTATGTAGAA	GATGGAACGC	CATGTGGCCC	TGTCATGATG	TGTTTAGATG	GGAAGTGCTC	2400		
35	ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCATTCGAT	TCCAAGGGTA	AAGTCTGTTG	2460		
	GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTTGT	GATTTCACTT	GGGCAGGGAC	2520		
	AGATTGCAAT	ATCCGGGATC	CAGTATAGAA	CTCTCACCCC	CCCCAAGGATG	AAGGACCCAA	2580		
	GGGTCTCTAG	GCCACCAATC	TCATAATAGG	CTCCATCGCT	GGTGGCACTG	TGGTACAGCC	2640		
	TATTTCTCCT	GGGGGCCACG	CTGTGGGATT	TAAAATGTG	AGCAAGAGAA	GTTTCGATGT	2700		
40	TACTCAGCAA	GGGCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACGTGTTG	2760		
	ATTCTCGGTA	TGACATACTC	CGACGAGTGT	TACTGGAACT	ATTAAAGTTT	TAAACAAAAC	2820		
	CTTTGGGTGT	TAATGACTAC	GGAGCTAAAG	TGTGGGTGAC	AGGATGTGGG	TAAAGAAAAA	2880		
	CTGTCTCTTT	TGGAATAAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTCTAGT	AAACGGGGGA	2940		
	GGGGGCCCCA	GACCATGCTA	TAAAAGAAGC	TGTTCCAGAA	TCCTTTTTTT	TCCCTAATGG	3000		
	ACGAAGGAAC	AACACACACA	CAAAAATTTA	ATGCAATGAA	GGAAATCATTA	AAAA			

Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

45	1	11	21	31	41	51	
	MKPPGSSSRQ	PPLAGCSLAG	ASCPQQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPLAASS	60
	RPRAWGAAAP	SAPHWNETAE	KNLGVLAEDS	NTLQONSSSN	ISYSNAMQKE	ITLPSRLTIYY	120
50	INQDSESPYH	VLDTKARHKQ	KHNKAHVLQA	ASFQTEAFGS	KFLZLDLFLVN	GLSSSDYVEI	180
	HYENGRKPYX	KGGEHCYVHG	SIRGVKDSK	ALSTCNGLHG	MFEDDTLVVM	IEPLELVADE	240
	KSTGRPHIIQ	KTLAGQYSKQ	MKNLTMERGD	QWPFLESLQW	LKRKRRAVNP	SRGIFEEMKY	300
	LELMIVNDHK	TYKHRSSHA	HTNNFAKSV	NLVDTSIYEKQ	LNTRVVLVNV	ETWTEKDQID	360
	ITTNPQMLH	EFYSKYRQRIK	QHADAHVHLS	RVTFFHYKRSS	LSYFGVGCSSR	TRGVGVNEYG	420
55	LPMVAHVQGS	QSLAQNLGIQ	WEPSSRRKPKC	DCTESWGCCI	MEETGVSHSR	KFSKCSILEY	480
	RDLFARQGGA	CLFNRPNTKLF	EPTCEGNGVY	EAGECDGCF	HVCEYGLCKC	CKSLSNGAHC	540
	SDGPPCNCNS	CLFQPRGYEC	RSADVNECDIT	EYCTGDSGQC	PPNLNLDQGY	ACNQNGQRCY	600
	NGECKTRDNG	QYIYIGTKKA	GDCKPCEYKEL	NCTEGTEKGC	KGKGDWRWICQ	SKHIDVCGFL	660
	LCNLNTRAPR	IQQLQGEIIP	TSFYHOGVRV	DCSGAHHVLD	DDTDVGVYED	FTGPCGSPMMC	720
60	LDRRKCLQIQ	ALNMSSCLPDS	KGKVCSGHGV	CSNEATGCTC	FTWAGTDCSI	RPDPVRLNHP	780
	KDEGPKGPSA	NLNLIIGSIAG	AILVAAILVLG	DSGWFGRKND	KRRFDPPTQCG	PI	

Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

	1	11	21	31	41	51	
70	CTTCTCCAA	GACGGCCGGC	CATGCTCTCC	TCCTCTGCCA	GTCTCTCCCA	CCACTCTCTA	60
	ACCTGAGAGC	CTGTGGAAACC	TGCCCGTCTC	CCCTCTCCCA	TCAGACACAC	CTGCCTAGGA	120
	AACAGATGGA	AAAAGTGAGG	GACCCGTGAG	TGACTTGCTG	CTAAAGTTTA	TACCAGATGC	180
	AAATGATGCA	CGTGGAGTTC	TGCTGTGCCT	GGAAGGACC	TCGGAAGTCT	TCTAAGGAGA	240
	GTCAATGCGT	ATTACCAACA	GTCTTCAGTG	GAGAACTCCA	TCATCAAGTC	CTAAAGCAGG	300
75	GACTTTACCA	CCTTGGCGGA	TCACTGCCTG	AGCATGGGCC	GGAGCTTTAA	GGATGAGACA	360
	TTCCCCGAGC	CAGATTCTTC	CATAGGCCAG	AGGCTGTCTC	AGGAAATCAT	CCTCTTCAAT	420
	GTGATATGGA	AGCGGCCACA	GGATCTACCA	GAGGTCTCTC	CTCAACTACG	CTGGATGATG	480
	ATAAGCATCA	TTGACATCCA	ACAAGGAGGC	GCAGCTGACT	GCTGGTTCTT	GGCAGCAGTG	540
	GGATCCTTGA	CTCAGAACC	ACAGTAGCAG	CAGAGATCC	TGATGGTCCA	AAGCTTTTCA	600
80	CACCAGTATG	CTGGCATTTT	CCGTTTCCGG	TTCTGGCAAT	GTGGCGTAGC	GTGGAAAGTG	660
	GTGATTGATG	ACCGCTACCC	TGTCAGGGGA	GATAAATGCC	TCTTTGTGCG	TCTCGGCATC	720
	CAAAACCAAG	AGTTCTGGCC	CTGCTGCTGT	GAGAGGGCTC	ATGCCAAGCT	GCTCGGATCC	780
	TATTCCGATC	TGCATATGCG	TCTTCTCGAG	GATGCCCTGG	TGGACCTCAC	AGGAGGCGTG	840
	ATCACCAACA	TCCATCTGCA	CTCTTCCCCT	GTGGACCTGG	TGAAGGACAG	GAAGACACGG	900
	ACCAAGCGAG	GCTCCTGATC	AACCTGTGCC	ATCTCAAGTG	GGCCAACAGA	TACAGCAGCA	960
85	GCGATGGAGA	ATGGGCTGGT	GAGTCTCCAT	GCCTACACTG	TGACTGGGGC	TGAGCAGATT	1020
	CAATACCGAA	GGGGCTGGGA	AGAAATTATC	TCCTCTGTGA	ACCCCTGGGG	CTGGGGCGAG	1080
	CAAGATTGGA	GAGGCGCTGG	GAGTAATGTC	TCTCAGGAGT	GGGAGGAAAC	CTGTGATCCG	1140

	CGGAAAAGCC	AGCTACATAA	GAACCGGGAA	GATGGCGAGT	TTTGGATGTC	GTGTCAAGAT	1200
	TTCCAAACAGA	AATTCATCGC	CATGTTTATA	TGTAGCGAAA	TTCCAATTAC	CCTGGACCAT	1260
	GGAAACACAC	TCCACGAAGG	ATGGTCCCAA	ATAATGTTTA	GGAAGCAAGT	GATTCTAGGA	1320
5	AACACTGCGAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
	GAAGGCACCA	ATGTGTGCGT	GTGCGTCACA	GTGCTGTGCA	CACCATCAAA	TTTGAAAGCA	1440
	GAAGATGCAA	AATTTCCACT	CGATTTCCAA	GTGATTCTGG	CTGGCTCACA	GAACACTGT	1500
	CCAAAGCTCA	AATAATAAAT	TCCGCCGCAA	CTTCAACATG	ACTTACCATC	TGAGCCCTGG	1560
	GAACATATGT	GTGGTTGCAC	AGACACGGAG	AAAATCAGCG	GAGTTCCTGC	TCGGAATCTT	1620
10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGGGGCC	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1860
	GCCTCTCTTC	CTGGATCGTC	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGACTTTC	AAGCTGGAAT	GCAGAGCTTA	GAAGGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	ACCTTCTCTT	CTCTACTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTCCCT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCTCTAA	TGGCTTAATA	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	AAAAAAAAAA	2280
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

	1	11	21	31	41	51	
	MAYYQEPSVE	TSIIKPKDQD	FTTLRDHCLS	MGRTFKDET	PAADSSIGQK	LLQEKRLSNV	60
	IWKRPQDLPG	GPPHFILDDI	SRFDIQQGA	ADCWFLAALG	SLTQNPQYRQ	KILMVQSFSS	120
	QYAGIFRFRF	WQCQWVEV	IDRLPVQGD	KCLFVRPRHQ	NQEFWPCLE	KAYAKLLGSY	180
30	SDLHYGLFED	ALVDLTGGVI	TNHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YTVTGAEQIQ	YRRGWEEIIS	LWNPWGWGET	SWRGRWSDGS	QWEETCDPR	300
	KSQHLHKRED	GEFWMSCQDF	QQKFIAMFIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
	TAGGPRNDQA	FNFSVQEPME	GTNVVVCVT	AVTPSNLKA	DAKFLPLDFQ	ILAGSQKHCP	420
	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

	1	11	21	31	41	51	
	GTGGGTCAAG	TGAACCACTT	TTCCGCGGAA	ACCTGGTTGT	TGCTGTAGTG	GCGGAGAGGA	60
	TCGTGGTACT	GCTATGGCGG	AATCATCGGA	ATCCTTCACC	ATGGCATCCA	GCCCGGCCCA	120
45	GCCTCGGCGA	GGCAATGATC	CTCTCACCTC	CAGCCCTGGC	CGAAGCTCCC	GGCGTACTGA	180
	TGCCCTCAC	TCCAGCCCTG	GCGGTGACCT	TCCACCATT	GAGGATGAGT	CCGAGGGGCT	240
	CCTAGGCA	GAGGGGCCCC	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGGAGATGG	300
	CATGGAAGG	GACTACCGCG	CCATCCAGAG	GCTGGACGCC	TATGAGGCGG	AGGGACTGGC	360
	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGCGGCG	CGTGACCGGG	AGGCTGGCGG	GGGCGTGGGC	CGCATGCGCC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCAGCGAG	GACGGCGAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAAGGC	CACCTCTGTG	GCGAGTGGGT	GAGCATGGCG	GGCCCCGGCG	TGGAGATCCA	660
	CCACCGCTTC	AAGAACTTCC	TGCGCACTCA	CGTCGACAGC	CACGGCCACA	ACGTCTTCAA	720
55	GGAGCGCATC	AGCGACATGT	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCAAG	TGCTGGCCTA	CTTCTGCTCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACTGCTCT	CTGGTGGAGG	AGCTGCGCTC	960
	GCTGAGGCG	CTGCATCTGA	ACCAGCTGAT	CGGCACCACT	GGGGTGGTGA	CCAGCTGCAC	1020
60	TGGCGTCTCG	CCCCAGCTCA	GCATGCTCAA	GTACAACTGC	AACAAGTGCA	ATTTCTGCTC	1080
	GGGTCTCTTC	TGCCAGTCCC	AGAACCAAGG	GGTGAAACCA	GGCTCTGTGC	CTGAGTGCCA	1140
	GTGCGCGGCG	CCCTTTGAGG	TCAACATGGA	GGAGACCATC	TATCAGAACT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGAGTCCAG	GCAAAAGTGG	GGCTGGCCCG	CTGCCCGGCT	CCAAGGACGC	1260
	CATTCTCCTC	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
65	CATCTATCAC	AACAACATAT	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACCTGTATC	CTAGCCCAAC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAATC	1440
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCGGAGAGAA	1500
	GATCTTTGCC	AGCATTGTCT	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCCCTGG	1560
	TCTGGCCCTG	TTCCGAGGGG	AGCCCAAAAA	CCCAGGTGGC	AAGCACAAGG	TACGTGGTGA	1620
70	TATCAACGTG	CTCTTGTGCG	GAGACCTTGG	CACAGCGAAG	TCGCAAGTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACCTGGCCG	GGGGCGTCCG	CTGTGGGCTC	1740
	CACGGCGTAT	GTCCAGCGCG	ACCCTGTGAG	CAGGGAGTGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTTCTGGCT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAGGA	1860
	CAGAACCCAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
75	CGTCACCTCC	CTGCAGGCTC	GCTGCAAGGT	CATTGTCTGC	GCCCAACCCA	TAGGAGGGCG	1980
	CTACGACCCC	TGCTGACTTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCATCTCAAG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGGAC	CGTGGACCCA	GTCAGGACCG	AGATGCTGGC	2100
	CGCTTCTGTC	GTGGGCAAGC	ACGTCAGACA	CCACCCAGC	AACAAGGAGG	AGGAGGGGCT	2160
	GGCCAATGGC	AGCGCTGTGT	AGCCCGCCAT	GCCCAACAGC	TATGGCGTGG	AGCCCTGCTC	2220
80	CCAGGAGGTC	CTGAAGAAGT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAGAT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	GACAGGCAGC	ATCCCCATTA	CGGTGCGGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGTCAACA	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GCATGCGCAA	2520
85	GACTTTTGCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTGTC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
	CACATATTAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCC ACGACCTGAA 2760
 AAGGAAAAATG ATCCTCGCAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCCTTGGGA 2820
 TTTCTGGTTTG GGGTGGTTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
 TGAACCTCGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC 2940
 TGTTTGTTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTTGCCAGTG 3000
 TGTCTTACTT GGTGTCTGAA CATCTTGCCA CCTCGAGTG CTTTGTCTCC ACTCAGTACC 3060
 TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCSTGTGGT TTAGGTGTTA GCCTTCTTAC 3120
 ATGGATGTCA GGAGAGCTGC TGCCCTCTGT GCGTGAAGTG CGTATTGAGG CTGCTTTTGC 3180
 TGCCCTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CCTGCAGGTT 3240
 TCTGTGCCCC TGTGTGGGAA GAGGGCACGA CAGTGCCAGC GCAGCGTTCT GGGCTCCTCA 3300
 GTGCGAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT 3420
 TAATTTTAA TAAAGTTGAA TAAATATAA AAAAAA AAAAAA

Seq ID NO: 329 Protein sequence:
 Protein Accession #: AAH17490.1

1 11 21 31 41 51
 MAESSESFTM ASSPAQRRR NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE 60
 GPLEEEEDGE ELIGDGMERD YRAIPELDAE EAEGALDDE DVEELTASQR EAAERAMRQR 120
 DREAGRGLGR MRRLGLLYSD EDEEREPARK RRQVERATED GEEDEEMIES IENLEDLKGH 180
 SVREWVSMAG PRLEIHHRFK NFLRTHVDSH GHNVFERIS DMCKENRESL VVNYEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVVLM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 HLNQLRTSG VVTSCGTGLP QLSMVKYCN CNFVLGPFC QSQNQEVKPG SCPEQCSAGP 360
 FEVNMETIY QNYQRIRIQE SPQKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGLSNTAN GPPVPATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GGEFKNPGGK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGG ASAVGLTAYV QRHPVSREW TLEAGALVLAD RGVCLIDEFD KMDQDRTSI 600
 HEAMEQSSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSEVNDLT EPIISRFDIL 660
 CVVRDVTDPV QDEMLARFVV GSHVRHHPNS KEEGLANGS AAEPAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDVIYEDD VNMAIRVMLE SFIDTQKFSV MRSMRKT FAR YLSFRDNDNE LLLFILKQLV 840
 AEQVTVQRNR FGAQDDTIEV PEKDLVDKAR QINIHNLSAF YDSELFMRNK FSHDLRKKMI 900
 LQGF

Seq ID NO: 330 DNA sequence
 Nucleic Acid Accession #: M17254
 Coding sequence: 257-1645

1 11 21 31 41 51
 GTCCGCGCGT GTCCGCGCCC GCGTGTGCCA GCGCGCGTGC CTTGGCCGTG CGGCGCGAGC 60
 CGGGTGCAC TAACCTCCCTC GCGCGCGAGC GCGCGCGTAA CCTCTCGGTT ATTCCAGGAT 120
 CTTTGAGAGC CCGAGGAAAG CCGTGTGTAG CAAAAGCAG ACAAATGACT CACAGAGAAA 180
 AAAGATGGCA GAACCAAGGG CAACAAAGC CGTCAGGTTT TGAACAGCTG GTAGATGGGC 240
 TGGCTTACTG AAGGACATGA TTCAGACTGT CCCGACCCCA GCAGCTCATA TCAAGGAAGC 300
 CTTATCAGTT GTGAGTGAGG ACCAGTCTGT GTTTGAGTGT GCCTACGGAA CGCCACACCT 360
 GGCTAAGACA GAGTGTGAGC CGTCTCTCTC CAGCGACTAT GGACAGACTT CCAAGATGAG 420
 CCCACGCGTC CCTCAGCAGG ATTGGCTGTC TCAACCCCA GCCAGGGTCA CCATCAAAAT 480
 GGAATGTAAC CCTAGCCAGG TGAATGGCTC AAGGAACTCT CCTGATGAAT GCAGTGTGGC 540
 CAAAGGCGGG AGATGTGGTG GCAAGCCAGA CACCGTTGGG ATGAACACTG GCAGCTACAT 600
 GGAGGAGAAG CACATGCCAC CCCCAAACAT GACCAAGAAC GAGCGCAGAG TTATCGTGCC 660
 AGCAGATCCT ACGTATGGA GTACAGACCA TGTGCGGCAG TGGCTGGAGT GGGCGGTGAA 720
 AGAATATGGC CTTCCAGAGC TCAACATCTT GTTATCCAG AACATCGATG GGAAGGAACT 780
 GTGCAAGATG ACCAAGGACG ACTTCCAGAG GCTCACCCCC AGCTACAACG CCGACATCCT 840
 TCTCTCACAT CTCCACTACC TCAGAGAGAC TCCTCTTCCA CATTTGACTT CAGATGATGT 900
 TGATAAAGCC TTACAAAACCT CTCCACGGTT AATGCAATGCT AGAAACACAG ATTTACCATA 960
 TGAGCCCCC AGGAGATCAG CCTGGACCGG TCACGGCCAC CCCACGCCCC AGTCGAAAGC 1020
 TGCTCAACCA TCTCCTTCCA CAGTGCCCAA AACTGAAGAC CAGCGTCTCT AGTTAGATCC 1080
 TTATCAGATT CTTGGACCAA CAAGTAGCCG CCTTGCAAT CCAGGCAGTG GCCAGATCCA 1140
 GCTTTGGCAG TTTCTCTGG AGCTCCTGTC GGACAGCTCC AACTCCAGCT GCATCACCTG 1200
 GGAAGGCACC AACGGGAGT TCAAGATGAC GGATCCCGAC GAGGTGGCCC GCGCTGGGG 1260
 AGAGCGGAAG AGCAAAACCA ACATGAAC TAAGCTC AGCGCGCCCC TCCGTTACTA 1320
 CTATGACAAG AACATCATGA CCAAGGTCCA TGGGAAGCGC TACGCTTACA AGTTGCACTT 1380
 CCACGGGATC GCCCAGGCC TCCAGCCCCA CCCCCCGGAG TCATCTCTGT ACAAGTACCC 1440
 CTCAGACCTC CCGTACATGG GCTCCTATCA CGCCACCCCA CAGAAGATGA ACTTTGTGGC 1500
 GCCCCACCTT CCAGCCCTCC CCGTGACATC TTCCAGTTT TTTGCTGCCC CAAACCCATA 1560
 CTGGAATTCA CCAACTGGGG GTATATACCC CAACACTAGG CTCCCCACCA GCCATATGCC 1620
 TTCTCATCTG GGCACCTACT ACTAAAGACC TGGCGGAGGC TTTTCCATC AGCGTGCACT 1680
 CACCAGCCCA TGGCCAGAAA CTCTATCGGA GAACATGAAT CAAAAGTGCC TCAAGAGGAA 1740
 TGAAAAAAGC TTTACTGGGG CTGGGGAAGG AAGCGGGGA AGAGATCCAA AGACTCTTGG 1800
 GAGGAGTTA CTGAAGTCTT ACTACAGAAA TGAGGAGGAT GCTAAAGATG TCACGAATAT 1860
 GGACATATCA TCTGTGAGT GACCTTGTA AAGACAGTGT ATGTAGAAGC ATGAAGTCTT 1920
 AAGGACAAAG TGCCAAAGAA AGTGGTCTTA AGAAATGTAT AAACCTTAGA GTAGAGTTTG 1980
 AATCCCACTA ATGCAAACTG GGTGAAACT AAAGCAATAG AAACAAACCA GTTTTGACCT 2040
 AACATACCGT TTATAATGCC ATTTAAGGA AAACCTACCT TATTTAAAA TAGTTTCATA 2100
 TCAAAAACAA GAGAAAAGAC AOCAGAGAGA CTGTGGCCCA TCAACAGACG TTGATATGCA 2160
 ACTGCATGGC ATGTGCTGTT TTGGTTGAAA TCAAAATACAT TCCGTTTGAT GGACAGCTGT 2220
 CAGCTTCTC AAACCTGTGA GATGACCCAA AGTTTCCAAC TCCTTTACAG TAITACCGGG 2280
 ACTATGAAC AAAAGGTGGG ACTGAGGATG TGTATAGAGT GAGCGTGTGA TTGTAGACAG 2340
 AGGGGTGAAG AAGGAGGAG AAGAGGCAGA GAAGGAGGAG ACCAGGCTGG GAAAGAAACT 2400
 TCTCAAGCAA TGAAGACTGG ACTCAGGACA TTTGGGGACT GTGTACATG AGTTATGGAG 2460
 ACTCGAGGGT TCATGCAGTC AGTGTATATC CAAACCCAGT GTTAGGAGAA AGGACACAGC 2520
 GTAATGGAGA AAGGGAAGTA GTAGAATCA GAAACAAAA TGGCATCTC TTTCTTTGTT 2580
 TGTCAATGA AATTTTAA TGAATTTGTC TGATATTTAA GAGAAACATT CAGGACCTCA 2640
 TCATTATGTG GGGGCTTTGT TCTCCACAGG GTCAGGTAAG AGATGGCCTT CTGGCTGCC 2700

ACAATCAGAA ATCACGCAGG CATTTTGGGT AGGCGGCCTC CAGTTTTCCT TTGAGTCGCG 2760
 AACGCTGTGC GTTTGTGAGA ATGAAGTATA CAAGTCAATG TTTTCCCCC TTTTATATA 2820
 ATAATTATAT AACTTATGCA TTTATACACT ACGAGTTGAT CTCGCCACG CAAAGACACA 2880
 CGACAAAAGA GACAAATCGAT ATAATGTGGC CTTGAATTTT AACTCTGTAT GCTTAATGTT 2940
 TACAAATAGA AGTTATTAGT TCTTAGAATG CAGAATGTAT GTAATAAAAT AAGCTTGGCC 3000
 TAGCATGGCA AATCAGATTT ATACAGGAGT CTGCATTTGC ACTTTTTTTA GTGACTAAAG 3060
 TTGCTTAAATG AAAACATGTG CTGAATGTTG TGGATTTTGT GTTATAATTT ACTTTGTCCA 3120
 GGAACCTGTG CAAGGGAGAG CCAAGGAAAT AGGATGTTTG GCACCC

Seq ID NO: 331 Protein sequence
 Protein Accession #: AAA52398

1 11 21 31 41 51
 15 MIQTVDPDAA HIKEALSUVS EDQSLFECAY GTPHLAKTEM TASSSSDYQ TSKMSPRVPQ 60
 QDWLSQPPAR VTIKMECNPS QVNGSRNSPD ECSVAKGGKM VGPSPTVGMN YGSYMEEKHM 120
 PPPNMTTNSY RVIVPADPTL WSTDHVRQWL EWAVKEYGLP DVNILLFQNI DGKELCKMTK 180
 DDFQLRTFSY NADILLSHLH YLRETPPLPHL TSDDVDKALQ NSPRLMHARN TDLPEYFPRR 240
 20 SAWTGHGHPT PQSKAAQPSF STVPKTEDQR PQLDPYQILG PTSSRLANPG SGQIQLWQFL 300
 LELLSDSSNS SCITWBGTTG EFKMTDPDEV ARRWGERKSK PNMNYDKLSR ALRYYYDKNI 360
 MTKVHGKRYA YKDFHGIQA ALQPHPPSS LYKYPSDLPY MGSYHAHPQK MNFVAPHPPA 420
 LPVTSSSFFA APNPYMNSTP GGIYPNTRLP TSHMPSHLGT YY 462

Seq ID NO: 332 DNA sequence
 Nucleic Acid Accession #: NM_000020
 Coding sequence: 283-1794

1 11 21 31 41 51
 30 AGGAAACCGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTCCCGCGC CAGCTGCGCC 120
 GAGCGAGCCC CTCGCCGCT CCAGCCCGGT CCGGGGCGGC GCCGACCCC AGCCCGCGT 180
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
 AGGCTAGCGC CCGGCCACCC GCAGAGCGGG CCCAGAGGGA CCATGACCTT GGGCTCCCCC 300
 35 AGGAAAGGCC TTCTGATGCT CTGATGGGCC TTGGTGACCC AGGAGAGACC TGTGAAGCCG 360
 TCTCGGGGCC CGCTGGTGAC CTGCACGTGT GAGAGCCAC ATTGCAAGGG GCCTACCTGC 420
 CGGGGGGCGT GGTGCACAGT AGTGCTGGTG CCGGAGGAGG GGAGGCACCC CCAGGAACAT 480
 CGGGGCTGGG GGAACCTTGA CAGGAGGCTC TGCAGGGGGC GCCCACCAG GTTCGTCAAC 540
 40 CACTACTGCT GCGACAGCCA CCTCTGCAAC CACAACGTGT CCCTGGTGCT GGAGGCCACC 600
 CAACCTCCTT CGGAGCAGCC GGAACAGAT GGCCAGCTGG CCCTGATCCT GGGCCCCGTG 660
 CTGGCCTTGG TGGCCTTGGT GGCCTGGGT GTCTGGGCC TGTGGCATGT CCGACGGAG 720
 CAGGAGAAGC AGCGTGGCCT GCACAGCGAG CTGGGAGAGT CCACTCTCAT CCTGAAAGCA 780
 TCTGAGCAGG GCGACAGCAT GTTGGGGGAC CTCTGGACA GTGACTGCAC CACAGGGAGT 840
 45 GGCTCAGGGC TCCCTTCTCT GGTGCAGAGG ACAGTGGCAC GGCAGGTTGC CTTGGTGGAG 900
 TGTGTGGGAA AAGGCCGCTA TGGCGAAGTG TGGCGGGGCT TGTGGCACGG TGAGAGTGTG 960
 GCCGTCAAGA TCTTCTCTCT GAGGGATGAA CAGTCTTGGT TCCGGGAGAC TGAGATCTAT 1020
 AACACAGAT TGTCTAGACA GACAACATC CTAGGCTTCA TCGCCTCAGA CATGACCTCC 1080
 CGCAACTGGA GCACGAGCT GTGGCTCATC ACGCACTACC ACGAGCACGG CTCCTCTAC 1140
 50 GACTTTCTGC AGAGACAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGG 1200
 GCATGCGGCC TGGCGCACT GCACTGGAG ATCTTCGGTA CACAGGGCAA ACCAGCCATT 1260
 GCCCACCGCG ACTTCAAGAG CCGCAATGTG CTGGTCAAGA GCAACCTGCA GTGTGTCATC 1320
 GCCGACCTGG GCCTGGCTGT GATGCACTCA CAGGGCAGCG ATTACCTGGA CATCGGCAAC 1380
 AACCCGAGAG TGGGCACCAA GCGGTACATG GCACCCGAGG TGCTGGACGA GCAGATCCGC 1440
 55 ACGGACTGCT TTGAGTCTTA CAAGTGGACT GACATCTGGG CCTTTGGCCT GGTGCTGTGG 1500
 GAGATTGCCG GCGGACCAT CAGTGAATGG ATCGTGGAGG ACTATAGACC ACCCTTCTAT 1560
 GATGTGGTGC CCAATGACCC CAGCTTTGAG GACATGAAGA AGGTGGTGTG TGTGGATCAG 1620
 CAGACCCCA CCATCCTTAA CCGGTGGCT GCAGACCCGG TCTCTCAGG CCTAGCTCAG 1680
 ATGATGCGGG AGTGGTGGTA CCAAAACCC TCTGCCGAC TCACCGCGCT GCGGATCAAG 1740
 60 AAGACACTAC AAAAAATTAG CAACAGTCCA GAGAAGCCTA AAGTGATTCA ATAGCCCAGG 1800
 AGCAGCTGAT TCCTTTCTGC CTGACAGGGG CTGGGGGGGT GGGGGGAGT GGATGGTGGC 1860
 CTATCTGGT AGAGGTAGTG TGAGTGTGGT GTGTGCTGGG GATGGGAGC TGCGCCTGCC 1920
 TGCTCGGCC CCAGCCACC CAGCCAAAA TACAGCTGGG CTGAAACCTG ATCCCTGCT 1980
 GTCTGGCCTG CTCAAAGCGG CAGGCTCCCT GACGCTGGC TCTCTCCCCA CCCCTATGGC 2040
 65 CAGCATGGTG CACCCCTAC CACTCCCGG ACAGGATGCA AAAGAGGCTC CAGAGTCAGA 2100
 GTGCCAAGCC AGGGAATCCC AGTCCAGAC TCAGAGCCCG GGCCTGCACT TTGCCCCCTG 2160
 CCCTTGATCA ACCCACTGC CCCACCAGAG CTGCCAGGGT GGCACAGGGC CCTGTCCAGC 2220
 CCCTGGCACA CACTTCCCTG CCAGGCCTCA GCCTTAGCA TAAGCTCCAG AGAGCCAGGG 2280
 CCCATCAGTT TCTCTCTGTG GATTGTATC TCAGCTCCAT GATGCCTTGG GCTTTCTGTC 2340
 70 TCCTCAACAA GAGTGCAGCT TGCTGAATGT CAGCTGCCTG AGAGAGCTGG GGCCTGACTT 2400
 ACTAGGGCAT TAAATCCTAA GAGTCCCTAC TGAGGTGTGG CAGGATCACA GGCCAGTGGA 2460
 AAAAGGGCAG GTCAGATGGG CAAGGCCAG GACTTTCAGA TTAACCTAGA GGATATCGAG 2520
 GCCAAGCATG GCAGGGGAA GGTCAAGTGG TGTCAGAGA CCCAGTCTG ACCCGGATG 2580
 TTTGCTCCAT GTGACAAAAG CAGGCTGTG TCAGGACCTT TTTTCTCTT TTTTCTCTT 2640
 75 TTTTCTCTT GACACGAGT TCGCTCTTG TTGTCCAGGC TAGAGTGCAA TGGCATGATC 2700
 CCAGCTCACC GCAACGCTA CTCTCCAGGT TCAATCAT CTCTGCTCT AGACTCCCGA 2760
 GTAGCTGGGA TTACAGGCAC ATGCCACCAT GCCTGGCTAA TTTTGTATAT TTAGTAGAAA 2820
 CAGGGTTTCA CCAATGTGGC CATGCTGGT CTGAACTCC TGACCTCAGG TGTTCACCT 2880
 80 ACCTCAGCT CCAAGTGTG TGGGTTACA GGTGTAGCC ATCGCGCCTG GCCAGGACCT 2940
 TTGTTCTTCT TCTACATATT GGAAGATTG GTCTGATGT CCTTGAGGC TCTTTAGCT 3000
 CTAGTTCTCT GACACTCAG CCTATATCAC AGCTAACTTC YTCAGTCTCA TCTATTCTCT 3060
 ATGCTCCAGC CCCTGGCAAT TTGCTCAAG ATGGGGGTTT GAAAATAACT TTACCTGACT 3120
 CAAGGAGTGT CTGGAGCACC TCCTAGTCTA AGTCTGCAAG CTCAGTTCT TGCCTAAAC 3180
 CATGCCAGTG GCCACCTTG GGTCTAGACA GCTCTGGGCC TTTTGACCAC AAGCCAGCCC 3240
 85 CTGCGCTCT CTGTTGCTA GTCTCTCTG CCCCAGGACT GCAGGGCGGC TTCCTCCAAG 3300
 GCTTCCAAG CTCAAAAGAA ATTTGGCTCC ATCCAAGAAG GCTCCAGCTC CCCTACTGGC 3360
 CCCTGGCTTC AGGCCACAC CCCTGGGCCA GSCCAGAGA GTGTGTCTCA GGAGAAATCA 3420
 ATGGGCTCTA GAGAGACACA CAGAAAGTTT GGGCATTTGG GAATTTTCA AGRTGTATG 3480

TATGGYTCAC GTATGGWACA GGTGTGCTCTG GTCCYKGGGT GCAGGGAAGT GGGCTGCAGG 3540
 GAAAGTGGATT GGAGGGGAGC TTGAGGAATA TAAGGAGCGG GGGTGGAGAC TCAGGCTATG 3600
 GACAAGGACA GCCCCAAGGT TGGGAAGACC TGGCCTTAGT CGTCTCAGC CTAGGGCAGG 3660
 GCGATGAAGA AAGCTCTCCC CGCTCCTGCT GTAATGACCC AGAGTAGCCT CCCCAGGCGG 3720
 GCATCTTATG TGTGTCTTCC ACCATCTCTCA TGGTGGCACT TTTCTAGGCC TGTCTCCCAG 3780
 CATTGTGCAA GGTCTGGAAG AGAACCCAGG AGTGAAACTG GGTGAAACA GAAAGCTCAA 3840
 TGGATGGGCT AGGTTCGCCAG ATCATTAGGG CAGAGTTTGC ACGTCTCTG GTTCACTGGG 3900
 AATCCACCCA GCCCACGAAT CATCTCCCTC TTTGAAGGAT TTTWATTTCT ACTGGGTTTT 3960
 GGAAACAACT CCTGCTGAGA CCCCACAGCC AGAACTGAA AGCAGCAGCT CCCCAGGCC 4020
 TGGAAATCC CTAAGAGAAG GCCTGGGGGA MAGGAATGG AGTGACAGGG GACAGGTAGA 4080
 GAGAAGGGGG CCCAATGGCC AGGGAGTGAA GGAGGTGGCG TTGCTGAGAG CAGTCTGCAC 4140
 ATGCTTCTGT CTAGTGCAG GAAGGTGTTT CAGGGTCGAA ATTACACTTC TCGTACCTGG 4200
 AGACGCTGTT TGTGGGAGCA CTGGGCTCAT GCCTGGCACA CAATAGGTCT GCAATAAAC 4260
 ATGGTTAAAT CCTGAAAAA AAAAAAAA

Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

1 11 21 31 41 51
 MTLGSPRKGL LMLMALVLTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
 RHPQEHRCGG NLHRELRCGR PTEFVNHYCC DSHLCNHNVS LVLEATQPPS EQPGTDGQLA 120
 LILGPVLALL ALVALGLVGL WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLIDS 180
 DCTTGGSGSL PFLVQRTVAR QVALVECVGK GRYGEVVRGL WHGESVAVKI FSSRDEQSWF 240
 RETEYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLPHLAL 300
 RLAVSAACGL AHLVEIFGT QGKPAIAHRD FKSRNLVVK NSLQCCIDLG LAVMHSQSGD 360
 YLDIGNNPRV GTKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPYDVVP NDPSPFDMKK VVCVDQQTPT IPNRLAADPV LSLAQMMRE CWYPNPSARL 480
 TALRIKKTLLQ KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

1 11 21 31 41 51
 GGCACGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC 60
 AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGGTCTGCG GCGGAAAATG CCTGCCCTTC 120
 ACATCGAAGA TTTGCCAGAG AAGGAAAAC TGAAAATGGA AGTTGAGCAG CTTCGCAAAG 180
 AAGTGAAGTT GCAGAGACAA CAAGTGCTA AATGTTCTGA AGAAATAAG AACTATATG 240
 AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA 300
 AAGAAAAAGG CAGCTGTGTT ATTTCTATAA TAACTTGGGA GAAACTGCAT CCTAAGTGA 360
 AGAACTAGTT TGTTTTAGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420
 TGAAATTAAA AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTAAAGA GAGCAGAGAG TATCAGATGT 540
 ACAATTATGG AATAAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
 GCTTCAATAA AAGTTTGTGC TT

Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

1 11 21 31 41 51
 MPALHIEDLP EKEKLKMEVE QLRKEVKLQR QQVSKCEBI KNYIEERSGE DPLVKGIPED 60
 KNFFKEKGSC VIS

Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

1 11 21 31 41 51
 GCACGAGGGA ACAACCTCTC TCTCTSCAGC AGAGAGTGTC ACCTCCTGCT TTAGGACCAT 60
 CAAGCTCTGC TAACTGAATC TCATCCTAAT TGCAGGATCA CATTGCAAAG CTTTCACTCT 120
 TTCCACCTT GCTTGTGGGT AAATCTCTTC TGCGGAATCT CAGAAAGTAA AGTTCCATCC 180
 TGAGAAATATT TCACAAAGAA TTTCCTTAAG AGCTGGACTG GGTCTTGACC CCTGGAATTT 240
 AAGAAATCTT TAAAGACAAT GTCAAAATAG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
 GACAATTGTG CATATCGTCT AATAATAAAA ACCCATACTA GCCTATAGAA AACAAATATT 360
 GAATAATAAA AACCCATACT AGCCTATAGA AAACAATATT TGAAGAGATT CTACCACTAA 420
 AAGAAAAACT ACTACAACCT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACCTG 480
 ACAAGGTTGC TATAAAACAA GATTGCTACA ACTTCTAGTT TATGTTATAC AGCATATTTT 540
 ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCCTGTATTT TCTGGTCTCT TTGCCTTTTT 600
 TTATGATTCT TGTTACAGCA GAATTAGAAG AGAGTCTGTA GGACTCAATT CAGTTGGGAG 660
 TTACTAGAAA TAAATCATG ACAGCTCAAT ATGAATGTTA CCAAAAGATT ATGCAAGACC 720
 CCATTCAACA AGCAGAAAGG GTTTACTGCA ACAGAACCTG GGATGGATGG CTCTGCTGGA 780
 ACGATGTTGC AGCAGGAAC TGAATCAATG AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
 ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAACCTGGTT AGACATCCAG 900
 CAAGCAACAG AACATGGACA AATTATACCC AGTGTAATGT TAAACCCAC GAGAAAGTGA 960
 AGACTGCACT AAATTTGTTT TACCTGACCA TAATTGGACA CGGATTGTCT ATTGCATCAC 1020
 TGCTTATCTC GCTTGGCATA TTTTATTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
 TACAAAAAA TCTGTTCTTC TCATTTGTTT GTAACTCTGT TGAACAATC ATTCACTCA 1140
 CTGCAGTGGC CAACAACGAG GCCTTAGTAG CCACAATACC TGTAGTTGCA AAAGTGTCCT 1200
 AGTTCACTCA TCTTACCTG ATGGGCTGTA ATTACTTTTG GATGCTCTGT GAAGGCATTT 1260
 ACCTACACAC ACTCATTTGT GTGGCCGTGT TTGCAGAGAA GCAACATTTA ATGTGGTATT 1320
 ATTTCTTTGG CTGGGGAATT CCACTGATTC CTGCTGTGAT ACATGCCATT GCTAGAAGCT 1380

TATATTACAA TGACAAATTGC TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTGG TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
 TCATCACCAA GTTAAAAATT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACCTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCTGA 1740
 GAAGAAACTG GAATCAATAC AAATCCAAT TTGGAACAG CTTTCCAAC TCAGAAAGCTC 1800
 TTGCTAGTGC GTCTTACACA GTGTCAACAA TCAGTGTAGG TCCAGGTTAT AGTCATGACT 1860
 GTCTAGTGA ACACCTTAAAT GGAAGAAAGCA TCCATGATAT TGAATAATGTT CTCTTAAAC 1920
 CAGAAAATT TATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTGG TGTCTCTCT 1980
 AACTCAAGGA CTGGACCCA TGACTCTGTA GCCAGAAGAC TTCAATATTA AATGACTTTG 2040
 GGGAAATGTA TAAAGAAGAG CCTTCACATG AAATTAGTAG TGTGTTGATA AGAGTGTAA 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTGTAA TGTGTTGCA TAAATACTCC 2160
 CACTATGCCT GATGTGAGCG TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGTAAGCC AGTTCACGCA CACCATTGAT GAATTCAAAC 2280
 AAATGGCTGT AAAACATAAC ATACATGTTG GGCATGATT TACCTTATT CCCCCAAGA 2340
 GACCTAGCTA AGGTCTATAA ACATGAAGGG AAAATTAGCT TTTAGTTTAA AAACCTTTA 2400
 TCCCATCTTG ATTGGGGCAG TTGACTTTT TTTTTCCTCA GAGTGCCTGA GTCCTTTTG 2460
 TAACTACCT CTCAAAATGA CAATACCAGA AGTGAATTAT CCGTCTGCGC TTTCTTTTCT 2520
 CTATGAAAAG CAACAGTAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
 ATCTTGTGGC ATATCCATTG TGGAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC 2640
 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 TGTCTTACCA AACAGTGGGA GGGAAATCCT AGCTGTAAT ATAAATTTG CCCTTCCATT 2760
 TCTACTGTAT AAACAAATTA GCAATCATT TATATAAGA AAATCAATGA AGGATTCTT 2820
 ATTTTCTTGG AATTTGTAA AAAGAAATTG TGAATAATGA GCTTGTAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAT CAATACATA CAACCTATGT AATTTTAA GCAAAATATAT 2940
 AATGCAACAA TGTGTGTATG TTAATATCTG ATACTGTATC TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKKCTLYFL VLLPFFMILV TAELEESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVYCNRTWD GWLWVNDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WNTYTQCNVN THEKVKTALN LFVLTIIIGH LSIASLLISL GIFFYFKSL SQRITLHKNL 180
 FFSFVCNSV TIIHLTAVAN NQALVATNPV SKVVSQFIHL YLMGCNYFWM LCEGIYHL 240
 IVVAVFAEKQ HLMWYFLLGW GFPLIPACIH AIARSLYYND NCWISSDTHL LYIIHGPICA 300
 ALLVNLFFLL NIVRVLIYKL KVTHQAESNL YMKAVRATLI LVPLLGIEFV LIPWRPEGKI 360
 ABEVYDYIMH ILMHFQGLLV STIFCFNGE VQAILRRNWN QYKIQFGNSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNKSGIHDIE NVLLKPENLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
 GCACGATCTG TTCTCCTGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
 GCCTGCCTGG GCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA 120
 CGGGACACCC ACAGCTGCTG GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TTGATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTCCGAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 TTCCGGGTGC ATGCAGAGAC AGGAGACGTG TTGCGCATG AGAGGCTGGA CCGGGAGAAT 360
 ATCTCAGAGT ACCACCTCAC TGCTGTCAAT GTGGACAAGG ACCTGGTGA AAACCTGGAG 420
 ACTCCTTCCA GCTTCACCAT CAAAGTTTCA GACGTGAAAG ACACTGGGCC TGTGTTCAAG 480
 CATCGGTTGT TCAATGCGTC CGTGCCCTGAG TCGTGGCTG TGGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCTCTGT CATGTACCAA 600
 ATCCTGAAGG GGAAGAGTA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGGAAAG GCGAGATGCC 720
 CAGGGCTTCC GGGGGGACTC GGGCACGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACCTCC CCTTCTTCA CCGACCAAG TACACATTG TCGTGCCTGA AGACACCCGT 840
 GTGGGCACTT CTGTGGGCTC TCTGTTTGTG GAGGACCCAG ATGAGCCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGG GGGCGACTAC CAGGACGCTT TCACCATGTA GACAAACCCC 960
 GCCCACAACG AGGGCATCAT CAAGCCCATG AAGCCTCTGG ATTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCGAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC 1080
 GCGGGAACA GAGCCAGGT CATTATCAAC ATCACAGATG TGGACGAGCC CCCCATTTTC 1140
 CAGCAGCCTT TCTACCACTT CCAGCTGAAG GAAAACCAGA AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTTGA TGGCGTAGG CATAGCATTG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAGG GCCAGTTCTT CCGAGTACA AAAAAGGGGG ACATTTACAA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
 AATGACAATG CCCCAGAGTT TGCCAAGCCC TACCAGCCCA AAGTGTGTGA GAACGCTGTC 1500
 CATGGCCAGC TGGTCTTGCA GATCTCCGCA ATAGACAAG ACATAACACC ACGAAACGTG 1560
 AAGTTCAAAT TACCTTTGAA TACTGAGAAC AACTTTACCC TCACGGATAA TCACGATAAC 1620
 ACGGCCAACA TCACAGTCAA GTATGGGCG TTTGACCGGG AGCATACCAA GGTCCACTTC 1680
 CTACCCGTGG TCACTCTAGA CAATGGGATG CCAAGTCGCA CCGGACCCAG CACGCTGACC 1740
 GTGGCGGTGT GCAAGTGCAA CGAGCAGGGC GAGTTCACTT TCTGCGAGGA TATGGCGGCC 1800
 CAGGTGGGCG TGAGCATCCA GGCAGTGGTA GCCATCTTAC TCTGCATCCT CACCATCACA 1860
 GTGATCACCC TCTCTACTTT CTTGCGGCG GCGCTCCGGA AGCAGGCCCG GCGCACGGC 1920
 AAGAGCGTGC CCGAGATCCA CGAGCAGCTG GTCACTACG ACGAGGAGGG CCGCGCGGAG 1980
 ATGACACACA CCAGCTACGA TGTGTCGGTG CTCAACTCGG TCGCGCCGGG CCGGGCCAA 2040
 CCCCAGGGC CCGCGCTGGA GCGCCGGCCT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
 AGGCACGGC CTGGGCGACA CCGAGGGCCC GGGGAGATGG CAGCCATGAT CGAGGTGAAG 2160
 AAGGACGAGG CCGACACAGA CCGGACGGC CCCCCCTACG ACACGCTGCA CATCTACGGC 2220
 TACGAGGGCT CCGAGTCCAT AGCCGAGTCC CTCAGCTCCC TGGGACCGA CTCATCCGAC 2280

TCTGACGTGG ATTACGACTT CCTTAACGAC TGGGGACCCA GGTTTAAGAT GCTGGCTGAG 2340
 CTGTACGGCT CGGACCCCGG GGAGGAGCTG CTGTATTAGG CGGCGAGGT CACTCTGGGC 2400
 CTGGGGACCC AAACCCCTGT CAGCCAGGCG CAGTCAGACT CCAGGCACCA CAGCCTCCAA 2460
 AAATGGCAGT GACTCCCGAG CCGAGCACCC CTTCCTCGTG GGTCCAGAG ACCTCATCAG 2520
 CCTTGGGATA GCAAACCTCA GGTTCCTGAA ATATCCAGGA ATATATGTCA GTGATGACTA 2580
 TTCTCAATAT CTGGCAATAT CAGGCTGGTG TTCTGTCTGG GCTCAGACAT CCACATAACC 2640
 CTGTACCCCA CAGACCGCGG TCTAACTCAA AGACTTCCTC TGGCTCCCCA AGGCTGCAAA 2700
 GCAAAACAGA CTGTGTTTAA CTGCTGCAGG GTCTTTTCT AGGGTCCCTG AACGCCCTGG 2760
 TAAGGCTGGT GAGGTCCTGG TGCCATCTCG CCTGGAGGCA AAGGCTTGA CAGCTTGACT 2820
 TTGTGGGCGAG GATTCTCTGC AGCCCATTCG CAAGGGAGAC TGACCATCAT GCCCTCTCTC 2880
 GGGAGCCCTA GCCCTGTCTC AACTCCATAC TCCACTCCAA GTGCCCCACC ACTCCCCAAC 2940
 CCCTCTCCAG GCCTGTCAAG AGGGAGGAAG GGGCCCCATG GCAGCTCCTG ACCTTGGGTC 3000
 CTGAAGTGAC CTCACCTGGC TGCCATGCCA GTAACCTGTG TGTACTGAGC ACTGAACCAC 3060
 ATTCAGGGAA ATGCTTATTA AACCTTGAAG CAACCTGTGA TTCACTCTGG AGGGGCGAGT 3120
 GAGATCAGGA GTGACAGATC ACAGGGTGAG GGCCACCTCC ACACCCACCC CCTCTGGAGA 3180
 AGGCTCTGAA GAGCTGAGAC CTGTCTTGA GACTCCTCAG CACCCCTCCA GTTTTGCCTG 3240
 AGAAGGGGCA GATGTTCCCG GAGATCAGAA GACGTCTCCC CTCTCTGCTC TCACCTGGTC 3300
 GCCAATCCAT GCTCTCTTTC TTTTCTCTGT CTACTCCTTA TCCCTTGGTT TAGAGGAACC 3360
 CAAGATGTGG CCTTTAGCAA AACTGACAAT GTCCAAACCC ACTCATGACT GCATGACGGA 3420
 GCCGAGCATG TGTCTTTACA CCTGCTGTGT GTCCATCTC AGGGAACCTA CCCTCAGGCA 3480
 CACCTGTGAG AAGGAAGGCC CTGCCCTGCC CAACCTCTGT GGTCAACCAT GCATCAITCC 3540
 ACTGGAACGT TTCACTGCAA ACACACCTTG GAGAAGTGGC ATCAGTCAAC AGAGAGGGGC 3600
 AGGGAAGGAG ACACAAGACT CACCCCTCGT CATGGACCGA GGTTCCTCACT CTGGCAAAGC 3660
 CCCTCACACT GCAAGGAGAT GTAGATAACA CTGACTTGTT TGTTTTAAAC AATAACTAGC 3720
 TTCTTATAAT GATTTTITTA CTAATGATAC TTACAAGTTT CTAGCTCTCA CAGACATATA 3780
 GAATAAGGGT TTTTGCATAA TAAGCAGGTT GTTATTTAGG TTAACAAATAT TAATTCAGGT 3840
 TTTTGTAGTG GAAAAACAAT TCCTGTAAAC TTCTATTTTC TATAATTGTA GTAATGTCTC 3900
 TACAGATAAT GTCTATATAT TGGCCAAACT GGTGCATGAC AAGTACTGTA TTTTITTTATA 3960
 CCTAATAAAA GAAAAATCTT TAGCCTGGGC AACAAAAAA

Seq ID NO: 339 Protein sequence
 Protein Accession #: NP_001786

1 11 21 31 41 51
 MQRLLMLLAT SGACGLGLAV AAVAAAGANP AQRDTHSLLP THRRQKRDWI WNQMHIIDEK 60
 NTSPLPHVVG IKSSVSRKNA KYLLKGEYVG KVRVDAETG DVFAIERLDR ENISEYHLTA 120
 VIVDKDTGEN LETPSSSTIK VHDVNDNWPV FTHRLFNASV PESSAVGTSV ISVTAVDADD 180
 PTVGDHASVM YQILKGEYF AIDNSGRIIT ITKSLDREKQ ARYEIVVEAR DAQGLRGDSG 240
 TATVLVLTQD INDNPFPEFTQ TKYTFVVPED TRVGTSGSL FVEDPDEPQN RMTKYSILRG 300
 DYQDAFTIET NPAHNEGIIK PMKPLDYEYI QQYSFIVEAT DPTIDLRYMS PPAGNRAQVI 360
 INITDVDEPP IFQPPFYHFQ LKENQKKPLI GTVLAMPDPA ARHSIGYSIR RTSKQGPFR 420
 VTKKGDIYNE KELDREYVYP YNLTVAEAKEL DSTGTPTGKE SIVQVHIEVL DENDNAPEFA 480
 KPYQPKVCEN AVHQQLVLQI SAIDKDIIPR NVKFKFTLNT ENNFITLDNH DNTANITVKY 540
 GQFDREHTKV HFLPVVISDN GMPSTRGTST LTVAVCKCNE QGEFTFCEDM AAQVGVSIIQA 600
 VVAILLCLIT ITVITLILFL RRRLRKQARA HGKSVPEIHE QLVTYDEEGG GEMDTTSYDV 660
 SVLNSVRRGG AKPRPALDA RPSLYAQVQK PPRHAPGAHG GPGEMAAMIE VKKDEADHDG 720
 DGPPYDTLHI YGYEGSESSIA ESLSSLGTDG SDSVDVYDPL NDWGRPFKML AELYGSDPRE 780
 ELLY

Seq ID NO: 340 DNA sequence
 Nucleic Acid Accession #: NM_003088
 Coding sequence: 112-1593

1 11 21 31 41 51
 GCGGAGGGTG CGTGCAGGCC GCGGCAGCCG AACAAAGGAG CAGGGGCGCC GCCGCAGGGA 60
 CCGGCCACCC ACCTCCCGGG GCGCGCAGC GGCCTCTCGT CTACTGCCAC CATGACCGCC 120
 AACCGCACAG CCGAGCGCGT GCAGATCCAG TTCGGCTCA TCAACTGCGG CAACAAGTAC 180
 CTGACGGCCG AGCGGTTCGG GTTCAAGGTG AACGCGTCCG CCAGCAGCCT GAAGAAGAAG 240
 CAGATCTGGA CGCTGGAGCA GCGCCCTGAC GAGGCGGGCA GCGCGGCGT GTGCTTGGC 300
 AGCCACTGGT GCGCTACTCT GCGCGCGGAC AAGGACGGCA ACGTGACCTG CGAGCGCGAG 360
 GTGCGCGGTC CCGACTGCGG TTTCTCTATC GTGGCGCAGC ACGACGGTCG CTGCTCGCTG 420
 CAGTCCGAGG CGCACCGGCG CTACTTCGGC GGCACCGAGG ACCGCTGTCT CTGCTTCGG 480
 CAGACGGTGT CCGCGCGGCA GAAGTGGAGC GTGCACATCG CCATGCACCC TCAGGTCAAC 540
 ATCTACAGTG TCACCCGTAA GCGCTACGCG CACCTGAGCG CGCGGCGGCG CGACGAGATC 600
 GCCGTGGACC GCGACGTGCC CTGGGCGGTC GACTCGCTCA TCACCTCTCG CTTCAGGAC 660
 CAGCGCTACA GCGTGACAGC CGCGGACAC CGCTTCTCTG GCCACGACGG GCGCTGCTG 720
 GCGCGCGGCG AGCGGCGCAC TGGCTACAGC CTGGAGTTCC GCTCCGCGCA GGTGGCTTC 780
 CGCGACTGCG AGGGCGGTTA CTTGGCGCGG TCGGGGCCCA GCGGCACGCT CAAGGCGGGC 840
 AAGGCCACCA AGGTGGGCAA GGACGAGCTC TTTGCTCTGG AGCAGAGCTG CGCCAGGTC 900
 GTGCTGCAGG CGGCCAACGA GAGGAACGTG TCCACGCGCC AGGGTATGGA CCTGTCTGCC 960
 AATCAGGACG AGGAGACCGA CCAGGAGACC TTCCAGCTGG AGATCGACCG CGACACCAAA 1020
 AAGTGTGCTT TCCGTACCCA CAGGGCAAG TACTGAGCG TGACGGCCAC CGGGGCGTG 1080
 CAGTCCACCG CCTCCAGCAA GAATGCCAGC TGCTACTTTG ACATCGAGTG GCGTGACCGG 1140
 CGCATCACAC TGAGGGCGTC CAATGGCAAG TTTGTGACCT CCAAGAAGAA TGGGCGAGCT 1200
 GCGCCTCTCG TGGAGACAGC AGGGGACTCA GAGCTCTTCC TCATGAAGCT CATCAACCGC 1260
 CCCATCATCG TGTTCGCGG GGAGCATGGC TTCATCGGCT GCCGCAAGGT CACGGGCACC 1320
 CTGGAGCGCA ACCGCTCCAG CTATGACGTC TTCCAGCTGG AGTTCAACGA TGGCGCTTAC 1380
 AACATCAAGG ACTCCACAGG CAATACTGG ACGGTGGGCA GTGACTCCG GGTCAACGAG 1440
 AGCGGCGACA CTCTGTGGA CTCTCTCTTC GAGTTCTGG ACTATAACAA GGTGGCCATC 1500
 AAGGTGGGCG GCGCTACTCT GAAGGGCGAC CACGAGGCG TCCTGAAGGC CTGCGCGGAA 1560
 ACGGTGGACG CGGCTCTGCT CTGGGAGTAC TAGGGCGGCG CCGTCTTCC CGGCGCTG 1620
 CCACATGGCG GCTCTGCCA ACCCTCCCTG CTAACCCCTT CTCGCGCAGG TGGGCTCCAG 1680
 GCGGGGAGCG AAGCCCCCTT GCCTTTCAAA CTGGAACCC CAGAGAAAC GGTGCCCCCA 1740
 CCTGTGCGCC CTATGGACTC CCACTCTCTC CCTCGCGCG GGTTCCTTAC TCCCTCGG 1800

TCAGCGGCTG	CGGCTGGGCC	CTGGGAGGGA	TTCAGATGC	CCCTGCCCTC	TTGTCTGCCA	1860
CGGGGGAGT	CTGGCACCTC	TTTCTTCTGA	CCTCAGACGG	CTCTGAGCCT	TATTTCTCTG	1920
GAAGCGGCTA	AGGGACGGTT	GGGGGCTGGG	AGCCCTGGGC	GTGTAGTGTG	ACTGGAATCT	1980
TTTGCCTCTC	CCAGCCACCT	CCTCCAGACC	CCCCAGGAGA	GCTGGGCACA	TGTCCCAAGC	2040
CTGTCACTGG	CCCTCCCTGG	TGCACTGTCC	CGAAACCCC	TGCTTGGGAA	GGGAAGCTGT	2100
CGGGAGGGCT	AGGACTGACC	CTTGTGGTGT	TTTTTTGGGT	GGTGGCTGGA	AACAGCCCCC	2160
CTCCACGTG	GGAGAGGCTC	AGCCTGGCTC	CCTTCCCTGG	AGCGGCAGGG	CGTACGGGCT	2220
ACAGGGTCTG	CCCCGTGCAC	GTCTGCCTAA	GGTGTGGTGT	GCGGGCGGGT	AGGGGTGTGG	2280
GGGCGCTCTT	CCTCTGTCTT	CTTCTCTTTC	ACCCTAGCCT	GACTGGAAGC	AGAAAAATGAC	2340
CAAAATCAGTA	TTTTTTTAA	TGAAATATTA	TGCTGGAGG	CGTCCAGGC	AAGCCTGGCT	2400
GTAGTAGCGA	GTGATCTGGC	GGGGGGCGTC	TCAGCACCTC	CCCCAGGGGG	TGCATCTCAG	2460
CCCCCTCTTT	CCGTCTCTCC	CGTCCAGCCC	CAGCCCTGGG	CCTGGGCTGC	CGACACCTGG	2520
GCCAGAGCCC	CTGCTGTGAT	TGGTGTCTCC	TGGGCTCTCC	GGGTGGATGA	AGCCAGGGCT	2580
CGCCCCCTCC	GGGAGCCCTG	GGGTGAGCGG	CGGGGGCCCC	CCTGCTGCCA	GCCTCCCCCG	2640
TCCCCAACAT	GCACTCTCACT	CTGGGTGTCT	TGGTCTTTTA	TTTTTTGTAA	GTGTCAATTTG	2700
TATAACTCTA	AACGCCCATG	ATAGTAGCTT	CAAACTGGAA	ATAGCGAAAT	AAAATAACTC	2760
AGTCTGTC						

Seq ID NO: 341 Protein sequence
Protein Accession #: NP_003079

1	11	21	31	41	51	
MTANGTAEAV	QIQFGLINCG	NKYLTAEAFG	FKVNASASSL	KKKQIWTLEQ	PPDEAGSAAV	60
CLRSHLGRYL	AADKDGNVTC	EREVPGPDCR	FLIVAHDDGR	WSLQSEAHRR	YFGGTEDRLS	120
CFAQTVPSPAE	KWSVHIAMHP	QVNIYSVTRK	RYAHLRSARPA	DEIAVDRDVP	WGVDSLITLA	180
FQDQRYSVQT	ADHRFLRHDDG	RLVARPEPAT	GYTLBFRSGK	VAFRDCEGRY	LAPSGPSGTL	240
KAGKATKVGK	DELFALEQSC	AQVVLQAANE	RNVSTRQGM	LSANQDEETD	QETFQLEIDR	300
DTKKCAFRTH	TGKYWTLTAT	GGVQSTASSK	NASCYFDIEW	RDRRITLRAS	NGKFVTSKIN	360
GQLAASVETA	GDSLFLMKL	INRPIIVFRG	EHGFIGCRKV	TGTLIDANRSS	YDVFLQLEFND	420
GAYNIKDSTG	KYWTVGSDSA	VTSSGDTFPD	PFPEFCDYNK	VAIKVGGRYL	KGDHAGVLKA	480
SAETVDPASL	WEY					

Seq ID NO: 342 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 660..1705

1	11	21	31	41	51	
CGCTCCGCAC	ACATTTCTCTG	TCGCGGCCTA	AGGGAAACTG	TTGGCCGCTG	GGCCCGCGGG	60
GGGATTCTTG	GCAGTTGGGG	GGTCCGTCGG	GAGCGAGGGC	GGAGGGGAAG	GGAGGGGGAA	120
CCGGGTGGGG	GAAGCCAGCT	GTAGAGGGCG	GTGACCGCGC	TCCAGACACA	GCTCTGCGTC	180
CTCGAGCGGG	ACAGATCCAA	GTGGGAGCA	GCTCTGCGTG	CGGGGCTCA	GAGAATGAGG	240
CCGGCGTTTG	CCCTGTGCCT	CCTCTGGCAG	GCCTCTGGC	CCGGCCCGGG	CGCGCGCGAA	300
CACCCCACTG	CCGACCGTGC	TGGCTGTCTG	GCCTCGGGGG	CCTGCTACAG	CCTGCACCAC	360
GCTACCATGA	AGCGGCAGGC	GGCCGAGGAG	GCCTGCATCC	TGCGAGGTGG	GGCGCTCAGC	420
ACCGTGCCTG	CGGGCGCCGA	GCTGCGCGCT	GTGCTCGCGC	TCCTGCGGGC	AGGCCCAGGG	480
CCCGGAGGGG	GCTCCAAAGA	CCCTGCTGTC	TGGGTGCGAC	TGGAGCGCAG	CGCTTCCAC	540
TGCACCTCTG	AGAACGAGCC	TTTGGCGGGT	TTCTCTGGC	TGTCTCCGA	CCCGCGCGGT	600
CTCGAAGCG	ACAGCTGCA	GTGGGTGGAG	GAGCCCCAAC	GCTCCTGCAC	CGCGCGGAGA	660
TGCGCGGTAC	TCCAGGCCAC	CGGTGGGGTC	GAGCCCCCAG	CTGGAAGGAG	ATGCGATGCC	720
ACCTGCGCGC	CAACGGCTAC	CTGTGCAAGT	ACCACTTTGA	GGTCTTGTGT	CCTGCGCCGC	780
GCCTCGGGGG	CGCTCTTAAC	TTGAGCTATC	GCGCGCCCTT	CCAGCTGCAC	AGCGCGCTC	840
TGGACTTCAG	TCCACCTGGG	ACCGAGGTGA	GTGCGCTCTG	CCGGGACAG	CTCCGATCT	900
CAGTTACTTG	CATCGCGGAC	GAAATCGGCG	CTGCTGGGA	CAAACTCTCG	GGCGATGTGT	960
TGTGTCCCTG	CCCCGGGAGG	TACCTCCGTG	CTGGCAAAATG	CGCAGAGCTC	CCTAACTGCC	1020
TAGACGACTT	GGGAGGCTTT	GCCTGCGAAT	GTGCTACGGG	CTTGGAGCTG	GGGAAGGAGC	1080
GCCGCTCTTG	TGTGACCACT	GGGGAAGGAC	AGCCGACCCT	TGGGGGGACC	GGGGTCCCA	1140
CCAGGCGCCC	GCCCGCCACT	GCAACCAAGC	CCGTGCGCGA	GAGAACATGG	CCAATCAGGG	1200
TCGACGAGAA	GCTGGGAGAG	ACACCACTTG	TCCTGAACA	AGACAATTCA	GTAACATCTA	1260
TTCTCTGAGT	TCCTCGATGG	GGATCACAGA	GCACGATGTC	TACCTTCAA	ATGTCCCTTC	1320
AAGCCGAGTC	AAAGGCCACT	ATCACCCCAT	CAGGGAGCGT	GATTTCCAAG	TTTAATTCTA	1380
CGACTTCTCT	TGCCACTCCT	CAGGCTTTTG	ACTCTCTCTC	TGCCGTGGTC	TTTCAATTTG	1440
TGAGCACAGC	AGTAGTAGTG	TTGGTGATCT	TGACCATGAC	AGTACTGGGG	CTTGTCAAGC	1500
TCTGCTTTCA	CGAAAGCCCC	TCTTCCAGC	CAAGGAAGGA	GTCTATGGGC	CCGCCGGGCC	1560
TGGAGAGTGA	TCCTGAGCCC	GCTGCTTTGG	GCTCCAGTTC	TGCACATTGC	ACAAACAATG	1620
GGGTGAAAGT	CGGGGACTGT	GATCTGCGGG	ACAGAGCAGA	GGGTGCCCTG	CTGGCGGAGT	1680
CCCTCTTGG	CTCTAGTGAT	GCATAG				

Seq ID NO: 343 Protein sequence
Protein Accession #: FGENESH predicted

1	11	21	31	41	51	
MGKDFMTKTP	KAFATKAKID	KWDLIKLKSP	CTAKETIIRV	NSQPTDWQKT	FAIYPSDKGV	60
IARIYKELEQ	IYKKKKPKTK	LRTHFLSRPK	GNCWPLGPRG	DSWQLGGPSG	ARAEGKGGGT	120
GLGKPAVEGG	DRAPDTALRP	RAGQIQVGS	SACGASENEA	GVRPVPLLAG	ALARAGRRRT	180
PHCRPCWLLG	LGGLLQAPAP	YHEAAGGRGG	LHPARWGAQH	RACGRRAARC	ARAPAGRERA	240
RRGLQRPAVL	GRGTAQAFPL	HPGERAFAGF	LLAVLRFRRS	RKRHAHVGGG	APTLHLRAEM	300
RGTPGHRWGR	ARSWGEMRCH	LRANGYLCKY	QFEVLCAPAP	PGAASNLSYR	APFQLHSAAL	360
DFSPPGTEVS	ALCRGQLPIS	VTCIADEIGA	RWDKLSGDVL	CPCPGRYLRA	GKCAELPNCL	420
DDLGGFACEC	ATGFELGKDG	RSCVTSSEGG	PTLGGTGVPT	RRPPATATSP	VPQRTWPIRV	480
DEKLGETPLV	PEQDINSVTSI	PEIPRWGSQS	TMSTLQMSLQ	AESKATITPS	GSVISKFNS	540
TSSATPQAFD	SSSAVVFIPV	STAVVVLVIL	TMTVLGLVKL	CFHSPSSSQP	RKESMGPPGL	600
ESDPEPAALG	SSSAHCTNNG	VKVGDCDLRD	RAEGALLAES	PLGSSDA		

Seq ID NO: 344 DNA sequence
Nucleic Acid Accession #: NM_012072
Coding sequence: 149-2107

5
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
AAAGCCCTCA	GCCTTTGTGT	CCTTCTCTGC	GCCGGAGTGG	CTGCAGCTCA	CCCTCAGCT	60
CCCTTGGGG	CCCAGTGGG	AGCCGAGATA	GAAGCTCCTG	TCGCCGCTGG	GCTTCTGCC	120
TCGCCGAGAG	GGCCACACAG	AGACCGGGAT	GGCCACCTCC	ATGGGCTGCG	TGCTGCTGCT	180
GCTGCTGCTC	CTGACCCAGC	CCGGGGCGGG	GACGGGAGCT	GACACGGAGG	CGGTGGTCTG	240
CGTGGGGACC	GCCTGTCTACA	CGGCCCCACTC	GGGCAAGCTG	AGCGCTGCCG	AGGCCAGAA	300
CCACTGCAAC	CAGAACGGGG	GCAACCTGGC	CACTGTGAAG	AGCAAGGAGG	AGGCCAGCA	360
CGTCCAGCGA	GTACTGGCCC	AGCTCCTGAG	GCGGGAGGCA	GCCCTGACGG	CGAGGATGAG	420
CAAGTCTTGG	ATTGGGCTCC	AGCGAGAGAA	GGGCAAGTGC	CTGGACCCTA	GTCTGCCGCT	480
GAAGGGCTTC	AGCTGGGTGG	GCGGGGGGGA	GGACACGCCT	TACTCTAACT	GGCACAAGGA	540
GCTCCGGAAC	TCGTGCATCT	CCAAGCGCTG	TGTGTCTCTG	CTGCTGGACC	TGTCCAGGCC	600
GCTCTCTCCC	AACCGCTGCG	CCAAGTGGTG	TGAGGGCCCC	TGTGGGAGCC	CAGGCTCCCC	660
CGGAAGTAAC	ATTGAGGGCT	TCGTGTGCAA	GTTTCACTTC	AAAGGATGTG	GCCGGCTCT	720
GGCCCTGGGG	GGCCAGGCTC	AGGTGACCTA	CACCACCCCC	TTCAGACCA	CCAGTTCCTC	780
CTTGGAGGCT	GTGCCCTTTG	CCTCTGCGGC	CAATGTAGCC	TGTGGGGAAG	GTGACAAGGA	840
CGAGACTCAG	AGTCATTATT	TCCTGTGCAA	GGAGAAGGCC	CCCGATGTGT	TGACTGGGG	900
CAGCTCGGGC	CCCCTCTGTG	TCAGCCCCAA	GTATGGCTGC	AACTTCAACA	ATGGGGGCTG	960
CCACCAGGAC	TGCTTTGAAG	GGGGGGATGG	CTCTTCTCTC	TGCGGCTGCC	GACCAGGATT	1020
CCGGCTGTCTG	GATGACCTGG	TGACCTGTGC	CTCTCGAAAC	CCTTGCAGCT	CCAGCCCATG	1080
TCGTGGGGGG	GCCACGTGGC	TCTTGGGACC	CCATGGGAAA	AACTACACGT	GCCGCTGCCC	1140
CCAAGGTTAC	CAGCTGGAAT	CGAGTCAGCT	GGACTGTGTG	GACGTGGATG	AATGCCAGGA	1200
CTCCCCCTGT	GCCCAAGAGT	GTGTCAACAC	CCCTGGGGGC	TTCGCTGCG	AATGTGGGT	1260
TGGCTATGAG	CCGGGCGGTC	CTGGAGAGGG	GGCCTGTGAG	GATGTGGATG	AGTGTGCTCT	1320
GGGTGCTGCG	CCTTGGCCCC	AGGGCTGCAC	CAACACAGAT	GGCTCATTTT	ACTGCTCCTG	1380
TGAGGAGGGC	TACGTCTCTG	CCGGGGAGGA	CGGGACTCAG	TGCCAGGACG	TGGATGAGTG	1440
TGTGGGCCCC	GGGGGGCCCC	TCTTGGACAG	CTTGTGCTTC	AACACACAAG	GGTCTTTCCA	1500
CTGTGGTCTG	CTGCCAGGCT	GGGTGCTGGC	CCCAAATGGG	GTCTCTTGCA	CCATGGGGCC	1560
TGTGTCTCTG	GGACCAACAT	CTGGGGCCCC	CGATGAGGAG	GACAAGGAGG	AGAAAGAAAG	1620
GAGCACGCTG	CCCCGCGCTG	CAACAGCCAG	TCCCAACAAG	GGCCCCGAGG	GCACCCCAAA	1680
GGCTACACCC	ACCACAAGTA	GACCTTCGCT	GTCACTGACG	GCCCCATCA	CATCTGCCCC	1740
ACTCAAGATG	CTGGCCCCCA	GTGGGTCTCT	AGGCGTCTGG	AGGGAGCCCA	GCATCCATCA	1800
CGCCACAGCT	GCCTCTGGCC	CCCAGGAGCC	TGCAGGTGGG	GACTCCTCCG	TGGCCACACA	1860
AAACAACGAT	GGCATGACG	GGCAAAAGCT	GCTTTTATTC	TACATCTAG	GCACCGTGGT	1920
GGCCATCCTA	CTCTGTCTGG	CCCTGGCTCT	GGGGCTACTG	GTCTATCGCA	AGCGGAGAGC	1980
GAAGAGGGAG	GAGAAGAAGG	AGAAGAAGCC	CCAGAATGCG	GCAGACAGTT	ACTCCTGGGT	2040
TCCAGAGCGA	GCTGAGAGCA	GGGCCATGGA	GAACCACTAC	AGTCCGACAC	CTGGGACAGA	2100
CTGCTGAAAG	TGAGGTGGCC	CTAGAGACAC	TAGAGTCACC	AGCCACCATC	CTCAGAGCTT	2160
TGAACTCCCC	ATTCCAAGGG	GGCACCCACA	TTTTTTTGAA	AGACTGGACT	GGAATCTTAG	2220
CAAAACAATTG	TAAGTCTCCT	CCTTAAAGGC	CCCTTGGAAC	ATGCAGGTAT	TTTCTACGGG	2280
TGTTTATGAT	TCCTGAAGTG	GAAGCTGTGT	GTGCGGTGCG	CACGGTGGGG	ATTTCTGTAC	2340
TCTATAATGA	TTGTTACTCC	CCCTCCCTTT	TCAAATTCGA	ATGTGACCAA	TTCGGATCA	2400
GGGTGTGAGG	AGGCTGGGGC	TAAGGGGCTC	CCCTGAATAT	CTTCTCTGCT	CACTTCCACC	2460
ATCTAAGAGG	AAAAGGTGAG	TGTCTCATGC	TGATTAGGAT	TGAAATGATT	TGTTTCTCTT	2520
CTTAGGATGA	AACTAAATC	AAATTAATTAT	TCAATTAGGT	AAGAAGATCT	GGTTTTTTGG	2580
TCAAAGGGAA	CATGTTCCGA	CTGGAACAT	TTCTTTACAT	TGCAATTCCT	CCATTTCGCC	2640
AGCACAGTCT	TTGCTAAATG	TGATACTGTT	GACATCCTCC	AGAAATGGCA	GAAGTGCAAT	2700
TAACCTCTTA	GGTGGCAAGG	AGGCAGGAAG	TGCCTCTTTA	GTTCTTACAT	TTCTAATAGC	2760
CTTGGGTTTA	TTTGCAAGG	AAGCTTGAAA	AATATGAGAA	AAGTTGCTTG	AAGTGCAATTA	2820
CAGGTGTTTG	TGAAGTCACA	TAATCTACGG	GGCTAGGGCG	AGAGAGGCCA	GGGATTGTGT	2880
CACAGATACT	TGAATTAATT	CATCCAAATG	TACTGAGGTT	ACCACACACT	TGACTACGGA	2940
TGTGATCAAC	ACTAACAAAG	AAACAAATTC	AAGGACAAAC	TGTCTTTGAG	CCAGGGCAGG	3000
CCTCAGACAC	CCTGCCTGTG	GCCCCGCCCTC	CAGTTTATCC	TGCCCGGAAT	GCCAGTGCTC	3060
CGAGCTCAGA	CAGAGGAAGC	CCTGCAGAAA	GTTCCATCAG	GCTGTTTCTT	AAAGGATGTG	3120
TGAACGGGAG	ATGATGCACT	GTGTTTGAAG	AGTTGTCAAT	TAAAGCATT	TAGCACAGT	3180
TCATAGTCCA	CAGTTGATGC	AGCATCCTGA	GATTTTAAAT	CCTGAAGTGT	GGGTGGCGCA	3240
CACACCAAGT	AGGGAGCTAG	TCAGGCAAGT	TGCTTAAGGA	ACTTTTGTTC	TCTGTCTCTT	3300
TTCTTTAAAA	TTGGGGGTAA	GGAGGGGAAG	AAGAGGGAAA	GAGATGACTA	ACTAAAAATCA	3360
TTTTTACAGC	AAAACTGCT	CAAGCCATT	TAAATTATAT	CCTCATTTTA	AAAGTTACAT	3420
TTGCAAAATAT	TTCTCCCTAT	GATAATGCAG	TCGATAGTGT	GCACTCTTTC	TCTCTCTCTC	3480
TCTCTCTCAC	ACACACACAC	ACACACACAC	ACACACACAC	AGAGACACGG	CACCATCTGT	3540
CCTGGGGCCTC	TGGAACACAT	TCCTGGGGGT	CACCGATGGT	CAGAGTCACT	AGAAGTTACC	3600
TGAGTATCTC	TGGGAGGCCCT	CATGTCTCCT	GTGGGCTTTT	TACCACCACT	GTGCAGGAGA	3660
ACAGACAGAG	GAAATGTGTC	TCCCTCCAAG	GCCCCAAAGC	CTCAGAGAAA	GGGTGTTTCT	3720
GGTTTGTGCT	TAGCAATGCA	TGGTCTCTG	AGGTGACACT	CTGGAGTGGT	TGAAGGGCCA	3780
CAAGGTGCGC	GGTTAAACT	CTTGCCAGTT	TGAAATATA	GATGCTATGG	TTCAGATTGT	3840
TTTTTAATAGA	AAACTAAAGG	GGCAGGGGAA	GTGAAAGGAA	AGATGGAGGT	TTTGTGCGGC	3900
TCGATGGGGC	ATTTGGAAC	TCTTTTAAA	GTCACTCAT	GGTCTCCAGT	TTTCAGTTGG	3960
AACTCTGGTG	TTTAACACTT	AAGGGAGACA	AAGGCTGTGT	CCATTGGGCA	AAACTTCTCT	4020
GGCCACGAGA	CTCTAGGTGA	TGTGTGAAGC	TGGGCAGTCT	GTGGTGTGGA	GAGCAGCCAT	4080
CTGTCTGGCC	ATTTCAGAGG	TTCTAAAGAC	ATGGCTGGAT	GCGCTGCTGA	CCAACATCAG	4140
CACTTAAATA	AATGCAAAATG	CAACATTCT	CCCTCTGGGC	CTTGAAAATC	CTTGCCCTTA	4200
TCATTTGGGG	TGAAGGAGAC	ATTTCTGTCC	TGGCTTCCC	ACAGCCCCAA	CGCAGTCTGT	4260
GTATGATTCC	TGGGATCCAA	CGAGCCCTCC	TATTTTCACA	GTGTTCTGAT	TGCTCTCACA	4320
GGCCAGGCCC	ATCGTCTGTT	CTCTGAATGC	AGCCCTGTTC	TCAACAACAG	GGAGGTCTATG	4380
GAACCCCTCT	GTGGAACCCA	CAAGGGGAGA	AATGGGTGAT	AAAGAATCCA	GTTCCTCAAA	4440
ACCTTCCCTG	GCAGGCTGGG	TCCTCTCCT	GCTGGGTGGT	GCTTCTCTCT	GCACACCACT	4500
CCACACAGGG	GGGGAGAGCC	AGCAACCCAA	CCAGACAGCT	CAGGTTGTGC	ATCTGATGGA	4560
AACCACTGGG	CTCAACACG	TGCTTTATTC	TCCTGTTTAT	TTTTGCTGTT	ACTTTGAAGC	4620
ATGGAAATTC	TTGTTTGGGG	GATCTTGGGG	CTACAGTAGT	GGGTAAACAA	ATGCCACCG	4680
GCCAAGAGGC	CATTAAACAA	TGCTCTTGT	CCTGAGGGGC	CCCAGCTTGC	TGGGGCGTGG	4740
CACAGTGGGG	AATCCAAGGG	TCACAGTAGT	GGGAGAGGTG	CACCTGCCCA	CCTGCTAACT	4800

TCTCGCTAGA CACAGTGTTC CTGCCAGGT GACCTGTTC GACAGAGAAC AAGCCAGGGC 4860
 CATGGGGAAC GGGGAAGTTT TCACTTGGAG ATGGACACCA AGACAATGAA GATTTGTGTG 4920
 CCAAAATAGT CAATAATCTT GGGAGACTCT TGGAAAAAAC TGAATATATT CAGGACCAAC 4980
 TCTCTCCTCT CCTCATCTCC ACATCTCAAA GCAGACAATG TAAAGAGAGA ACATCTCACA 5040
 CACCCAGCTC GCCATGCCTA CTCATTCTCG AATTTCAGGT GCCATCAGTG CTCTTTCTTT 5100
 CTCTTTGTTC ATTTGAGAAA GGTATGCAGG GACAAATTC CACAGATAAT CTGAGGAATG 5160
 CAGAAAAAAC AGGGCAGGAC AGTTATCGAC AATGCATTAG AACTTGGTGA GCATCTCTCG 5220
 TAGAGGGAAT CACCCCTGCG TCAACAGCTT GGCTTCCAGG CAAGACCAAC CACATCTGGT 5280
 CTCTGCCTTC GGTGGCCAC ACACCTAAGC GTCATCGTCA TTGCCATAGC ATCATGATGC 5340
 AACACATCTA CGTGTAGCAC TACGACGTTA TGTTTGGGTA ATGTGGGGAT GAATCTGCATG 5400
 AGGCTCTGAT TAAGATATGT GGGAAAGTGG CTGCGGTCTC TGTGCGCCTT GCAAGGCCAC 5460
 CTGGAGGCCT GTCTGTAGC CAGTGGTGGG GGAGCAAGGC TTCAGGAAGG GCCAGCCACA 5520
 TGGCATCTTC CCTGCGATCA GGCAAAAAAG TGGAAATAAA AAGTCAAACC TTTATATGCA 5580
 TGTGTTATGT CCATTTTGCA GGATGAACCT AGTTTAAAAG AATTTTCTTT TCTCTTCAAG 5640
 TTGCTTTGTC TTTTCCATCC TCATCAACAAG CCCTTGTGTT AGTGTCTTAT CCTGAGCAA 5700
 TCTTTCGATG GATGGAGATG ATCATTAGGT ACTTTTGTTC CAACCTTTAT TCCTGTAAAT 5760
 ATTTCTGTGA AAATAGGAG AACAGAGATG AGATTTGACA AAAAAAATTT GAATTAATAA 5820
 TAACACAGT TTTTAAAC TAACATAGGA AAGCCTTTC TATTATTCTT CTCTTAGCT 5880
 TCTCCATTGT CTAATCAGG AAAACAGGAA AACACAGCTT TCTAGCAGCT GCAAAATGGT 5940
 TTAATGCCCC CTACATATTT CCATCACCTT GAACAATAGC TTAGCTTGGG GAATCTGAGA 6000
 TATGATCCCA GGAACATCTT GTCTTACTT CGGCTGCAAA ACCCATGGTT TAAATCTATA 6060
 TGGTTTGTGC ATTTTCTCAA CTAATAATAG AGATGATAAT CCGAATTCTC CATATATTC 6120
 CTAATCAAAG ACATATTTT CACTACTAGT TCCTGAGACA AATACTCACT GAAGGGCTTG 6180
 TTTAAAAATA AATTGTGTT TGGTCTGTT TGTAGATAA TGCCCTTCTA TTTTAGTAG 6240
 AAGCTCTGGA ATCCCTTTAT TGTGCTGTT CTCTTATCTG CAAGGTGGCA AGCAGTCTT 6300
 TTCAGCAGAT TTTGCCACT ATTCTCTGA GCTGAAGTTC TTTGCATAGA TTTGGCTTAA 6360
 GCTTGAATTA GATCCCTGCA AAGGCTTGT CTGTGATGTC AGATGTAATT GTAAATGTCA 6420
 GTAATCACTT CATGAATGCT AAATGAGAAT GTAAGTATTT TTAATGTGT GTATTTCAA 6480
 TTTGTTTGA TAATCTGGA ATTACAAGAT TTCTATGCAG GATTACCTT CATCTGTGC 6540
 ATGTTTCCCA AACTGTGAG AGGGAAGGCT CAGAGATCGA GCTTCTCTC TGAGTTCTAA 6600
 CAAATAGGTG CTTTGGGGT CAGCCTTAG GAAGGTGCAG CTTTGTGTC CTTTGAGCTT 6660
 TCTGTTATGT GCCTATCCTA ATAACTCTT AAACACATT

Seq ID NO: 345 Protein sequence
 Protein Accession #: NP_036204

1 11 21 31 41 51
 MATSMGLLLL LLLLLTPQGA GTGADTEAVV CVGTACYTAH SGKLSAAEAQ NHCNQNGGNL 60
 ATVKSKEEAQ HVQRVLAQLL RREAALTARM SKFWIGLQRE KGKCLDPSLP LKGFSSVWGGG 120
 EDTFYSNWHK ELRNSISLKR CVSLLLDLSQ PLLPNRLPKW SEGPGSPSGS PGSNIEGFVC 180
 KFSFKGMCRP LALGGPGQVT YTFPQTSS SLEAVPFASA ANVACGEGDK DETQSHYFLC 240
 KEKAPDVFDW GSSGPLCVSP KYGCNFNNGG CHQDCFEEDG GSFLGCRPG FRLLDDLVT 300
 ASRNPSSSPS CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDECG DSPCAQECVN 360
 TPGGFRCECW VGYEPGGPGE GACQDVDECA LGRSPCAQGC TNTDGSFHC SCEEYVLAGE 420
 DGTQCQDVDE CVGPGGPLCD SLFCNTQGSF HCGCLPGWVL APNGVSCSTM FVSLGPPSPGP 480
 PDDEKGEKE GSTVPRATA SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLKMLAPSGS 540
 SGVWREPSIH HATAASGPQE PAGDSSSVAT QNNDGTDGQK LLLFYILGTV VAILLLLALA 600
 LGLLVYRKR AKREEKKEKK PQNAADSYSW VPERAESRAM ENQYSPTPGT DC

Seq ID NO: 346 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: <1-966

1 11 21 31 41 51
 CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCCGGG CCCGCAGCAA 60
 ACTTCGGGGG GCGGCGGGCG CAATCCACCC GCGGCGGGCG CCGGCGGCAA CCAGAAAAAC 120
 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGTTCCCG CCGGCAGCGG 180
 CGCAAGATGG CCCAGAGAAA CCCCAGATG CACAACCTCG AGATCAGCAA GCGCCTGGGG 240
 GCGGAGTGGG AACTTTTGTG GGAGACGGAG AAGCGGCGGT TCATCGACGA GGCTAAGCGG 300
 CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAACCC 360
 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGCTGCTGGC CCCGCGGGCG 420
 AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCGGCGCTGG GCGGCGGGCG GAACCAAGCG 480
 ATGGACAGTT ACGCCGACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540
 CAGCTGGGCT ACCCGCAGCA CCGGGGCTCT AATGCCGACG GCGCAGCGCA GATGCAGCCC 600
 ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACCTCA TGACAGCTC GCAGACCTAC 660
 ATGAACGGCT CCGCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTCTGG GTTCAAGTCC GAGGCCAGCT CCAGCCCCCC TGTGGTTACC 780
 TCTTCTCTCC ACTCCAGGGC GCCTTGCAG GCGGGGAGC TCCGGGACAT GATCAGCATG 840
 TATCTCCCCG GCGCGAGGTT GCGGGAACCC GCGGCCCCCA GCAGACTTCA CATGTCCAG 900
 CACTACCAGA GCGGCCCGGT GCGGCCGACG GCCATTAAAC GCACACTGCC CCTCTCAC 960
 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACAGGGGAAA 1020
 TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAA 1080
 AAAAA

Seq ID NO: 347 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
 HSARMYNMME TELKPPGPQQ TSGGGGNGST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR 60
 RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRLHMKRHP DYKYPRRRQ 120
 KTLMKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGYSMMQD 180
 QLGYFQHPGL NAHGAQMOP MHRVDVSLQ YNSMTSSQTY MNGSPYTSMS YSQGTPGMA 240
 LGSMSVVK SSSSPVVVT SSSSRAPCQ AGDLRDMISM YLPGAEPVPEP AAPSRLEHMSQ 300
 HYQSGVPVPT AINGTLPLSH M

Seq ID NO: 348 DNA sequence
Nucleotide Accession #: NM_002638
Coding sequence: 120-473

```
5      1      11      21      31      41      51
      |      |      |      |      |      |
      CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
10     GCTGGAGTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
      TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
      AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
      TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAA 300
      CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
15     TCCGCTGCGC CATGTTGAAT CCCCTAACCC GCTGCTTGA AGATACTGAC TGCCACAGGA 420
      TCAAGAAGTG CTGTGAAGGC TCTTGGCGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
      CGGTCTCTGC TGCACTCTGT CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
      TGCTGCCCTT CCCCTCCCA CACTGTCCAT TCTTCTCCC ATTCAAGATG CCCACGGCTG 600
      GAGCTGCCCTC TCTCATCCAC TTTCCAATAA A
```

Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

```
25     1      11      21      31      41      51
      |      |      |      |      |      |
      MRASSFLIVV VFLIAGTLVL EAAVTGVFVK GQDTVKGKRP FNGQDPVKQ VSVKQDKVK 60
      AQEPVKGPVS TKPGSCPIIL IRCAMLNPFN RCLKDTDCPG IKKCEGSCG MACFVPQ
```

Seq ID NO: 350 DNA sequence
Nucleic Acid Accession #: NM_007183
Coding sequence: 75-2468

```
35     1      11      21      31      41      51
      |      |      |      |      |      |
      GAATTCCGGA CAGGACGTGA AGATAGTTGG GTTTGGAGGC GGCCGCCAGG CCCAGGCCCG 60
      GTGGACCTGC CGCATGCAG GACGGTAACT TCCTGCTGTC GGCCCTGCAG CCTGAGGCCG 120
      GCGTGTGCTC CCTGGCGCTG CCCTCTGACC TGCAGCTGGA CCGCCGGGGC GCCAGGGGGC 180
      CGGAGGCCGA GCGGCTGCGG GCAGCCCGCG TCCAGGAGCA GGTCCGGGCC CGCCTCTTGC 240
      AGCTGGGACA GCAGCCCGCG CACAACGGGG CCGCTGAGCC CGAGCCTGAG GCCGAGACTG 300
40     CCAGAGGCAC ATCCAGGGGG CAGTACCACA CCCTGCAGGC TGGCTTCAGC TCTCGCTCTC 360
      AGGSCCTGAG TGGGACAAG ACCTCGGGCT TCCGGCCCAT CGCAAAGCG GCCTACAGCC 420
      CAGCCTCTCTG GTCTCTCCGC TCCGCCGTGG ATCTGAGCTG CAGTCGGAGG CTGAGTTTCA 480
      CCCACAATGG GGGCAGCGCC TTGGGGCCCG CTGGGTACGG GGGTGCCAG CCCACCCCTC 540
      CCATGCCACAG CAGGCCCGTG TCCTTCCATG AGCGCGGTGG GGTGGGAGC CGGGCCGACT 600
45     ATGACACACT CTCCTGCGC TCGCTGCGGC TGGGGCCCGG GGGCCTGGAC GACCCTACA 660
      GCCTGGTGTG TGAGCAGCTG GAGCCCGCGG CCACCTCCAC CTACAGGGCC TTTGCGTACG 720
      AGCGCCAGGC CAGTCTCAGC TCAGCCCGG CAGGGGGGCT GAGCTGGCCC GAGGCCACTG 780
      AGGTTTCCCC GAGCCGAGC ATCCGTGCCC CTGCCGTGCG GACCCTGCAG CGATTCCAGA 840
      GCAGCCACCG GAGCCCGGGG GTAGGCGGGG CAGTGCCGGG GGGCGTCTG GAGCCAGTGG 900
50     CTGAGAGGCC ATCTGTGCGC AGCCTCAGCC TCAGCTGGC TGACTCGGGC CACTTGCCTG 960
      ACGTGCATGG GTTCAACAGC TAGGTAGCC ACCGAACCTT GCAGAGACTC AGCAGCGGTT 1020
      TTGATGACAT TGACCTGCCC TCAGCAGTCA AGTACCTCAT GGCTTCAGAC CCCAACCTGC 1080
      AGGTGCTGGG AGCGGCTTAC ATCCAGCACA AGTGCTACAG CGATGCAGCC GCCAAGAAGC 1140
      AGGCCCGCAG CCTTCAGGCC GTGCCTAGGC TGGTGAAGCT CTTCACCCAC GCCAACAGG 1200
55     AAGTGCAGCG CCATGCCACA GGTGCCATGC GCAACCTCAT CTACGACAA GCTGACAACA 1260
      AGCTGGCCCT GGTGGAGGAG AACGGGATCT TCGAGTCTGT CGGACACTG CGGGAGCAGG 1320
      ATGATGAGCT TCGCAAAAT GTACAGGGA TCCTGTGAA CCTTTCATCC AGCGACCAAC 1380
      TGAAGGACCG CCTGGCCAGA GACACGCTGC AGCAGCTCAC GAGCCTGGT TTGAGCCCC 1440
      TGTGGGGGCG TGGGGGTCCC CCCCTCATCC AGCAGAACGC CTCGGAGGCG GAGATCTTCT 1500
60     ACAAGCCAC CGGCTTCTCT AGGAACCTCA GCTCAGCCTC TCAGGCCACT CGCCAGAAGA 1560
      TGCGGGAGTG CCAGGACAAG AGCGTGGAGA ACGCGGTGTG CGTCTGCGG AACCTGTCTT 1680
      CGGGCAATG CGAGGACAAG AGCGTGGAGA ACGCGGTGTG CGTCTGCGG AACCTGTCTT 1680
      ACCGCTCTA CGAGGAGATG CCGCGCTCCG CGCTGCAGCG GCTGGAGGGT CGCGGCCGCA 1740
      GGGACCTGGC GGGGGCGCG CCGGAGAGG TCGTGGGCTG CTTACGCGC CAGAGCCGCG 1800
65     GGCTGCGCGA GCTGCCCTCT GCGCGCGATG CGCTCACCTT CGCGGAGGTG TCCAAGGACC 1860
      CCAAGGGCCT CGATGCTGTG TGGAGCCCC AGATGCTGGG GCTGTACAAC CGGCTGTCTG 1920
      AGCGCTGCGA GCTCAACCGG CACACGACGG AGGCGGCGCG CGGGGCGCTG CAGAACATCA 1980
      CGGCAGGCGA CCGCAGGTGG GCGGGGTGTC TGAGCCGCTT GGCCTGGAG CAGGAGCGTA 2040
      TTCTGAACCC CCTGCTAGAC CGTGTAGGA CCGCGACCA CCACAGCTG CGCTCACTGA 2100
70     CTGGCCTCAT CCGAAACCTG TCTCGGAACG CTAGGAACAA GGACGAGATG TCCACGAAGG 2160
      TGGTGAAGCA CCTGATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTGG CCCCAGCGCG 2220
      AGGTGCTGGT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCCATCGCTG 2280
      CCCAGACCT GCTGTATTTT GACGGACTCC GAAAGCTCAT CTTATCAAG AAGAAGCGGG 2340
      ACAGCCCGGA CAGTGAGAAG TCCTCCCGGG CAGCATCCAG CCTCTGGCC AACCTGTGGC 2400
75     AGTACAACAA GCTCCACCGT GACTTTGCGG CGAAGGGCTA TCGGAAGGAG GACTTCTTGG 2460
      GCCATAGGT GAGCCCTTCT GGAGGAGAAG GTGACGTGGC CCAGCGTCCA AGGGACAGAC 2520
      TCAGCTCCAG GCTGCTTGGC AGCCAGCCT GGAGGAGAAG GCTAATGACG GAGGGGCCCC 2580
      TCGCTGGGCG CCTGTGTGTC ATCTTTGAGG GTCCTGGGCC ACCAGGAGGG CAGGGTCTT 2640
80     ATAGCTGGGG ACTTGGCTTC CGCAGGGCAG GGGGTGGGGC AGGGCTCAAG GCTGCTCTGG 2700
      TGTATGGGGT GGTGACCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCCTGGCAGT 2760
      ATCTTGGGAT AGCAGCACT GGAATAAAG ATGGCCATGA ACAGTCACAA AAAAAAAAAA 2820
      AAAAGGAATT C
```

Seq ID NO: 351 Protein sequence:
Protein Accession #: NP_009114.1

```
85     1      11      21      31      41      51
```

MQDGNFLLSA LQPEAGVCSL ALPSDLQLDR RGAEGPEAER LRAARVQEQV RARLLQLGQQ 60
PRHNGAAEPE PEAEATARGTS RGQYHTLQAG FSSRSQGLSG DKTSGFRPIA KPAYSASPWS 120
SRSAVDLSCS RRLSSAHNGG SAFGAAGYGG AQPTPPMPTR PVSFHERGGV GSRADYDTLS 180
5 LRSRLRLPGGG LDDRYSLVSE QLEPAATSTY RAFAYERQAS SSSSRAGGLD WPEATEVSPS 240
RTIRAPAVRT LQRFQSSHRS RGVGGA VPGA VLEPVARAPS VRSLSLSLAD SGHLPDVHGF 300
NSYGSHTLQ RLSSGFDDID LPSAVKYLMA SDPNLQVLGA AYIQHKCYSD AAAKKQARSL 360
QAVPRLVKLF NHANQEVQRH ATGAMRNLIY DNADNKLALV EENGI FELLR TLREQDDELRL 420
KNVTGILWNL SSSDHLKDR LARDTLEQLTD LVLSPLSGAG GPPLIQNAS EAEIFYNATG 480
10 FLRNLSSASQ ATRQRMRECH GLVDALVTSI NHALDAGKCE DKSVENAVCV LRNLRYLYD 540
EMPFSALQRL EGRGRRLDAG APPGEVVGCF TPQSRRLREL PLAADALTFA EVSKDPKGLE 600
WLWSPQIVGL YNRLLQRCCL NRHTTEAAAG ALQNTAGDR RWAGVLSRLA LEQERILNPL 660
LDRVRTADHH QLRSLTGLIR NLSRNARNKD EMSTKVVSHL IEKLEPGSVGE KSPPAEVLVN 720
15 IIAVLNNLVV ASPIAARDLL YFDGLRLKLF IKKKRSDSPS EKSSRAASSL LANLWQYNKL 780
HRDFRAKGYR KEDFLGP

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

1 11 21 31 41 51
ATGGCTGCGC AGGGAGAGCC CCAGGTCCAG TTCAAACCTG TATTGGTTGG TGATGGTGGT 60
25 ACTGGAAAAA CGACCTTCGT GAAACGTCAT TTGACTGGTG AATTGTAGAA GAAGTATGTA 120
GCCACCTTGG GTGTGTAGGT TCATCCCCCTA GTGTTCCACA CCAACAGAGG ACCTATTAAAG 180
TTCAATGTAT GGGACACAGC CGGCCAGGAG AAATTCGGTG GACTGAGAGA TGGCTATTAT 240
ATCCAAGCCC AGTGTGCCAT CATAATGTTT GATGTAACAT CGAGAGTTAC TTACAAGAAT 300
GTGCCTAACT GGCATAGAGA TCTGGTAGCA GTGTGTGAAA ACATCCCCAT TGTGTTGTGT 360
30 GGCAACAAAG TGGATATTAA GGACAGGAAA GTGAAGGCGA AATCCATTGT CTTCACCGA 420
AAGAAGAATC TTCAGTACTA CGACATTCTT GCCAAAAGTA ACTACAACCT TGAAGAAGCCC 480
TTCTCTGGC TTGCTAGGAA GCTCATTTGA GACCCTAACT TGGAAATTGT TGCCATGCCT 540
GCTCTCGCCC CACCAAGAGT TGTATGGAC CCAGCTTTGG CAGCACAGTA TGAGCAGCAC 600
35 TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG ATGACCTGTG A

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

1 11 21 31 41 51
MAAQGEPOVQ FKLVLVGDGG TGKTFVVKRH LTGEFEKKYV ATLGVEVHPL VFHTNRGPIK 60
40 FNVWDTAGQE KFGGLRDGYI IQAQCAIIMF DVTSRVITYKN VPWHRDLVR VCENIPIVLC 120
GNKVDIKDRK VKAKSIVFHR KKNLQYYDIS AKSNYNFEKP FLWLARKLIG DPNLEFVAMP 180
45 ALAPPEVVM D PALAAQYEH D LEVAQTALP DEDDDL

Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

1 11 21 31 41 51
CCGTTTCGCA AAGAAGCTGA CTTAGAGGG GGAACCTTC TTCTTTTAGG AGGCGGTTAG 60
55 CCCTGTTCCA CGAACCCAGG AGAAGCTGCTG GCCAGATTAA TTAGACATTG CTATGGGAGA 120
CGTGTAACA CACTACTTAT CATTGATGCA TATATAAAAC CATTTTATT TCGCTATTAT 180
TTCAGAGGAA GCGCTCTCGA TTTGTTTCTT TTTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
GTTTGGAGAA AGCAGAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCGAGC GCGAGCGGAG 300
ACGATGCAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCTGCT GAGCTACGCG 360
60 GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT 420
GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTCT 480
CTTCACCATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC 540
CCTAACTCCA AGCCTCTCCT CAACACAAAG AACCACCCCG TCCGATTGGG GTCTGATGAT 600
GAGGGCAGAT ACCTAACTCA GGAAGCTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC 660
65 AAGACACCTG GGAAGAAAAA GAAAGGCAAG CCCGGGAAAC GCAAGGAGCA GGAAGAGAAA 720
AAAGCGCGAA CTCGCTCTGC CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG 780
GACCACCTGT CTGACACCTC CACACAGCTG CTGGAGCTCG ATTCACGGTA ACAGGCTTCT 840
CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTTT GGAGCCTCCC TTCTGCCTTG 900
70 GCTTGGACAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA 960
CAGAGAATAA CTCAGAATAT TGTCTGCCTT AAAGCAGTAC CCCCCTACCA CACACACCCC 1020
TGTCTCCAG CACCATAGAG AGGCGCTAGA GCCCATTCCT CTTTCTCCAC CGTCACCCAA 1080
CATCAATCCT TTACCACTCT ACCAAATAAT TTCATATTCA AGCTTCAGAA GCTAGTGACC 1140
ATCTTCATAA TTGCTGGAG AAGTGTATT TTTCCCTTCA CTCTCACACC TGGGCAAACT 1200
75 TTCTTCAGTG TTTTTCATT TTTACGTTCT TTCACITCAA GGGAGAATAT AGAAGCATTT 1260
GATATTATCT ACAACACTG CAGAACAGCA TCATGTGATA AACGATTCTG AGCCATTAC 1320
ACTTTTATT TAATTAATG TATTTAATTA AATCTCAAAT TTATTTTAA GTAAAGAACT 1380
TAAATTATGT TTTAAACACA TGCCTTAAAT TTGTTTAATT AAATTTAACT CTGTTTCTTA 1440
CCAGCTCATA CAAAATAAAT GGTTCCTGAA AATGTTTAA TATTAACITTA CAAGGATATA 1500
80 GGTTCCTCTC ATGTATCTTT TTGTTTCTG GCAAGATGAA ATAAATTTTC TAGGGTAATG 1560
CCGTAGGAAA AATAAAACTT CACATTTAAA AAAAA

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

1 11 21 31 41 51
MQRRVQQWS VAVFLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRPFL 60
85 HHLIAEIHIA EIRATSEVSP NSKPSPTNKN HPVRFSGSDE GRYLTQETNK VETYKEQPLK 120

TPGKKKKGKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR

Seq ID NO: 356 DNA sequence

Nucleic Acid Accession #: NM_017522

Coding sequence: 1-2100

5
10
15
20
25
30
35
40
45
50

1 11 21 31 41 51
| | | | | |
ATGGGCTCC CCGAGCCGG CCTCTCOGG CTCTGCGCG TGCTGCTGCT GCTGCTGCTG 60
CTGCTGCTGC TCGGCTTCCA GCATCTTGG GCGGCAGCG CTGATCCGCT GCTCGGCGGC 120
CAAGGGCCGG CCAAGGAGTG CGAAAAGGAC CAATTCCAGT GCGGAAACGA GCGCTGCATC 180
CCCTCTGTGT GGAGATGCGA CGAGGACGAT GACTGCTTAG ACCACAGCGA CGAGGACGAC 240
TGCCCCAAGA AGACCTGTGC AGACAGTGAC TTCACCTGTG ACAACGGCCA CTGCTCCAC 300
GAACGGTGA AGTGTGACGG CGAGGAGGAG TGTCTGTATG GCTCCGATGA GTCCGAGGCC 360
ACTTGCACCA AGCAGGTGTG TCCTGCAGAG AAGCTGAGCT GTGGACCCAC CAGCCACAAG 420
TGTGTACTTG CCTCGTGGCG CTGCGACGGG GAGAAGGACT GCGAGGGTGG AGCGGATGAG 480
GCGGGCTGTG CTACCTCACT GGGCACCTGC CGTGGGGACG AGTTCACAGT TGGGGATGGG 540
ACATGTGTCC TTGCAATCAA GCATGTCAAC CAGGAGCAGG ACTGTCCAGA TGGGAGTGAT 600
GAAGCTGGCT GGCTACAGGG GCTGAACGAG TGTCTGCACA ACAATGGCGG CTGCTCACAC 660
ATCTGCACAG ACCTCAAGAT TGGCTTTGAA TGCACTGCC CAGCAGGCTT CCAGCTCCTG 720
GACCAAGA CTTGTGGCGA CATTGATGAG TGCAAGGACC CAGATGCCCT CAGCCAGATC 780
TGTGTCAATT ACAAGGGCTA TTTTAAGTGT GAGTGTCTACC CTGGCTGCGA GATGGACCTA 840
CTGACCAAGA ACTGCAAGGC TGCTGCTGGC AAGAGCCCAT CCCTAATCTT CACCAACCCG 900
ACGAGTGGCG AGGATGACCC TGTGAAGCGG AACTATTAC GCCTCATCCC CATGCTCAAG 960
AATGTGCTGG CACTAGATGT GGAAGTTGCC ACCAATCGCA TCTACTGGTG TGACCTCTCC 1020
TACCGTAAGA TCTATAGCG CTACATGGAC AAGGCCAGTG ACCCGAAAGA GCGGGAGGTC 1080
CTCATTTACG AGCAGTTGCA CTCTCCAGAG GGCTTGGCAG TGGACTGGGT CCACAAGCAC 1140
ATCTACTGGA CTGACTCGGG CAATAAGACC ATCTCAGTGG CCACAGTTGA TGGTGGCCGC 1200
CGACGCACTC TCTTCAGCGG TAACCTCAGT GAACCCCGGG CCATCGCTGT TGACCCCTCTG 1260
CGAGGGTTCA TGTATTGGTC TGACTGGGGG GACCAGGCCA AGATTGAGAA ATCTGGGCTC 1320
AACGGTGTGG ACCGGCAAC ACTGGTGTCA GACAATATTG AATGGCCCAA CGGAATCACC 1380
CTGGATCTGC TGAGCCAGCG CTGTACTTGG GTAGACTCCA AGCTACACCA ACTGTCCAGC 1440
ATTGACTTCA GTGGAGGCAA CAGAAAGACG CTGATCTCCT CCACTGACTT CCTGAGCCAC 1500
CCTTTTGGGA TAGCTGTGTT TGAGGACAAG GTGTTCTGGA CAGACCTGGA GAACGAGGCC 1560
ATTTTCAGTG CAAATCGGCT CAATGGCCTG GAAATCTCCA TCCTGGCTGA GAACCTCAAC 1620
AACCACATG ACATTGTGCT CTTCATGAG CTGAAGCAGC CAAGAGCTCC AGATGCGCTG 1680
GAGCTGAGTG TCCAGCTTAA TGGAGGCTGT GAATACCTGT GCCTTCCTGC TCCTCAGATC 1740
TCCAGCCACT CTCCAAGTA CACATGTGCG TGTCTGACA CAATGTGGCT GGGTCCAGAC 1800
ATGAAGAGGT GCTACCGAGA TGCAAAAGAA GACAGTAAGA TGGGCTCAAC AGTCACTGCC 1860
GCTGTTATCG GGATCATCGT GCCCATAGTG GTGATAGCCC TCCTGTGCAT GAGTGGATAC 1920
CTGATCTGGA GAAACTTGA ACGGAAGAAC ACCAAAGCA TGAATTTTGA CAACCCAGTC 1980
TACAGGAAAA CAACAGAAGA AGAAGATGAA GATGAGCTCC ATATAGGGAG AACTGCTCAG 2040
ATTGGCCATG TCTATCTCTG ACGAGTGGCA TTAAGCCTTG AAGATGATGG ACTACCTCGA 2100
GGATGGGATC ACCCCCTTGC TGCCTCATGG AATTCACTCC CATGCACTAC ACTCCGATG 2160
GTGTATGACT GGATGAATGG GTTCTATAT ATGGGTCTGT GTGAGTGAT GTGTGTGTGT 2220
GATTTTTTTT TTTAAATTTA TGTTCGCGAA AGGTAACCCAC AAGATTATGA TGAAGTCAA 2280
ACATCCAAAG GATGCTGAGG TTTTCTATG TATAATGTTT TATACACTTT TTAAGTGGT 2340
GCACTACCCA TGAGGAATTC GTGGAATGGC TACTGCTGAC TAACATGATG CACATAACCA 2400
AATGGGGGCC AATGGCACAG TACCTTACTC ATCATTAAAA AACTATATTT ACAGAAGATG 2460
TTTGGTTGCT GGGGGGCTTT TTAGGTTTT GGGCATTGTG TTTTGTGAAA TAAGATGATT 2520
ATGCTTTGTG GCTATCCATC AACATAAGT

Seq ID NO: 357 Protein sequence

Protein Accession #: NP_059992

55
60
65
70

1 11 21 31 41 51
| | | | | |
MGLPEPGPLR LLALLLLLLL LLLRLQLHLA AAAADPLLGG QGPAKECEKD QFQCRNERCI 60
PSVWRCDDED DCLDHSDEDD CPKKTCAUSD FTDNGHCIH ERWKCDGEEE CPDGSDESEA 120
TCTKQVCPAE KLSGCPSTSH CVPASWRCDG EKDCGEGADE AGCATSLGTC RGDEFQCGDG 180
TCVLAIRKCN QEQDCPDGSD EAGCLQGLNE CLHNNGGCSH ICTDLKIGFE CTCFAGFQLL 240
DQKTCGDIDE CKDPDACSQI CVNYKGYFKC ECPYGCMDL LTKNCKAAAG KSPSLIFTNR 300
TSAEDRPVKR NYSRLIPMLK NVVALDVEVA TNRIYWCDSL YRKIYSAYMD KASDPKEREV 360
LIDBQLHSPE GLAVDWNVHKH IYVTDGSGNKT ISVATVDGGR RRTLFNRNLS EPRAIADVPL 420
RGFMYHSDWG DQAKIEKSGI NGVDRQTLVS DNIEWPNGIT LDLLSQRLYW VDSKLHQLSS 480
IDFSGGNRKT LISSTDFLSH PFGIAVFEDK VFWTDLENEA IFSANRLNGL EISILAENLN 540
NPHDIVIFHE LKQPRAPDAC ELSVQPNGGC EYLCLPAPQI SSHSPKYTCA CPDTMWLGPD 600
MKRCYRDANE DSRMGSTVTA AVIGIIVPIV VIALLCMSGY LIWRNWKRN TSMNPNPNV 660
YRKTEREDE DELHIGRTAQ IGHVYPARVA LSLEDDGLP

Seq ID NO: 358 DNA sequence

Nucleic Acid Accession #: M27826

Coding sequence: <1-503

75
80
85

1 11 21 31 41 51
| | | | | |
AGCCCAAGAA ACATCTCACC AATTTCAAAT CTGATCTATT CGGCTTAGCG ACTGAAGATT 60
GACGCTGCCG GATCGCTCG GAAGTCCCCT GGACCATCAC AGAAGCCGAG CTTCGGGTAA 120
CTCTCACAGT GGAGGGTAAG TCCATCCCCT GTTTAATCGA TACGGGGGCT ACCCACTCCA 180
CGTTCGCTTC TTTTCAAGGG CTGTTTCCC TTGCCCCCAT AACTGTTGTG GGTATTGACG 240
GCCAAGCTTC AAAACCCCTG AAAACTCCCC CACTCTGGTG CCAACTTGGA CAACACTCTT 300
TTATGCACTC TTTTGTAGTT ATCCCCACCT GCCCACTTCC CTTATTAGGC CGAAATATTT 360
TAACCAAAAT ATCTGCTTCC CTGACTATTG CTGGAGTACA GCTACATCTC ATTGCTGCCG 420
TTCTTCCCAA TCCAAAGCCT CCTTTGTGTC CTCTAACATC CCCACAATAT CAGCCCTTAC 480
CACAAAGACCT CCCTTCAGCT TAATCTCTCC CACTCTAGGT TCCACGCGCG CCCCTAATCC 540
CACTTGAAGC AGCCCTGAGA AACATGCGCC ATTCTCTCTC CATACCACCC CCAAAAAATT 600
TTCGCGCTC CAACACTTCA AACTATTATT GTTTTATTG TCTTATTAAT ATCAGAAGGC 660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACTGAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAACCTG 780
 ATGACATTC ACCATTGTGA TTGTTCCTG CCCACCCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCTTAAGAA GGTTCCTTGT AATTCTCCCC ACCCTTGAGA ATGTACTTTG 900
 TGAGATCCAC CCCTGCCAC CAGAGAACAA CCCCTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAAATCT ATAAACAGC CCCACCCCTA TCTTCCTTCA CTGACTCTCT TTTGGGACTC 1020
 AGCCACGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFNS DLFLGATEDW RCPIASEVFW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSFQGPVSL APITVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLLRNLI 120
 TKLSASLTIP GVQLHLIALAL LPNPKPPLCP LTSFQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAA TTAGAAGAA AAAGCCCTTT GACTTTTTC CCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCTCTTA 180
 GGTGGAAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCCCTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAA GCACATAGATT 300
 TTCACATTC TCACAGAGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAATT 360
 CTAAGAGGCTC AGATACCTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCAGGTGGA ACTTCCACAG AAGACTTTTC AATACTATT ACAGTAAAAAC 480
 CAAAAAAGG AATTCACTCT TTCCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
 TTGGTGTGTA GGTGGGAGA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAACACCTG 600
 CCCAGAGAGA CTATCCCTC TTCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGAGAGAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTTGATAC CAATGGAATC ACGGTTTTTG 780
 GAACAAGATT TTTGATGAA GAAATTTTGG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTTATG TCACAGTGT GACTCTTCAG 900
 CACCAAGGCG TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATAA 960
 TCGAATATGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020
 GACCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGGAACA ATGGAAGATT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
 GGACAAATGA GCCAAATCCA GTTGAAGAAA TATTTACTGA AGAATATCTA ACGGGAGAGG 1200
 ATTATGATTC CCAGAGGAAA AATTCTGAGG ATACACTATA TGAAAACAAA GAAATAGACG 1260
 GCAGGGATTC TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320
 AAGAATATGA AGATAAACCA ACAAGCCCCC CTAATGAAGA ATTTGGTCCA GGTGTACCAG 1380
 CAGAAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCAATGGA GAGAAAGGAC 1440
 AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CCAGGACCAG 1500
 CAGGACCTGC AGGTATTATG GGTCTCCAG GTCTACAAGG CCCACTGGA CCCCTGGTG 1560
 ACCCTGGCGA TAGGGGCCCC CCAGGACGTC CTGGCTTACC AGGGGCTGAT GGTCTACCTG 1620
 GTCCTCCTGG TACTATGTTG ATGTTACCGT TCCGTTATGG TGGTGATGGT TCCAAAGGAC 1680
 CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC 1740
 TGAGAGGCCC ACTGGGCCCA ATGGGTCTAA CTGGAAGACC AGGTCTCTGT GGGGGGCTG 1800
 GTTCATCTGG GGCCTAAGGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGCGTCC 1860
 AGGGTCCCCC TGGTCCAACG GGAACACCTG GAAAAAGGGG TCGTCCAGT GCAGATGGAG 1920
 GAAGAGGAAT GCCAGGAGAA CCTGGGGCAA AGGGAGATCG AGGGTTTGT GACTTCCGG 1980
 GTCTGCCAGG TGACAAAGGT CACAGGGGTG AACAGGTCC TCAAGTCTCT CCAGGTCTCT 2040
 CTGGTGATGA TGAATGAGG GGAAGATG GAGAAATTGG ACCAAGAGGT TCTCCAGGTG 2100
 AAGCTGGCCC ACGAGGTTTG CTGGGTCCAA GGGGAACTCC AGGAGCTCCA GGGCAGCCTG 2160
 GTATGGCAGG TTGATAGTGC CCCCAGGAC CAAAAGGGAA CATGGGTCCC CAAGGGGAGC 2220
 CTGGGCCTCG AGGTCAACAA GGAATCCAG GACCTCAGGG TCTTCTGGT CCAAGGTC 2280
 CAATGGTCC TCCTGGTGAA AAAGGACCAC AAGGAAAACC AGGACTTGCT GACTTCTCTG 2340
 GTGCTGATGG GCTCTCTGT CATCTGGGA AAGAAGGCCA GTCTGGAGAA AAGGGGGCTC 2400
 TGGGTCCCCC TGGTCCACAA GGTCTATTG GATNNCCGGG CCCCAGGGGA GTAAAGGGAG 2460
 CAGATGTTGT CAGAGGTCTC AAGGGATCTA AAGGTGAAAA GGGTGAAGAT GGTTTTCCAG 2520
 GATTCAAAGG TGACATGGGT CTAAGAGGTG ACAGAGGAGA AGTTGGTCAA ATTGGCCCAA 2580
 GAGGNAAGA TGGCCCTGAA GGACCCAAAG GTCGAGCAGG CCAACTGGA GACCCAGGTC 2640
 CTTAGGTCA AGCAGGAGAA AAGGGAACAC TTGGAGTTCC AGGATTACCA GGATATCCAG 2700
 GAAGACAAGG TCCAAAGGGT TCCACTGGAT TCCTGGGTT TCCAGGTGCC AATGGAGAGA 2760
 AAGGTGCAAG GGGAGTAGCT GGCAAAACAG GCCCTCGGG TCAGCGTGGT CCAACGGGTC 2820
 CTCGAGGTTC AAGAGGTGCA AGAGGTCCCA CTGGGAAACC TGGGCCAAG GGCACCTCAG 2880
 GTGGCGATGG CCTCCTGGC CCTCCAGTG AAAGAGGTCC TCAAGGACCT CAGGGTCCAG 2940
 TTGGATTCCC TGGACCAAAA GGCCCTCTGT GACCACAGG AAGGATGGGC TGCCACGAGC 3000
 ACCCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCCT GGGCCAGGGG 3060
 GAGTGGTTGG ACCACAGGTG CCAACCGGTG AGACTGGTCC AATAGGGGAA CGTGGGTATC 3120
 CTGGTCTCTC TGGCCCTCCT GTGTGAGCAAG GTCTTCTCTG TGCTGCAGGA AAAGAAGGTG 3180
 CAAAGGGTGA TCAGGTCTCT CAAGGTATCT CAGGGAAGA TGGACACGA GGATTACGTG 3240
 GTTTCCAGG GGAAGAGGT GTCTCTGGAG CTCAGGTTGC ACCTGGACTG AAAGGAGGTC 3300
 AAGGTCCCCA GGGCCACCA GGTCCAGTTG GCTCACCAGG AGAACGTGGG TCAGCAGGTA 3360
 CAGCTGGCCC AATTGGTTTA CGAGGGGCC CGGACCTCA GGGTCTCTCT GGTCCAGCTG 3420
 GAGAGAAAGG TGCTCTCTGA GAAAAAGGTC CCAAGGGGCC TGCAGGAGA GATGGAGTTT 3480
 AAGGTCTCTG TGGTCTCCCA GGGCCAGCTG GTCTGCGGG CTCCTCTGGG GAAGACGGAG 3540
 ACAAGGGTGA AATTGGTGG CCGGACAAA AAGGCAGCAA GGGTGGCAAG GGAGAAAATG 3600
 GCCCTCCGG TCCCCAGGT CTTCAAGGAC CAGTTGGTGC CCTGGAATT GCTGGAGGTG 3660
 ATGTGAAAC AGGTCTTAGA GGACAGCAGG GATGTTTGG GCAAAAAGGT GATGAGGGTG 3720
 CCAGAGGCTT CCTGGACCT CTTGGTCCAA TAGGTCTTCA GGGTCTGCA GGGCCACCTG 3780
 GTGAAAAGG TGAATATGG GATGTTGGTC CATGGGGGCC ACTGGTCTCT CCAGGCCCAA 3840

5
10
15
20
25
30
35
40

GAGGCCCTCA AGGTCCCAAT GGAGCTGATG GACCACAAGG ACCCCCAGGT TCTGTTGGTT 3900
CAGTTGGTGG TGTGGAGAA AAGGGTGAAC CTGGAGAAGC AGGAAACCCA GGGCCTCCTG 3960
GGGAAGCAGG TGTAGGCGGT CCCAAGGAG AAAGAGGAGA GAAAGGGGAA GCTGGTCCAC 4020
CTGGAGCTGC TGGACCTCCA GGTGCCAAGG GGCCGCCAGG TGATGATGGC CTAAGGGTA 4080
ACCCGGGTCC TGTGTTTCTT CTGGAGATC CTGGTCTCTC TGGGGAACCT GGCCCTGCAG 4140
GTCAAGATGG TGTGTTGTTT GACAAAGGTT AAGATGGAGA TCCTGGTCAA CCGGGTCCCTC 4200
CTGGCCCATC TGTGAGGCT GGCCACCAG GTCCTCTGG AAAACGAGGT CCTCTGGAG 4260
CTGCAGGTGC AGAGGGAAGA CAAGTGAAA AAGGTGTAA GGGGAAGCA GGTGCAGAA 4320
GTCCTCCTGG AAAAACCGGC CCAGTCGGTC CTCAGGGACC TGCAGGAAAG CCTGGTCCAG 4380
AAGGTCTTCG GGGCATCCCT GGTCTGTGG GAGAACAAGG TCTCCCTGGA GCTGCAGGCC 4440
AAGATGGACC ACCTGTCTCT ATGGGACCTC CTGGCTTACC TGGTCTCAA GGTGACCCTG 4500
GCTCCAAGGG TGAAGAGGGA CATCTGGTT TAATTGGCCT GATTGGTCT CCAGGAGAAC 4560
AAGGGGAAAA AGGTGACCGA GGGCTCCCTG GAACCTAAGG ATCTCCAGGA GCAAAAGGGG 4620
ATGGGGGAAT TCCTGTCTCT GCTGGTCCCT TAGGTCCACC TGGTCTCCA GGCTTACCAG 4680
GTCCTCAAGG CCCAAAGGGT AACAAAGGCT CTACTGGACC CGCTGGCCAG AAAGTGACA 4740
GTGGTCTTCC AGGGCCTCCT GGGCCTCCAG GTCCACCTGG TGAAGTCATT CAGCCTTTAC 4800
CAATCTTGTG CTCCAAAAAA ACGAGAAGAC ATACTGAAGG CATGCAAGCA GATGCAGATG 4860
ATAATATTCT TGATTACTCG GATGGAATGG AAGAAATATT TGGTCCCTC AATTCCCTGA 4920
AACAAAGCAT CGAGCATATG AAATTTCCTA TGGGTACTCA GACCAATCCA GCCCGAATT 4980
GTAAAGACCT GCAACTCAGC CATCTGACT TCCCAGATGG TGAATATTGG ATTGATCCTA 5040
ACCAAGGTTG CTCAGGAGAT TCCTTCAAAG TTTACTGTAA TTTACATCT GGTGGTGAGA 5100
CTTGCAATTA TCCAGACAAA AAATCTGAGG GAGTAAGAAT TTCATCATGG CCAAAGGAGA 5160
AACCAGGAAG TTGTTTATG GAATTTAAGA GGGGAAAACT GCTTTCATAC TTAGATGTTG 5220
AAGGAAATTC CATCAATATG GTGCAATGA CATTCTGAA ACTTCTGACT GCCTCTGCTC 5280
GGCAAAATTT CACCTACCAC TGTCATCAGT CAGCAGCCTG GTATGATGTG TCATCAGGAA 5340
GTTATGACAA AGCACTTCGC TTCCTGGGAT CAAATGATGA GGAGATGTCC TATGACAATA 5400
ATCCTTTTAT CAAAACACTG TATGATGGTT GTACGTCCAG AAAAGGCTAT GAAAAAACTG 5460
TCATTGAAAT CAATACACCA AAAATTGATC AAGTACCTAT TGTGATGTC ATGATCAGTG 5520
ACTTTGGTGA TCAGAAATCAG AAGTTCGGAT TTGAAGTTGG TCCTGTTTGT TTTCTTGGCT 5580
AAGATTAGA CAAAGACAT ATCAAAATCA CAGAAAAATG ACCTTGGTGC CACCAACCCA 5640
TTTTGTGCCA CATGCAAGTT TTGAATAAGG ATGTATGGAA AACAACGCTG CATATACAGG 5700
TACCATTAGG GAAATACCGA TGCCCTTTGTG GGGGCAGAA CACAGACAAA AGCTTTGAAA 5760
ATCATAAAGA TATAAGTTGG TGTGGCTAAG ATGGAAACAG GGCTGATTCT TGATTCCCAA 5820
TTCTCACTC TCCTTTTCTT ATTTGAATTT CTTTGGTGTG GTAGAAAAA AAAAAAGAAA 5880
AATATATATT CATAAAAAAT ATGGTGCTCA TTCTCATCCA TCCAGGATGT ACTAAACAG 5940
TGTGTTAAT AAATTGTAAT TATTTTGTGT ACAGTTCTAT ACTGTTATCT GTGTCCATTT 6000
CCAAACTTG CAGGTGCTCC TGAATCCCG TGACTCTAAT TTATGAGGAT GCCGAACCTC 6060
GATGGCAATA ATATATGTAT TATGAAAAAT AAGTTATGAT TTCCGATGAC CCTAAGTCCC 6120
TTCTTTTGGT TAATGATGAA ATCTCTTGT GTGTGTTT

Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

45
50
55
60
65
70
75

1 11 21 31 41 51
MEPWSRWKT KRWLWDFTVT TLALTFLFQA REVRGAAPVD VLKALDFHNS PEGISKTTGF 60
CTNRNRSKGS DTAYRVSKQA QLSAPTKQLF PGGTFFEDFS ILFTVKPKKG IQSFLLSIYN 120
ERGIQIGIVE VGRSPVFLFE DHTGKPAPE YLFRFTVNI A DGKWHRAIS VEKKTVTMIV 180
DCKKRTTKPL DRSERAVDT NGITVFGTRI LDEEVFEGDI QQFLITGDPK AAYDYCEHYS 240
PDCSSAPKA AQAGQEPIDE YAPEDIEVD YEYGEAEYKE AESVTEGPTV TEETIAQTEA 300
NIVDDFQEVN YGTMESQTE APRHVSQTNE PNPVEEIFTE EYLTEGEDIYS QRKNSIEDTLY 360
ENKEIDGRDS DLLVDGDLGE YDFYKEYEY DKPTSPPNEE FGPGVPAETD ITETSINGHG 420
AYEKGKQGE PAVVEPGLMV EGPPGPAGPA GIMGPPGLQG PTGPPGDPGD RGPPGRPGLP 480
GADGLPGPPG TMLMLPFYRG GDGSKGPTIS AQEAQAQAIL QQARIALRG PGPMGLTGRP 540
GPDGLPGLPG DKGHRGERGP QGPPGPPGDD GMRGEDGEIG PRGLPGEAGP RGLLGPRTGP 600
GAPGPGMAG VDGPPGPKGN MGPGGEPGPP GQQGNFGPQG LPGPQGPFGP PGEKGPQKGP 660
GLAGLPGADG PPGHPKKEQG SGEKALGPP GPQGPPIKPG PRGVKGADGV RGLKGSKEK 720
GEDGFPFGK DMGLKGRGE VQIGPRGXG GPEGPKRAG PTGDPGSPQG AGEKGLGVP 780
GLPGYVGRQG PKGSTGPPF PGANGKRGAR GVAGKPPRG QRGPTGPRGS RGARGPTGK 840
GPKGTSGGDG PPGPPGERGP QGQGPVGF PPQGPVGF PPQGPVGF AAGKSGAKGD PGFPQISGD 900
GPPGPGGVVG PQGTGTGTGP IGERGYPPGP GPPGQGLPG AAGKSGAKGD PGFPQISGD 960
GPAGLRGPPG ERGLPQAQGA PGLKGGEGQP GPPGVPVSPG ERGSAGTAGP IGLRGRPGPQ 1020
GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLFGPAGPAG SPGEDGDKGE IGEPGQKGSK 1080
GGKGENGPPG PPGLQGPVGA PGIAGGDGEP GPRGQQMFG QKDEGARGF PGPPGPIGLQ 1140
GLPGPPGEGK ENGDDVGPWP PPFGPPRGPQ GPNGADGPPG PPGSVGSVGG VGEKGEPEGA 1200
GNPGPPGEAG VGGPKGERGE KGEAGPPGAA GPPGAKGPPG DDGPKGNPVP VGFPDGPDP 1260
GELGPAGQDG VGGDKGEDGD PGQPGPPGPS GEAGPPGPPG KRGPFGAAGA EGRQGEKGA 1320
GEAGAGPPG KTGVPVGPQP AGKPPGPEGLR GIPGPVGEQG LPGAAGQDGP PGPMGPPGLP 1380
GLKGDPSKG EKGHPGLIGL IGPPGEQGEK GDRGLPGTQG SPGAKGDGGI PGPAFLGPP 1440
GPPGLPGPQG PKGNKSGTGP AGQKGDGSLP GPPGPPGPPG EVIQPLPILS SKTTRRHTG 1500
MQADADDNLL DYSDEMEIF GSLNSLKQDI EHMKPFMTQ TNPARTCKDL QLSHPDFPDG 1560
EYWDPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPKKPPGS WFSEFKRGKL 1620
LSYLDVEGNS INMQMTFLK LLTASARQNF TYHCHQSAW YDVSSGSYDK ALRFLGSND 1680
EMSVDNPPFI KTYLDGCTSR KGYEKTVEI NTPKIDQVFI VDVMSIDFGD QNQGKGFV 1740
PVCFLG

Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

85

1 11 21 31 41 51
TTCCCCAGCA TTCCAGAAAC TCCTCTCTAC TTTAGCACGG TCTCCAGACT CAGCCGAGAG 60
ACAGCAAAC CTGACGCGGT GAGAGAGCGA GAGAGAGGGA GAGAGAGACT CTCAGCCTG 120
GGAACATATA CTCTCTCTCG AGAGGCGGAG AACTCCTTCC CCAATCTTT TGGGACTTT 180

TCTCTCTTTA CCCACCTCCG CCCCTGCGAG GAGTTGAGGG GCCAGTTGGG CCGCCGCGGG 240
 CGTCTTCCCG TTCCGGGTGT GCTTGGCCCG GGAACCGGG AGGGCCCGGC GATCGCGCGG 300
 CGGCGCGCGC GAGGGTGTGA GCGCGCGTGG GCGCCCGCG AGCGAGAGCC ATGTTGTCAGC 360
 AAACCAACAA TGCCGAGAAC ACGGAAGGCG TGCTGGCCGG CGAGAGCTCG GACTCGGGCG 420
 CCGGCCTCGA GCTGGGAATC GCCTCCTCCC CCACGCCCGG CTCCACCGCC TCCACGGGCG 480
 GCAAGGCGGA CGACCGGAGC TGGTGCAAGA CCCCGAGTGG GCACATCAAG CGACCCATGA 540
 ACGCTTTCAT GGTGTGGTGG CAGATCGAGC GCGCAAGAT CATGGAGCAG TCGCCCGACA 600
 TGCACAACGC CGAGATCTCC AAGCGGCTGG GCAACGCTG GAAGCTGCTC AAAGACAGCG 660
 ACAAGATCCC TTTCATTCGA GAGGCGGAGC GGTGTCGCTT CAAGCACATG GCTGACTACC 720
 CGACTACAA GTACCGGCC TCCAAACCGG TGAAGTCCGG CAACGCCAAC TCCAGCTCCT 780
 CCGCCGCGCG CTCTCCAAAG CCGGGGAGAG AGGGAGACAA GGTGCTGGC AGTGGCGGGG 840
 GCGGCCATGG GGGCGGCGCG GCGCGCGGGA GCAGCAACGC GGGGGGAGGA GCGCGCGGTG 900
 CGAGTGGCGT GCTGCGCCCT TCCAAACCGG CGCAGAAAAA GAGCTGCGCG TCCAAAGTGG 960
 CCGGCGCGCG GGGCGGTGGG GTTAGCAAA CCGACGCCAA GCTCATCTCG GCGAGCGGCG 1020
 GCGGCGCGCG GAAAGCAGCG GCTGCCGCG CCGCCTCCTT CGCCGCGGAA CAGGCGGGGG 1080
 CCGCGCGCCT GCTGCCCTCG GCGCGCGCG CCGACCAACA CTCGCTGTAC AAGGCGCGGA 1140
 CTCGCCAGCG CTCGCGCTCC GCCTCCTCGG CAGCCTCGGC CTCGCGAGCG CTCGCGCCCC 1200
 CGGGCAAGCA CCTGGCGGAG AAGAAGGTGA AGCGCGTCTA CCTGTTCGCG GGCTGGGCA 1260
 CGTCTGCTGC CCGCTGGGCG GCGGTGGGCG CGGGAGCCGA CCCCGAGCGC CCCCTGGGCC 1320
 TGTACGAGGA GGAAGGCGCG GGTGCTCGC CCGACGCGCC CAGCCTGAGC GCGCGCAGCA 1380
 GCGCGCGCTC GTCCCGCGCG GCGCGCGCT CGCCGCGGA CCAACGCGCG TACGCCAGCC 1440
 TCGCGCGCGC TCGCGCGCG CCGTCCAGCG CGCCCTCGCA CGCGTCTCTC TCGCGCTCGT 1500
 CCCACTCCTC CTCTTCTCTC TCCTCGGGCT CCTCGTCTCT CGAAGCAGAG TTCGAAGACG 1560
 ACCTGCTCGA CCTGAACCCC AGCTCAAACT TTGAGAGCAT GTCCCTGGCG AGCTTCAGTT 1620
 CGTCTGCGCG GCTCGACCGG GACCTGGATT TTAACCTCGA GCGCGGCTCC GGCTCGCACT 1680
 TCGAGTTCCC GGACTACTCG ACGCCCGAGG TGAGCGAGAT GATCTCGGGA GACTGGCTCG 1740
 AGTCACGATC CTCACACTCG GTTTTCACTT ACTGAAGGCG GCGCAGGCG GAGAGAGGGC 1800
 CCGGGGGGGT AGGAGAGGAG AAAAAAAG TGAAAAAAG AAACGAAAG GACAGACGAA 1860
 GAGTTTAAAG AGAAAAAGGA AAAAAGAAAG AAAAGTAAAG CAGGGCTCGT TCGCCCGCGT 1920
 TCTGCTGCTC GGATCAAGGA GCGCGCGCGC GTTTTGGACC CGCGCTCCCA TCCCCACCT 1980
 TCCCGGGCGG GGAACCCACT CTGCCAGCC GGAGGGACGC GGAGGAGGAA GAGGGTAGAC 2040
 AGGGGCGACC TGTGATTGTT GTTATTGATG TTGTTGTTGA TGGCAAAAAA AAAAAGCGAC 2100
 TTGAGTTTG CTCCCTTTG CTGAAAGAGA CCCCCCTCCC CTTCACAGCA GCTTCCGAGC 2160
 TTGTTCTGAC CCGCAGCAAG AAGCGAGTT AGTTTCTAG AGACTTGAAG GAGTCTCCCC 2220
 CTCTCTGCAT CACCACCTTG GTTTTGTITT ATTTTGCTTC TTGTTCAAGA AAGGAGGGGA 2280
 GAAACCAAGG CACCCCTCCC CCCCCTTTT TAAACGCGTG ATGAAGACAG AAGGCTCCGG 2340
 GGTGACGAAT TTGGCGATG GCAGATGTTT TGGGGGAACG CCGGAGCTGA GAGACTCCAC 2400
 GCAGGCGAAT TCCCGTTTGG GGCCTTTTTC TCCTCCCTCT TTTCCCTTG CCCCCTCTGC 2460
 AGCCGAGGGA GGAGATGTTG AGGGGAGGAG CCGAGCCAGT GTGACCGGCG CTAGGAAATG 2520
 ACCCGAGAAC CCGTTTGGAA GCGCAGCAGC GGGAGCTAGG GCGCGGGGCG GAGGAGGACA 2580
 CGAACTGGAA GGGGTTTAC GGTCAAACTG AAATGGATTG GCACTTGGG GAGCTGGCGG 2640
 CCGCGGCTGC TGGGCTCCCG CTTCTTTTC TAGTGAAAT CAGTGAGGTG AGACTTCCCA 2700
 GACCCCGGAG GCGTGGAGGA GAGGAGACTG TTTGATGTGG TACAGGGGCA GTCAGTGGAG 2760
 GCGAGTGGT TTCGAAAAA AAAAAGAAA AAAAGGG

Seq ID NO: 363 Protein sequence
 Protein Accession #: NP_003098

1 11 21 31 41 51
 MVQQTNNAE TEALLAGESS DSGAGLELGI ASSPTPGSTA STGGKADDPG WCKTPSGHIK 60
 RPMNFMVWS QIERRKIMEQ SPDMHNAEIS KRLGKRWKLL KDSDKIPFIR EAERLRLKHM 120
 ADYDPYKYRP RKIVKSGNAN SSSSAAASSK PGEKGDKVGG SGGGGHGGGG GGGSSNAGGG 180
 GGGASGGGAN SKPAQKSCG SKVAGGAGGG VSKPHAKLIL AGGGGGGKAA AAAAASFPAE 240
 QAGAAALLPL GAAADHHSLY KARTPSASAS ASSAASASAA LAAPGKHLAE KKVIRVLPFG 300
 GLGTSSSPVG GVGAGADPSD PLGLYEEEGA GCSPPAPSLG GRSSAASSPA AGRSPADHRG 360
 YASLRAASPA PSSAPSHASS SASHSSSSSS SSGSSSSDDE FEDDLLDLNP SSNFESMSLG 420
 SFSSSSALDR DLDFNFEPGS GSHFEPPDYC TPEVSEMISG DWLESSISNL VFTY

Seq ID NO: 364 DNA sequence
 Nucleic Acid Accession #: U10860
 Coding sequence: 123-2204

1 11 21 31 41 51
 TGCCGGCTGC TCCTCGACCA GGCCTCCTTC TCAACCTCAG CCCGCGGCGC CGACCCCTCC 60
 GGCACCCCTC CGCCCGCTCT CTAAGTGTGC CCGTCACCGC CGCGGCTCGG GCGCTGGCCC 120
 CGATGGCTCT GTGCAACGGA GACTCCAAGC TGGAGAATGC TGGAGGAGAC CTTAAGGATG 180
 GCCACCAACA CTATGAAGGA GCTGTTGTCA TTCTGGATGC TGGTGTCTAG TACGGGAAAG 240
 TCATAGACCG AAGAGTGAGG GAACTGTTGC TGCACTCTGA AATTTTCCCC TTGGAAACAC 300
 CAGCATTTCG TATAAAGGAA CAAGGATTCC GTGCTATTAT CATCTCTGGA GGACCTAATT 360
 CTGTGTATGC TGAAGATGCT CCGTGGTTTG ATCCAGCAAT ATTCACTATT GGCAAGCCTG 420
 TTCTTGGAA TGTCTATGGT ATGCAGATGA TGAATAAGGT ATTGGAGGT ACTGTGCACA 480
 AAAAAAGTGT CAGAGAAGAT GGAGTTTCA ACATTAGTGT GGATAATACA TGTTCATTAT 540
 TCAGGGGCTT TCAGAAAGGA GAAGTTGTTT TGCTTACACA TGGAGATAGT GTAGACAAAG 600
 TAGCTGATGG ATTCAAGGTT GTGGCAGGTT CTGGAAACAT AGTAGCAGCG ATAGCAAATG 660
 AATCTAAAAA GTTATATGGA GCAAGTTCC ACCCTGAAGT TGGCCTTACA GAAAAAGGAA 720
 AAGTAATACT GAAGAAATTC CTTTATGATA TAGCTGGATG CAGTGGAAAC TTCACCGTGC 780
 AGAACAGAGA ACTTGAAGTGT ATTCAGAGGA TCAAGAGAG AGTAGGACAG TCAAAAGTTT 840
 TGGTTTTACT CAGTGGTGA GTAGACTCAA CAGTTTGTAC AGCTTTGCTA AATCGTGCTT 900
 TGAACCAAGA ACAAGTCATT GCTGTGCACA TTGATAATGG CTTTATGAGA AAACGAGAAA 960
 GCCAGTCTGT TGAAGAGGCC CTCAAAAAGC TTGGAATTC GGTCAAAGTG ATAAATGCTG 1020
 CTCAATCTTT CTACAATGGA ACAACAACCC TACCAATATC AGATGAAGAT AGAAACCCAC 1080
 GGAAAGAAT TAGCAAAACG TTAATATGGA CCACAAGTCC TGAAGAGAAA AGAAAAATCA 1140
 TTGGGGATAC TTTTGTAAAG ATTGCCAATG AAGTAATTGG AGAAATGAAC TTGAACACAG 1200
 AGGAGGTTTT CTTGCCCCAA GGTACTTTAC GGCCTGATCT AATTGAAGAT GCATCCCTTG 1260

TTGCAAGTGG CAAAGCTGAA CTCATCAAAA CCCATCACA TGACACAGAG CTCATCAGAA 1320
AGTTGAGAGA GGAGGGAAAA GTAATAGAAC CTCTGAAAGA TTTTCATAAA GATGAAGTGA 1380
GAATTTTGGG CAGAGAACTT GGACTTCCAG AAGAGTTAGT TTCCAGGCAT CCATTTCCAG 1440
GTCCTGGGCT GGAATCAGA GTAATATGTG CTGAAGAAC TTATATTTGT AAGGACTTTC 1500
CTGAAACCAA CAATATTTT AAAATAGTAG CTGATTTTTC TGCAAGTGT AAAAAGCCAC 1560
ATACCCATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620
AAATTACCAG TCTGCTTCA CTGAATGCCT TCTTGCTGCC AATTAAAACT GTAGGTGTGC 1680
AGGGTGACTG TCGTCTCTAC AGTTACGCTG GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740
GGGAATCACT TATTTTCTG GCTAGGCTTA TACCTCGCAT GTGTCAACAC GTTAACAGAG 1800
TTGTTTATAT ATTGCGCCCA CCAGTTAAAG AACCTCTTAC AGATGTTACT CCCACTTTCT 1860
TGACAACAGG GGTGCTCAGT ACTTTACGCC AAGCTGATTT TGAGGCCCAT AACATTCTCA 1920
GGGAGTCTGG GTATGCTGGG AAAATCAGCC AGATGCCGGT GATTTTGACA CCATTACATT 1980
TTGATCGGGA CCCACTTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGGTT ATTCGAACCT 2040
TTATTACTAG TGACTTCATG ACTGGTATAC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100
AGGTGGTATT AAGATGGTC ACTGAGATTA AGAAGATTCC TGGTATTTCT CGAATTATGT 2160
ATGACTTAAC ATCAAAGCCC CCAGGAACCTA CTGAGTGGGA GTAATAAAT TC

Seq ID NO: 365 Protein sequence
Protein Accession #: AAA60331

1 11 21 31 41 51
MALCNGDSKL ENAGGDLKDG HHYEGAVVI LDAGAQQYKV IDRRVRELFV QSEIFPLETP 60
AFAIKEQGFRI AIIISGGPNS VYAEDAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
KSVREDGVFN ISVDNTCSLF RGLQKEEVVL LTHGDSVDKV ADGFKVVARV GNIVAGIANE 180
SKKLYGAQFH PEVLGTENGK VILKNFLYDI AGCSGTPTVQ NRELECIREI KERVGTSKVL 240
VLLSGGVDST VCTALNRLAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRII GDTFVKIANE VIGEMNLKPE 360
EVFLAQGTLR PDLESASLV ASGKAELIKT HINDTELIRK LREEGKVIEP LKDFHKDEV 420
ILGRELGLPE ELVSRHPPFG PGLAIRVICA EEPYICKDFP ETMNLKIVA DFSASVKKPH 480
TLLQRVKACT TEEDQELLMQ ITSLSLNAF LLPKTVGVQ GDCRSYSYVC GISSKDEPDW 540
ESLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADPEAHNLR 600
ESGYAGKISQ MPVILTPLHF DRDPLQKQPS CQRSVVIRTF ITGDFMTGIP ATPGNEIPVE 660
VVLKMTVEIK KIPGISRIMY DLTSKPPGTT EWE

Seq ID NO: 366 DNA sequence
Nucleic Acid Accession #: NM_004219
Coding sequence: 46-654

1 11 21 31 41 51
GCGGCCCTCAG ATGAATGCGG CTGTTAAGAC CTGCAATAAT CCAGAATGGC TACTCTGATC 60
TATGTTGATA AGGAAAATGG AGAACACGGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
CTGGGGTCTG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAAGTTTC AACACCACGT 180
TTTGCCAAAA CGTTCGATGC CCCACCAGCC TTACCTAAAG CTACTAGAAA GGCTTTGGGA 240
ACTGTCAACA GAGCTACAGA AAAGTCTGTA AAGACCAAGG GACCCCTCAA ACAAAAACAG 300
CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTTCT 360
GCCTCAGATG ATGCCTATCC AGAAATAGAA AAATCTTTTC CCTTCAATCC TCTAGACTTT 420
GAGAGTTTTG ACCTGCCTGA AGAGCACCAG ATTGCGCACC TCCCCTTGAG TGGAGTGCTT 480
CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAGAGCTG TTCAGCTGGG CCCCCTTCA 540
CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCACTCTCC TTCAAGCATT 600
CTGTGACCCC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAATTTTCT 660
TAGTGCTTCA GAGTTTGTGT GTATTTGTAT TAATAAAGCA TTCTTCAACA GAAAAAATAA 720
AAAAAATA

Seq ID NO: 367 Protein sequence
Protein Accession #: NP_004210

1 11 21 31 41 51
MATLIYVDKE NGEPTGRVVA KDGLKLGSGP SIKALDGRSQ VSTPRFGKTF DAPPALPKAT 60
RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KIMTEKTVKA KSSVPASDDA YPEIEKFFPF 120
NPLDFESFDL PEEHQIAHLF LSGVPLMILD EERELEKLFQ LGPPSPVKMP SPPWESNLLQ 180
SPSSILSTLD VELPPVCCDI DI

Seq ID NO: 368 DNA sequence
Nucleic Acid Accession #: NM_000597
Coding sequence: 118-1104

1 11 21 31 41 51
ATTCGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCCGCTGCA GGGCGGTGCA 60
CCTGCCCGCC CGCCCGCTGC CTGCGCTGCC CGCCCGCGCG CGCTGCCGAC CGCCAGCATG 120
CTGCCGAGAG TGGCTGCGCC CGCGCTGCCG CTGCGCGCGC CGCCGCTGCT GCGCGTCTG 180
CCGCTGCTGC TGCTGCTACT GGGCGCGAGT GCGCGCGCGG GCGGGGCGCG CGCGGAGGTG 240
CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCGG CCTGCGGGCC CCGCGCGGTT 300
GGCGCGCGCG AGGCGCTGGT CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC 420
GGCGTCTACA CCCCCTGCTG CGGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
CTGCCCTGCG AGGCGCTGGT CATGGGCGAG GGCACCTGTG AGAAGCGCGG GGACGCGGAG 540
TATGGCGCCA GCCCGAGGCA GGTTCAGAC AATGGCGATG ACCACTCAGA AGGAGGCGCTG 600
GTGGAGAACG ACGTGGACAG CACCATGAAC ATGTTGGGCG GGGGAGGCGG TGCTGGCCCG 660
AAGGCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG 720
CACCGGCAGA TGGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG 780
CGACCAACCC CTGCCAGGAC TCCTTGCCAA CAGGAACCTG ACCAGTCTCT GGAGCGGATC 840

TCCACCATGC GCCTTCGGGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
 CCCAACTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
 CAGCGTGGGG AGTGTGGTGT TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
 ACCATCGGGG GGGACCCCGA GTGTCACTCTC TTCTACAATG AGCAGCAGGA GGCTTGCGGG 1080
 GTGCACACCC AGCGGATGCA GTAGACCGCA GCCAGCGGGT GCCTGGCGCC CCTGCCCCCC 1140
 GCCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGTCTTG GTGGTGGGTG CTGGAGGATT 1200
 TTCCAGTTCT GACACACGTA TTTATATTG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
 CCCGGCTCTC CTCTCCAG CTGCAGATGC CACACCTGCT CCTTCTGTCT TCCCCGGGG 1320
 GAGGAAGGGG GTTGTGTCG GGGAGCTGGG GTACAGTTT GGGAGGGGG AAGAGAAATT 1380
 TTTATTTTGG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

Seq ID NO: 369 Protein sequence
 Protein Accession #: NP_000588

1 11 21 31 41 51
 MLPRVGCPL PLPPPLLLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
 VAPPAVAAV AGGARMPGAE LVREPGCGCC SVCARLEGEA CGVYTPRCQG GLRCYPHFGS 120
 ELPLQALVMG EGTCEKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGSAG 180
 RKPLKSKMKE LAVFREKVT EHRQMGKGGK HHLGLEBPCK LRPPPARTPC QQELDQVLER 240
 ISTMLPDER GPLEHLYSLH IPNCDKHLGLY NLKQCKMSLN GQRGECWCVN FNTGKLIQGA 300
 PTIRGDPECH LFYNEQEEAC GVHTQRMQ

Seq ID NO: 370 DNA sequence
 Nucleic Acid Accession #: NM_004264
 Coding sequence: 6-440

1 11 21 31 41 51
 GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
 TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCTCTC TGCCCTCTTC AATAATATTC 120
 AGACAGCAAT TAACAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTGT 180
 CAGCACTGAT TGCACGAACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
 AAGAATCTAC AGCTGCTTTA CAGGCTGCTA GCTTGATATA GCTAGAAGAA GAAAACCATG 300
 AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
 AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
 AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
 GTGCCATTAA GAATCTGCA TCAGACTTAG ATACAAGCCT TACCAACAAT TACAGAAACA 540
 TTAACACTA TGACACATTA CCTTTTATAG TATTTTAAAT AGTCTTCTAT TTTCACTCTT 600
 GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTAACTT 660
 GAGTGAATTT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
 AATTCGTGTA TGACATAATT TATGTCTCCA TTTTGTGTTA TTGGCCAGTA CTTTACAAAT 780
 C

Seq ID NO: 371 Protein sequence
 Protein Accession #: NP_004255

1 11 21 31 41 51
 MADRLTLQLD AVNSLADQFC NAIGVLQCG PPASFNNIQT AINKDQPANP TEEYAQLFAA 60
 LIARTAKDID VLIDSLPSEE STAALQAASL YKLEENHEA ATCEDVDVYR GDMLEKIQS 120
 ALADIAQSQL KTRSGTHSQS LPDS

Seq ID NO: 372 DNA sequence
 Nucleic Acid Accession #: AJ271091
 Coding sequence: 1-1113

1 11 21 31 41 51
 ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
 CTGGCGGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAAAGTGCTG 120
 CATTTCAAAG CTCAGGACCA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
 TTCTTAGACC TTGTGAACCC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
 ACAGTACAGA AGAAAGTGGG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAAGCGACCA 300
 CTGTTTTTGG CTCTGACTTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
 AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCGACTGGG AAAGCGAAGG CTCTCCTGAA 420
 ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
 TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCTTTT 540
 TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
 GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
 CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
 AAAGCTGTGG TTTTCTTTGT GTTTTATTGG TGGAGTGCAA TTGAATTTT CAGGTACTCT 780
 TTCTACATGC TGACGTGCAT TGACATGGAT TGGAGGTGTC TCACATGGCT TCGTTACACT 840
 CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCAGTCC 900
 ATTCGAATAT TCAATAGAGC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAATAATC 960
 AAAGTTAGAT TTTCTTTTTC TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
 ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
 CATGCCCTGG ATCCAGCGC TTTGGGAGGC TGA

Seq ID NO: 373 Protein sequence
 Protein Accession #: CAB69070

1 11 21 31 41 51
 MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
 FLDLVKPEPV YKLTRQVNI TVQKVSQWW ERLTKQEKRP LPLAPDFDRW LDESDAEMEL 120
 RAKEERELNK LRLESGSPE TLTLNRKGYL FMYNLVQPLG FSWIFVNLTV RFCILGKESF 180

YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLP SLIQ LLGRNFILPI IFGTMEEMQN 240
KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYT LWIPLYPLGC LAEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
HACDPSALGG

Seq ID NO: 374 DNA sequence
Nucleic Acid Accession #: NM_016395
Coding sequence: 1-1113

1 11 21 31 41 51
| | | | | |
ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
CTGCCCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
CATTTCAAAG CTCAAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAACATT 240
ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTGTGCA ATTCTTGGGA 480
TTCTCCTGGA TCTTTGTCAA CTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
AAAGCTGTGG TTTTCTTTGT GTTTTATTGG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTACACT 840
CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAATAATC 960
AAAGTTAGAT TTTCTTTTTC TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
ATAAATTTTC GTCACCTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
CATGCCTGTG ATCCAGCGC TTTGGGAGGC TGA

Seq ID NO: 375 Protein sequence
Protein Accession #: NP_057479

1 11 21 31 41 51
| | | | | |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
FLDLVKPEPV YKLTRQVNI TVQKKVSQWV ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
RAKEERENLN LRLESEGSPE TLTLNRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESP 180
YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLP SLIQ LLGRNFILPI IFGTMEEMQN 240
KAVVFFVFFYL WSAIEIFRYS FYMLTCIDMD WKVLTWLRYT LWIPLYPLGC LVEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFPLQI YLIMIFLGLY INFRHLYKQR RRRYGGKKRKR 360
STKKKDLDFG LPV

Seq ID NO: 376 DNA sequence
Nucleic Acid Accession #: NM_005987
Coding sequence: 1-270

1 11 21 31 41 51
| | | | | |
ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
GTGAAACAAC CTTGCCAGCC TCCACCCAGG GAACCATGCA TCCCAAAAC CAAGGAGCCC 120
TGCCAAACCA AGGTGCTGTA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
ATTCCAGAGC CTTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTCAACGGT CACTCCAGCA 240
CCAGCCAGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
Protein Accession #: NP_005978

1 11 21 31 41 51
| | | | | |
MNSQQKQPC TPPPQPPQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPCH PKVPSPQPK 60
IPEPCQPKVP EPCPSTVTPA PAQQKTKQK

Seq ID NO: 378 DNA sequence
Nucleic Acid Accession #: NM_002105
Coding sequence: 74-505

1 11 21 31 41 51
| | | | | |
ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTTTG AGCCGTGCTG CTTCAACGGT 60
CTACCTCGCT AGCATGTCGG GCCGCGGCAA GACTGGCGGC AAGGCCGCG CCAAGGCCAA 120
GTGCGGCTCG TCGCGGCGCG GCCTCCAGTT CCACTGGGCG CGGTACACC GGCTGCTGCG 180
GAAGGGCCAC TACGCCGAGC GCGTTGGCGC CGGCGGCCCA GTGTACCTGG CGGCAGTGCT 240
GGAGTACCTC ACCGCTGAGA TCCTGGAGCT GGCGGGCAAT GCGGCCGCG ACAACAAGAA 300
GACCGGAATC ATCCCCGCGC ACCTGCAGCT GGCCATCCGC AACGACGAGG AGCTCAACAA 360
GCTGCTGGGC GCGGTGACGA TCGCCAGGG AGGCGTCTG CCCAACATCC AGGCGGTGCT 420
GCTGCCCAAG AAGACAGCG CCACCGTGGG GCCGAAGGCG CCTCGGGCG GCAAGAAGGC 480
CAACCAAGGC TCCAGAGGCT ACTAAGAGG CCGCGCGCGC GCGCGGCGC CCCAGCTCCC 540
CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACGCGCC TCATGGAAAG AGCTGAGCCG 600
CTTCAGACTG CGGGGCAAGC GGGCCGCGGC TCCCTTCCCC TCCCTCCCC TCGCCGCGCT 660
TCGCGCGCGC GCTCGAGTC CCGCGCGGCC CCGCTCCCG TCCCGCACCG CTTGCGCGCT 720
CGGCTCGGG CCGCGCTGCT CCGCGCTCG CCGTCCGGTA GGGTTCGGGC CTTCCGGATG 780
CGGCTTGGGC GCTCTTGGG GACCTCCGTG GCGCGGAAGA CCCGAGCCTG CCGGGGGAG 840

GCGGCGGGG CCGCACTGC CCGCTCGGC GTTGTGACT CAGCGCCCC ATCCCGAGTC 900
 GCTAAGGGG TGGGGGAGG CCGCAGCAC TTCTGGAAGA CTGGCCCTTC CGCTCTGACG 960
 CAGGGCCGAG GTGGGCAGTC CAGGCCGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCGGGGTG GTGCTTAGCC CAGGACTTTC 1080
 AGACGGCCG TGGCCGGGAG GCTTTGGTGG GAGAGACGCG ATCGCCGATT TCGGTCTGGC 1140
 GCGCTTCTG CCGCCGGGAC CCAGGCCTTT CACATCAGCT CTCCCTCCAT CTTCATTCAT 1200
 AGGTCTGCG TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA 1260
 CTGCCTCTA GGAGGACATT TAGGGGAGGG CAGAGGCCTG CAGTTTGGCT TCACGGCTGG 1320
 CTATGTGGAG AGCAAGATGC GTTTTGCAGA ACGGAGCTGG CAGCCAGGCC TGTGGGGCCC 1380
 CCGACGCGCG CCCATTTCCC TTCCAGCAAA CTCAACTCGG CAATCCAAGC ACCTAGATAC 1440
 CAGCACAAAT CGGTTAATCC CTGTCTGGAG TGAGCCTCCG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGGAATAAT 1560
 TTTATTAAG GATTGTTTTT TTTTT

Seq ID NO: 379 Protein sequence
 Protein Accession #: NP_002096

1 11 21 31 41 51
 MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKHY AERVGAGAPV YLAHVLEYLT 60
 AEILELAGNA ARDNKKTRII PRHLQLAIRN DEELNKLGG VTIAQGGVLP NIQAVLLPKK 120
 TSATVGPAPK SGGKATQAS QEY

Seq ID NO: 380 DNA sequence
 Nucleic Acid Accession #: AL136942
 Coding sequence: 184-864

1 11 21 31 41 51
 ACGGCTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCG GCGGGCGCAC 60
 GGGCGAGCGG GCCGGGAGCC GGAGCGCGCG AGGAGCCGCG AGCAGCGGCG CGCGGGGCTC 120
 CAGGCGAGGC GGTGACGCT CCTGAAAACCT TGCGCGCGCG CTGCGCCAC TGCGCCCGGA 180
 GCGATGAAGA TGGTCCGCGC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 CATGTCCGCA CCGGCACCAT CCTGCTCGGC GTCTGGTATC TGATCATCAA TGCTGTGGTA 300
 CTGTTGATTT TATTGAGTGC CTGGCTGAT CCGGATCAGT ATAACCTTTC AAGTCTGAA 360
 CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAATCATGT GCATTGCCAT TCGGATTTCT 420
 CTTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 TGGATCATCC CATTCTTCTG TTACCAGATC TTTGACTTTG CCTGGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTATATCC AAATCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT 600
 TTCCCTACA GAGATGATGT CATGTCAGTG AATCCTACCT GTTTGGTCCG TATTATCTCT 660
 CTGTTATTA GCATTATCTT GACTTTTAAAG GGTACTTGA TTAGCTGTGT TTGGAACCTG 720
 TACCGATACA TCAATGGTAG GAATCCTCT GATGTCCTGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCG GTATGATGAT GCCACTGTGA ATGGTGCTCG CAAGGAGCCA 840
 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA 900
 CTTTGCAGAC ATCTGAGCAA TAGTCTGTT ATTTCACCTT TGCCATGAGC CTCTCTGAGC 960
 TTGTTTGTG CTGAAATGCT ACTTTTAAA ATTTAGATGT TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGTCTAGA ACACCTGTAT AGATTAACTG TAGAATCTCT CCGTAGCAT 1080
 TGGGATATA ACGGGCTTCA CTAACCTTCC CTAGGCATTG AAATCTCCCC CAAATCTGAT 1140
 GGACCTAGAA GTCTGCTTTT GTACCTGCTG GCGCCCAAAG TTGGGCATT TTTCTCTGT 1200
 TCCCTCTCT TTGAAATATG AAAATAAAAC CAAAAATAGA CAATTTTTTC TTCAGCCATT 1260
 CCAGCATAGA GAACAAACCT TATGGAAC AGGAATGTCA ATGTGTGAAT CATGTTCTTA 1320
 ATTAGTAAA TAGAAGTCTT TATGATGTG TTACAAGAAT TTCCCCACA ACATCCTTTA 1380
 TGACTGAAGT TCAATGACAG TTTGTGTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT 1440
 TAAGACCATT AGAAGCACC AGGCCGTGGG AGCAGTGACC ATCTACTGAC TGTTCTTGTG 1500
 GATCTTGTGT CCAGGACAT GGGGTGACAT GCCTCGTATG TGTAGAGGG TGAATGGAT 1560
 GTGTTTGGCG CTGCATGGGA TCTGGTGCCC CTCTTCTCCT GGATTCACAT CCCCACCCAG 1620
 GGCCCGCTTT TACTAAGTGT TCTGCCCTAG ATTGGTTCAA GGAGGTCATC CAACTGACTT 1680
 TATCAAGTGG AATTGGGATA TTTTGATAT ACTTCTGCTT AACACATAGG AAAAGGGTTT 1740
 TCTTTTCCCT GCAAGCTACA TCCTACTGCT TTGAATCTCC AAGTATGCT AGTCACCTTT 1800
 TAAAATGTAA ACATTTCTAG AAAATGAGG ATTGCCTTCC TTGTATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGG ATTTTATAT ATTCATATGT TACAAAGTCA GCAACTCTCC 1920
 TGTGTTTCA TTATTGAATG TGCTGTAAAT TAAGTCGTTT GCAATTAATA CAAGTTTTC 1980
 CCACATCCAA AAAAAAAAAA AAAAA

Seq ID NO: 381 Protein sequence
 Protein Accession #: CAB66876

1 11 21 31 41 51
 MKMVAPWTRF YSNSCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDFFEMDDA NMCIATISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DFLNMLVAI 120
 TVLIYPNSIQ EYIRQLPFNF PYRDDVMSVN PTCLVLIILL FISIIITFKG YLISCVWNCY 180
 RYINGRNSSD VLVVTSNDT TVLLPPYDDA TVNGAAKEPP PPVUSA

Seq ID NO: 382 DNA sequence
 Nucleic Acid Accession #: NM_002510
 Coding sequence: 92-1774

1 11 21 31 41 51
 CAGATGCCAG AAGAACACTG TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAAITCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTTATG ATGTGCTGGG 180
 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAAATGGCT GGTCTTCTGA 240
 TGAATATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CGGGGAGACA TGAGGTGGA 300
 AAATCCTGAG AAGGGAGGCC GTGTGACGCG GGTCTGACC AGTGACTCAC CAGCCCTCGT 360

GGGCTCAAAAT ATAACATTTC CGGTGAACCT GATATTCCCT AGATGCCAAA AGGAAGATGC 420
 CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT CTGCTGATCC 480
 ATATGTTTAC AACTGGACAG CATGGTCAGA GGACAGTGAC GGGGAAAATG GCACCGGCCA 540
 AAGCCATCAT AACGCTCTCC CTGATGGGAA ACCTTTTCCT CACCACCCCG GATGGAGAAG 600
 ATGGAAATTC ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG 660
 TTCAGTGAGA GTTTCGTGTA ACACAGCCAA TGTGACACTT GGGCCTCAAC TCATGGAAAGT 720
 GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCCTATC GCACAAGTGA AAGATGTGTA 780
 CGTGGTAACA GATCAGATTG CTGTGTTTGT GACTATGTTT CAGAAGAACG ATCGAAATTC 840
 ATCCGACGAA ACCCTTCTCA AAGATCTCCC CATTATGTTT GATGTCTCGA TTCATGATCC 900
 TAGCCACTTC CTCGAATTAT CTACCATTA CTACAAGTGG AGCTTCGGGG ATAATACTGG 960
 CCTGTTTGTG TCCACCAATC ATACTGTGAA TCACACGTAT GTGCTCAATG GAACCTTCAG 1020
 CCTTAACCTC ACTGTGAAGC CTGCAGCACC AGGACCTTGT COGCCACCGC CACCACCACC 1080
 CAGACCTTCA AACCCAGCCC TTCTTTTAGG ACCTGCTGGT GACAACCCCG TGGAGCTGAG 1140
 TAGGATTCTC GATGAAAAC GGCAGATTAA CAGATATGGC CACTTTCAAG CCACCATCAC 1200
 AATTGTAGAG GGAATCTTAG AGGTAAACAT CATCCAGATG ACAGACGTCC TGATGCCGGT 1260
 GCCATGGCCT GAAAGCTCCC TAATAGACTT TGTGCTGACC TGCCAAGGGA GCATTTCCAC 1320
 GGAGGTCTGT ACCATCATTT CTGACCCAC CTGCGAGATC ACCCAGAAC CAGTCTGCG 1380
 CCCTGTGGAT GTGGATGAGA TGTGTCTGCT GACTGTGAGA CGAACCTTCA ATGGGTCTGG 1440
 CGGTACTGT GTGAACCTCA CCCTGGGGGA TGACACAAGC CTGGCTCTCA CGAGCACCCT 1500
 GATTTCTGTT CTGACAGAG ACCCAGCCTC GCCTTTAAGG ATGGCAAACA GTGCCCTGAT 1560
 CTCGTTGGC TGCTTGGCCA TATTTGTGAC TGTGATCTCC CTCITGGTGT ACAAAAAACA 1620
 CAAGGAATAC AACCCTATAG AATAATAGTCC TGGGAATGTG GTCAGAAGCA AAGGCCTGAG 1680
 TGTCTTTCTC AACCGTGCAA AAGCCGTGTT CTTCGCGGGA AACCAGGAAA AGGATCCGCT 1740
 ACTCAAAAC CAAGAATTAA AAGGAGTTTC TTAATTTTCG ACCTTGTTC TGAAGCTCAC 1800
 TTTTCAGTGC CATTGATGTG AGATGTGCTG GAGTGGCTAT TAACCTTTTT TTCCTAAAGA 1860
 TTATTGTTAA ATAGATATTG TGGTTTGGGG AAGTTGAATT TTTTATAGGT TAAATGTCAT 1920
 TTTAGAGATG GGGAGAGGGA TTATACTGCA GGCAGCTTCA GCCATGTTGT GAAACTGATA 1980
 AAAGCAACTT AGCAAGGCTT CTTTTCATTA TTTTATATGT TTCACTTATA AAGTCTTAGG 2040
 TAACTAGTAG GATAGAAACA CTGTGTCCTG AGAGTAAGGA GAGAAGCTAC TATTGATTAG 2100
 AGCCTAACCC AGGTAACTG CAAGAAGAGG CGGGATACTT TCAGCTTTCC ATGTAACCTG 2160
 ATGCATAAAG CCAATGTAGT CCAGTTTCTA AGATCATGTT CCAAGCTAAC TGAATCCAC 2220
 TTCATATAC ACTCATGAAC TCCTGATGGA ACAATAACAG GCCCAAGCCT GTGGTATGAT 2280
 GTGCACACTT GCTGACTCA GAAAAAATAC TACTCTCATA AATGGGTGGG AGTATTTTGG 2340
 TGACAACCTA CTTTCTTGG CTGAGTGAAG GAATGATATT CATATATTCA TTTATTCCAT 2400
 GGACATTTAG TTAGTGCTTT TTATATACCA GGCATGATGC TGAGTGACAC TCTTGTTGAT 2460
 ATTTCAAAT TTTTGTATAG TCGCTGCACA TATTTGAAAT CATATATTAA GACTTTCCAA 2520
 AGATGAGGTC CCTGTTTCTT CATGGCAACT TGATCAGTAA GGATTTCAAC TCTGTTTGT 2580
 ACTAAAAACA TCTACTATAT GTTAGACATG ACATTCTTTT TCTCTCCTTC CTGAAAAATA 2640
 AAGTGTGGGA AGAGACAAAA AAAAAAAA

Seq ID NO: 383 Protein sequence
 Protein Accession #: NP_002501

1 11 21 31 41 51
 MECLYYFLGF LLLAARFLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60
 VWKRGDMRWK NSWKGGRVQA VLTGDSPLV GSNITFAVNL IFPRCQKEDA NGNIVYEKNC 120
 RNEAGLSADP YVYNWTAWE DSDGENTGQ SHENVFPDGK PFPHPGWRR WNFIVVFHTL 180
 GQYFQKLGRS SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDVI VVTDQIPVFI 240
 TMFQKNDNRNS SDETLFKDLF IMFDVLHDP SHFLNYSTIN YKWSFGDNTG LFFVSTNHTVN 300
 HTYVLNGTFS LNLTKVAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENQCIN 360
 RYGHFQATIT IVEGILEVNI IQMTDVLMPV PWPESLIDF VVTCQGSIFT EVCTIISDPT 420
 CEITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALATSL ISVFPDRDPAS 480
 PLRMANALI SVGCIAIFVT VISLLVYKXH KEYNPIENSP GNVVRSKGLS VFLNRAKAVF 540
 FPGNQEKDPL LKNQEPKGVG

Seq ID NO: 384 DNA sequence
 Nucleic Acid Accession #: NM_001134
 Coding sequence: 48-1877

1 11 21 31 41 51
 TCCATATTGT GCTTCCACCA CTGCCAATAA CAAAATAACT AGCAACCATG AAGTGGGTGG 60
 AATCAATTTT TTTAATTTTC CTACTAAATT TTACTGAATC CAGAACACTG CATAGAAATG 120
 AATATGGAAT AGCTTCCATA TTGGATTCTT ACCAATGTAC TGCAGAGATA AGTTAGCTG 180
 ACCTGGCTAC CATATTTTTT GCCCAGTTTG TTCAAGAAGC CACTTACAAG GAAGTAAGCA 240
 AAATGGTGAA AGATGCAATTG ACTGCAATTG AGAAACCCAC TGGAGATGAA CAGTCTTCAG 300
 GGTGTTTAGA AAACAGCTA CCTGCCTTTC TGGAGAAGCT TTGCCATGAG AAAGAAATTT 360
 TGGAGAAGTA CGACATTCA GACTGCTGCA GCCAAAGTGA AGAGGGAAGA CATAACTGTT 420
 TTCTTGACCA CAAAAGGCC ACTCCAGCAT CGATCCCACT TTTCCAAGTT CCAGAACCTG 480
 TCACAAGCTG TGAAGCATAT GAAGAAGACA GGGAGACATT CATGAACAAA TTCAATTATG 540
 AGATAGCAAG AAGGCATCCC TTCTGTATG CACCTACAAT TCTTCTTTGG GCTGCTCGCT 600
 ATGACAAAAA AATTCCATCT TGCTGCAAG CTGAAAATGC AGTTGAATGC TTCCAACAA 660
 AGGCAGCAAC AGTTACAAAA GAATTAAGAG AAAGCAGCTT GTTAAATCAA CATGCATGTG 720
 CAGTAATGAA AAATTTTGGG ACCCGAAGCT TCCAAGCCAT AACTGTTACT AAAGTGAATC 780
 AGAAGTTTAC CAAAGTTAAT TTTACTGAAA TCCAGAAACT AGTCTGGATG GTGGCCCATG 840
 TACATGAGCA CTGTTGACGA GGAGATGTGC TGGATTGTCT GCAGGATGGG GAAAAATCA 900
 TGTCTACAT ATGTTCTCAA CAAGACACTC TGTCAACAA AATAACGAA TGCTGCAAC 960
 TGACCAAGCT GGAACGTGGT CAATGTATAA TTCATGCAGA AAATGATGAA AAACCTGAAG 1020
 GTCTATCTCC AATCTAAAC AGGTTTCTAG GAGATAGAGA TTTTAACCAA TTTTCTTCAG 1080
 GGGAAAAAAA TATCTTCTTG GCAAGTTTTC TTTCAATAA TTCAAGAAGA CATCCTCAGC 1140
 TTGCTGTCTC AGTAATTTCTA AGAGTTGCTA AAGGATACCA GGAGTTATG GAGAAGTGT 1200
 TCCAGACTGA AAACCTCTCT GAATGCCAAG ATAAAGGAGA AGAAGAATTA CAGAAATACA 1260
 TCCAGGAGAG CCAAGCATTG CCAAAGCGAA GCTGCGGCTT CTTCAGAAA CTAGGAGAAT 1320
 ATTACTTACA AAATGCGTTT CTCGTGCTT ACACAAAGAA AGCCCCCAG CTGACCTCGT 1380
 CGGAGCTGAT GGCATCACG AGAAAAATGG CAGCCACAGC AGCCACTTGT TGCCAACCTA 1440
 GTGAGGACAA ACTATTGGCC TGTGGCGAGG GAGCGGCTGA CATTATTATC GGACACTTAT 1500

GTATCAGACA TGAAATGACT CCAGTAAACC CTGGTGTGG CCAGTGCTGC ACTTCTTCAT 1560
 ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGGG TGAACATAT GTCCTCCTG 1620
 CATCTCTGA TGACAGTTTC ATTTTCCATA AGGATCTGTG CCAAGCTCAG GGTGTAGCGC 1680
 TGCAACGAT GAAGCAAGAG TTCTCATTAC ACCTTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAAC TGAGGCTGTG ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTGTCTGAAG AGGGACAAAA ACTGATTTC AAAAACTCGT 1860
 CTGCTTTGGG AGTTTAAAT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTCATTGG 1920
 TGTGAACCTT TCTCTTAAAT TTAACTGAT TTAACACTTT TTGTGAATTA ATGAAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence

Protein Accession #: NP_001125

1 11 21 31 41 51
 MKWVESIFLI FLNFTESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF PAQFVQEATY 60
 KEVSKMVKDA LTAIEKPTGD EQSSGCLENQ LPALFLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIPLFQ VPEPVTSCBA YEEDRETSMN KFIYBIARRH PFLYAPTILL 180
 WAARYDKIIP SCCCAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNP GTRTFQAITV 240
 TKLSQKFTKV NPTBIQKLVV DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QODTSLNKIT 300
 ECCKLTTLER GQCIHAEND EKPEGLSPNL NRFLGDRDFN QFSSGEKNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAQYQEL LEKCFQTEHP LECQDKGEE LQKYIQESQA LAKRSCGLFQ 420
 KLGEYLLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CCQLSEDKLL ACGEAADI 480
 IGHLCIRHEM TPNVPGVGGC CTSSVANRRP CFSSLVVDET YVPPAFSDDK PIFHKDLCCA 540
 QGVALQTMKQ EFLINLVKQK PQITEQLEA VIADFSGLLE KCCQGEQEV CFAEEGQKLI 600
 SKTRALGV

Seq ID NO: 386 DNA sequence

Nucleic Acid Accession #: NM_002205.1

Coding sequence: 1..3149

1 11 21 31 41 51
 ATGGGGAGCC GGACGCCAGA GTCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC CGCTSSGTGC GCTGCTGTTG CTGCTSSGTG CGCCGCCACC CAGGGTGGGG 120
 GGCTTCAACT TAGACGCCGA GGCCTCAGCA GTACTCTCGG GGCCTCCTTC CTCCTTCTTC 180
 GGATTCTCAG TGAGATTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC 360
 CTGAGTCTCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCTCTGAC 420
 TGGTTCCGGG CAACAGTTTG AGCCCATGGC TCCTCCATCT TGGCATGGCG TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCCGAATTCG GGAGTATGCA CCTGCGCGCT CAGATTTCAG CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCAGTTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAA CTATTATCCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA TTTCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGTGA 840
 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAATT CTCAGGGGAA 960
 CAGATGGGCT CTACTTTGG CTATGCAGTG CCGCCACAG ACGTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCCTGACGG GCGGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140
 CTACCCCTCA CTGGCCATGA TGAGTTTGGC CGATTCTGAC GCTCCTGGGG CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTGTTG ATTTCTTGGG GGCACAGGAG GGCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCTGC AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCTTTGGT 1440
 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGTAGTGC CTCCTCACC 1500
 ATCTTCCCGG CCATGTTTCA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCCTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACAAGTTGC TGACTCCATT 1620
 GGTTCACAG TGGAACTTCA GCTGGAAGTG CAGAAGCAGA AGGGAGGGGT ACGCGGGGCA 1680
 CTGTTCTCTG CCTCCAGGCA GGCAACCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
 CTCTGCGCGA TTCACTATGC TCTCAACTTC TCCTTGGAAC CCCAAGCCCC AGTGGACAGC 1860
 CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGTCTG ACTGTGGAGA AGACAACATC TGTGTGCTGT ACCTGCAGCT GGAAGTGT 1980
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040
 CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCAACGC CCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCTGAG CTGTGACTAC 2160
 TTTGCGGTGA ACCAGAGCCG CCGTCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TGGTATTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGAGTGGTT 2340
 TCCTTTCCGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAAC CTGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT 2580
 GTGACCAAGG TTAGCGGACT CAACTGCACC ACCAATCACC CCATTAAACC AAAGGGCTG 2640
 GAGTTGGATC CCGAGGGTTC CCGTGCACC CAGCAAAAAC GGGAGAGTCC AAGCCGAGC 2700
 TCTGCTCTCT CGGGACCTCA GATCTGAAA TGCCCGGAGG CTGAGTGT 2760
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGTCA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTGA GCCTGCAAGT TGAGGCTGTG 2880
 TACAAGCCCT TGAAGATGCC CTACCGAATC CTGCTCGGCG AGCTGCCCCA AAAAGAGCGT 2940
 CAGGTGGGCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120
 CTCAGCCCTC CAGCCACCTC TGATGCTGA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

5 1 11 21 31 41 51
MGSRTPESPL HAVOLRWGPR RRPPLPLLLL LLLPPFPRVG GFNLDAEAPA VLSGPPGSFF 60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSESE EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLSL 180
10 DNFTRILEYA PCRSDFSWAA GGGYCGGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPFYL INLVQQLQT RQASSIYDD5 YLGVSVAVGE FSGDDTEDFV AGVPKGNLTY 300
GVYVILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DLLLVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDDEF RFGSSLTPLG DLDQDGYNDV AIGAPFGET 420
QGGVVFVFPF GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YPDLIVGSFG 480
15 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW QKQKGVVRA LFLASRQATL TQTLIIQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNF SLDPQAPVDS HGLRPLALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLG D KNALNLTFHA QNVGEGGAYE AELRVATPPE AEYSGLVHRP GNFSLSLSDY 720
20 FAVNQSRLLV CDLGNPMKAG ASLWGLLRFT VPHLRDTKKT IQPFDQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTLNNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGGQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHH QKREAPSR5 900
SASSGPQILK CPEABCFRLR CELGLPHQOE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALMMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
25 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA

Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

30 1 11 21 31 41 51
AAAGAAGSTA AGGGCAGTGA GAATGATGCA TCTTGCATTC CTGTGCTGT TGTGTCTGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCAGCAAA TACTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
35 AAAGGACAGT AATCTCATTT TAAAAAAT CCAAGGAATG CAGAAGTTC TGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
40 TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGGAAAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTCGCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT GGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAAGTCT GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
45 TTTGATGATC CCATCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCCGAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCTCT GCTCTACTG AGGAACCCCT 840
GGTGCCACCA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCTGTCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTCAT TGTATTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTGCG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTTTAT 1080
50 TTTTAAAGGA AATGATGATC CTGAGGATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAGG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAG 1260
TAGCCAGTCC ATGGAGCAAG GTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
55 ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTATC TAATGTATTA TGAGCCAAA TGGTTAATTT TTCTGCTATG TTCTGTGACT 1560
GAAGAAGATG AGCCTTGACG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTTCTT 1620
60 ACTTGCTTTT GAATTGCAT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTTC 1740
CTT

Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

65 1 11 21 31 41 51
MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RRKDSNLIVK 60
KIQQMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
70 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS PAVKEHGDYF SFDGPGHSLA 180
HAYPPGPGLY GDHIFDDDEK WTEDASGTNL FLVAHAELGH SLGLFHSANT EALMYPLYNS 240
FTELAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDF ALSFDAISTL 300
RGEYLFPPDR YFWRRSHWNP EPEFLISAF WPSLPSYLD AYEVSNRDVT FIPKNEFWA 360
75 IRGNEVQAGY PRGIHTLGFPT PIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420
PRLIADDPFG VEPKVDVQLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

80 1 11 21 31 41 51
ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60
CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CTGGAAAAA 120
85 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAGAGC GGAGAAATAG TGGCCAGTG 180
GTTGAAAAAT TGAAGCAAA GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGTCTAGTTT 300

GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACACGCCAG ATTTGCCAAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
 TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCACTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAACAA CCCCAGAACG ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA ACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
 GGAATTGGCC ACAAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTTCTA TTTCTTTTCT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSPPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLRQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGQADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEED ERWNTNRFREY NLHRVAAHEL GHSLGLSHST DIGALMYPYSY 240
 TFSGDVQLAQ DDIDGIAQIY GRSQNPVQPI GPQTPKACDS KLTFFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEAFADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSPGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRY DEYKRSMOPG YPKMIAHDFP 420
 GIGHKVDAVF MKDGFYFFPH GTRQYKFDEPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 392 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAAAC TGAAGAAATGA TGGGAGGCAA GTTGAAAAAGC GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
 TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCTTCACTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAACAA CCCCAGAACG ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA ACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
 GGAATTGGCC ACAAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTTCTA TTTCTTTTCT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 MHSPPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLRQMGEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGQADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDEED ERWNTNRFREY NLHRVAAHAL GHSLGLSHST DIGALMYPYSY 240
 TFSGDVQLAQ DDIDGIAQIY GRSQNPVQPI GPQTPKACDS KLTFFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFIISVF WPQLPNGLEA AYEAFADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSPGF PRTVKHIDAA LSEENTGKTY FFFVANKYWRY DEYKRSMOPG YPKMIAHDFP 420
 GIGHKVDAVF MKDGFYFFPH GTRQYKFDEPK TKRILTLQKA NSWFNCRKN

Seq ID NO: 394 DNA sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

1 11 21 31 41 51

	ATGGTCAGAA	AGCCTGTTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCCTTCCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
5	GGAACTCTCA	TCTCTCTTAA	GGGCGTGCTC	CAGAACAACG	GCAGCGTGGG	CATGTCTCTG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTGTGCA	CTATTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAAACAATA	TAAAGAAATC	TGGAGGTCAT	TACACATATA	TTTTGGAAAGT	CTTTGGTCCA	360
	TTACCAGCTT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGCG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
10	CCTGAACCTG	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTCTAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACTTTTGG	CAAGCTCACA	600
	GCATTTCTGA	TAAATATAGT	CCCTGGAGTT	ATGCAGCTAA	TTAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTTCAGG	AAGAGATTCA	AGTATTACGC	GGTGGCCACT	GGCTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTACTGTA	AGAAGTAGAA	780
15	AACCCGAAA	AAACCATTCC	CCTTGCAATA	TGTATATCCA	TGGCCATTGT	CACCATTTGGC	840
	TATGTGCTGA	CAATATGTCG	CTACTTTACG	ACCATTAATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGG	CAGTACCTTT	TTCTGAGCGG	CTACTGGGAA	ATTTCTCATT	AGCAGTTCCG	960
	ATCTTTGTGT	CCCTCTCTGT	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGCTCCAGG	1020
	TTATTTCTATG	TGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCCTCTCCAT	GATTCTATGC	1080
20	CGCAAGCACA	CTCCTCTACC	AGCTGTTATT	GTTTTCACAC	CTTTGACAA	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAG	TCCTTTGAAT	TTCTCTAGTT	TTGCCAGGTG	GCTTTTATT	1200
	GGCTGGGAG	TTGCTGGGCT	GATTTATCTT	CGATACAAAT	GCCAGATAT	GCATGCTCCT	1260
	TTCAAGGTGC	CAGTGTTCAT	CCCAGCTTTG	TTTTCTTTCA	CATGCCCTCT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCCGACCC	ATTAGTACA	GGGATTGGCT	TCGTCATCAC	TCTGACTGGA	1380
25	GTCCCTGGGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAACCAAGAC	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAGATAAG	1500
	TTATGAACATA	ATGAGCTTGA	GATCTTGCGA	ATCTGCCCAA	GGGAGAGCAC	AAAAAGGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACTT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCATATA	TTTTAGCATA	TTGCAACTAA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACCTATATG	AGTTATAGAA	AGTGAATATG	CAGTTATTTCT	ATGAGTCGCA	CAATTTCTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACAAC	ATATGTTAGC	ACGGCAAGAA	ACCTTCAAAT	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGCTATACT	GTGAAAAGTG	1920
35	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
	ATTTTACATT	GACATTGCAT	TGCTTCCCT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTTG	AACAAAGGTC	AGTGGGGATT	GTGAAATACA	2100
	TTAAAGAAGA	GTTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAGT	2160
	AAAAATCCTT	GAGAATTTAT	TATGTAGAT	GTTTTCAT	TCATTATCAG	GAAATTTTAG	2220
	TTATCTGTCA	TTTTTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGATATA	CACATCTTAG	2280
40	AGCAAGAGTT	AGTTTGGTAT	TAAATCCTCA	TTAGAACAA	CACCTGTTTC	ACTAATAACT	2340
	TACCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAGCC	TTCAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAAA	GAAAGTGTTC	AAAATAATAG	TCCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTGC	ATTTCTTTTA	TACATTTTAT	ATTTCTCTGT	TAAATATCT	2580
45	CTTCAGATGA	AACCTGTCCG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTTGCA	2640
	AAGAAATGTC	GCTGTAAATA	AGATTTCACA	CTGATGTTTC	TAGAAAATTT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTCAGTAAT	TTCCACACCT	TAATTATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAAAATGAA	ATGAGAATCT	GTGGATAAGT	GTTTGTGTTT	AGAAGATGTT	2820
	GTTTGGCCAG	TATTAGAAAA	TACTGTGAGC	CGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACCTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTCGG	GAGTTCTAGA	CCAGCCTGAC	2940
	CAACATGGAG	AAACCCCATC	CTTACTAAAA	ATACAAAATT	AGCTGGGCAT	GGTGGCAGAT	3000
	GCTGGTAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCG	TGAGCCAAGA	TTGCACCACT	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAAATA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

	1	11	21	31	41	51	
60	MVRKPVVSTI	SKGGYLQGNV	NGRLPSLGNK	EPFGQEKVQL	KRKVTLLRGV	SIIGTIIGA	60
	GIFISPKGVL	QNTGSGVMSL	TIWTVCGVLS	LFGALSVAEL	GTTIRKSGGH	YTYILEVFGP	120
	LPAPVRVWVE	LLIIRPAATA	VISLAFGRYI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWASRI	QIFLTPCKLT	AILIIIVPGV	MLIKGQTQN	FKDAFSGRDS	SITRLPLAFY	240
	YGMAYAGWFI	YLNFTVEEVE	NPEKTIPLAI	CISMAITIGV	YVLTNVAYFT	TINAEELLS	300
65	NAVAVTFSEF	LLGNFSLAVP	IFVALSCFGS	MNGGVPAVSR	LPYVASREGH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	FSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLPIPAL	FSFTCLFMVA	LSLYSDPPST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	480
	SEKITRTLQI	ILEVVPEEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

	1	11	21	31	41	51	
75	GCCGCCAGCG	GCTTTCTCGG	ACGCCCTTGC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
	ACCCGCTCG	CCCCCTGGGG	CTGTCGATTC	TGCTGCTTTT	CCTGACGGAG	GCTGCACTGG	120
80	GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCCCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCTT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCCT	TAATCTAAGT	TCCATGACAT	420
85	GTGAAAAATT	CTTTTCCGCT	GGGTGTCACC	GGAACCCGAT	TGAGAACAGG	TTTCCAGATG	480
	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAAATCC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCCAATGTGA	CTCGCTATTA	TTTTAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTATG	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCOGG AAAATTCOGGA AGAAGCAATT TTAACCATTC TTAATATGTC 780
 ATCTTGTGTTG TCTTTATGGC TTATTTGCCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAATCATT GGTGATTAT TCACCAAGTTT TTATTAATAC AAGTCACATT 900
 TTCAAAATTT TGGATTTTT TATATATAAC TAGCTGCTAT TCAAAATGTA GTCTACCATT 960
 TTTAATTTAT GGTTCACACTG TTTGTGAGAC GAATTCCTGC AATGCATAAG ATATAAAAGC 1020
 AAATATGACT CACTCATTTC TTGGGGTCGT ATTCCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACACATA AGACAAATATA ATCATGTGCT TTAAACATAT TTGAGAATAA AAAGGACTAG 1140
 CC

Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
 MDPARPLGLS ILLFLLEA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYDRTYQS 60
 CRQFLYGGCE GNANFYTYE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPSPFCYS PKDEGLCSAN VTRYFNPRI 180
 RTCDAPTYTG CGGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC 120
 TTCGTGATGG GCCTTCTGGG GAACAGCGTC ACCATTGCGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
 TTGGTGTTC TCACTCGGAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300
 ACGTCCAGCT ACACCTGTCT GACGCTCAGC TTTGAGGCT ACATCGCCAT CTGTCACCCC 420
 GCTACGCTGC TGCACGTGCT GAGCACTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 540
 GTCACTCCG CCTGTGGTGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 600
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCAG CCACCCAGAG 660
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 720
 CAGTCCAGCA TCTTCGGCGC CTTCTGGTGC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 780
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 840
 ACGCGGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 900
 ACCATCATCT TCTTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 960
 ATTCCGAGGA TCATGCTGTC GGCCAAACCC AAGCAGGACT GGACGAGGTC CTACTTCCGG 1020
 CGGTACATGA TCTCTCTCCC CTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCACTCAAC 1080
 CCGCTCCTGT ACACGGTGTG CTGCGAGCAG TTTCCGGCGG TGTTCTGTGA GGTGCTGTGC 1140
 TGCCGCTGT CGCTGCAGCA CGCCAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1200
 ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1260
 TCTGCAAGGA GAACGTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1320
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCCAGC 1380
 AATTCTGCTG CAGAGAAATG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

1 11 21 31 41 51
 MASPSLPDSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLNSV TIRVTQVLQK 60
 KGYLQKEVTD HMYSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAGTEYPL 180
 VNVPSHRGLT CNRSSTRHIE QPETSNSMIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 MCWNMMQVLM KSKQGLSLAG TRPPQLRKSE SEESRTARRQ TIIFLRLLIV TLAVCMWPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSVIN PLLYTVSSQG FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEQ 420
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV

Seq ID NO: 400 DNA sequence
 Nucleic Acid Accession #: NM_006475.1
 Coding sequence: 28..2538

1 11 21 31 41 51
 AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA 60
 TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAATCATT ATGACAAGAT CTTGGCTCAT 120
 AGTGTATATCA GGGGTGCGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
 ACCAAAAGA AATACTTACG CACTTGTAA GAACTGTGTA AAAAGTCCAT CTGTGGACAG 240
 AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAGGC 300
 TGCCCGAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
 ACAACGCGAG GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
 TTCACTTACT TTGACCCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA 480
 GGTGTGAGGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
 AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
 TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
 ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
 CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
 GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
 TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCTCTAGA AAGGTTCTAG 900
 GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
 TCTGAGTCTA TTAGTGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

5
 10
 15
 20
 25
 30
 35
 40

```

GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
GTGACAAATA ATGGTGTGAT CCATTGTGATT GATCAGGTCC TAATTCTCTGA TCTGCCAAA 1140
CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATT 1200
GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260
GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAATTAAT TCTGCAGAA 1320
CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAACC 1380
ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAATAATT 1440
TGATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCAG TTCACATATT CCGCGAGATC 1500
ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560
TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620
ACATTATTGT TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680
CTGATACGGG ACAAATAATG TCCTCAAAAC ATCATTCTT ATCACTGAC ACCAGGAGTT 1740
TTCATTGGAA AAGGATTGTA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800
AAAACTCTTC TGAAGAAGT AAATGATACA CTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
TCTGACATCA TGACAACCAA TGGTGTAATT CATGTTGTAG ATAACTCCT CTATCCAGCA 1920
GACACACCTG TTGGAATGTA TCAACTGCTG GAAATACCTA ATAAATTAAT CAAATACATC 1980
CAAATTAAGT TTGTTCTGTT TAGCACCTTC AAAGAAATCC CCGTGAAGT CTATACAACT 2040
AAAAATTATA CCAAGTTTGT GGAACCAAAA ATTAAAGTGA TTGAAGGCAG TCTTCAGCCT 2100
ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATT 2160
AGACTGATTA AAGAAGGTGA AACATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220
AAATACACCA AAATCAATGA TGGAGTGCTT GTGGAATAAA CTGAAAAAGA GACACGAGAA 2280
GAACGAATCA TTACAGGTCC TGAATAAAA TACTAGTGA TTTCTACTGG AGGTGGAGAA 2340
ACAGAAGAAA CTCTGAAGAA ATTTGTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT 2400
GAAGGTGGTG ATGGTCATT ATTTGAAGAT GAAGAAATTA AAGAGCTGCT TCAGGAGAC 2460
ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAG GTTCTAGAAG ACGATTAAAG 2520
GAAGGTGCTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTATTACA ACCCTAAGTC 2580
AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACCT AAACATCAGC 2640
ACAAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTT TCTGGAATGA 2700
GAAACATGAG GGAATTTGTT GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAATATAA 2760
CACCTTACAC CCTTTTTCAT CTGACATTA AAAGTTCTGG CTAACCTTGG AATCCATTAG 2820
AGAAAAATCC TTGTACCAG ATTCAATACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880
CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
TCAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120
TCTCAACGTT TCAATAAAA CCATTTTTC GATATAAAGA GAATTACTTC AAATTGAGTA 3180
ATTCAAGAAA ACTCAAGATT TAAGTAAAA AGTGGTTTG ACTTGGGAA
  
```

Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

45
 50
 55

```

1 11 21 31 41 51
MIPFLPMFSL LLLLIIVNPIN ANNHDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC 60
KNWYKKSICG QKTTVLVECC PGYMRMEGMK GCPAVLPIDH VYGTGLGIVGA TTTQRYSDAS 120
KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSNVNVE LLNALHSHMI NKRLMTKDLK 180
NGMIIPSMYN NLGLFINHYP NGVTVNCAAR IIHGNQIATN GVHVHIDRVL TQIGTSIQDF 240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL 300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDDSDSITV NGIKMVNKKD IVTNNGVIHL 360
IDQVLIPDSA KQVIELAGKQ QTFPTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
VQRLKLLQL NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
RNGAIHIFRE IIKPAEKSLH ERLKQDKRFS TFLSLLEAED LKELLTPQPD WTLFVPTNDA 540
FKGMTSEKE ILIRDKNALQ NIIYLHLPFG VFIGKGFEPG VTNIKLTQSG SKIFLKEVND 600
TLLVNEKSKS ESDIMTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLIKY IQIKFVRGST 660
PKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVIEGEPE FRLIKEGETI 720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKLKL 780
QEEVTKVKFP IEGGDGHLFE DEEIKRLQGG DTPVRKLQAN KKVQGSRRRL REGRSQ
  
```

Seq ID NO: 402 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

65
 70
 75
 80
 85

```

1 11 21 31 41 51
ATCCAATACA GGAGTGACTT GGAACITCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTTT 60
TTCCTCTTGG GCATCATCTT GCTGGTCTCG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120
AAGGGTCGCT GTTCTTGCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA 180
GACCTTAAAC AATTGCCCC AAGCCCTTCC TGCGAGAAAA TTGAATCAT TGCTACACTG 240
AAGAATGGAG TTCAAACATG TCTAAACCCA GATTCAGCAG ATGTGAAGGA ACTGATTAAA 300
AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
AAGAAAGTTC TGAAGTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG 420
ACCCTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACGCTATCA 480
TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTAAAAAC 540
ATTACTCTGA AATTGTAAC AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600
TTGTTAAAGG CTATGATTGT CTTTGTCTT CTACCACCCA CCAAGTTAAT TTCATCATGC 660
TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTACCCCAA CCACATCCCA 720
CTCACACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG 780
TATCTGAGGC ACATGCTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT 840
TGAAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
CTACAGGCTT CACACACAAT GTGCTGAGG GATTATGCT GATTGTTATT GGGTATCACC 960
ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTGGAA AGCCATGTGA 1020
TTCCATCTTG CCGCTCAGG CTGACCATT TATTTCTTT TGTCCCTT TGCTTCATTC 1080
AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTCTCTCCA GTGCACCTGT 1140
CATATGCTCT GATTATCTG AGTCAACTCC TTTCTCATCT GTCCCCAAC ACCCCACAGA 1200
AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260
AAATAAACCT TTTTGGACAC ACAAATTATC TTAATACTCC TGTTTCACTT GGTTCAGTAC 1320
CACATGGGTG AACACTCAAT GGTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCAACC 1380
  
```

AGATTGTCAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACCT GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACACG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATCTCT TTTCCGAAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAAAGTAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920
 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCCGT 2040
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTCCAGG 2100
 GGAGGTTTCA TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CGGTGGGAGA 2220
 TCCCACCGCA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATAACTAAC AACCAAAGAC TACATATTGT CACTGACACA CACGTTATAA 2400
 TCATTTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAAATAAT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTTGTAATT TGAAATATTT TCTTTGTATA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 403 Protein sequence
 Protein Accession #: NP_002407

1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCCK 60
 IBIATLKNRG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120
 QKKTT

Seq ID NO: 404 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCAGCCCC 60
 AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCGGGGGCCC GCGCGCGGG 120
 GACGGGCGTC TGGCGGTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGGTG 240
 TCCGCCAGC CCGCGCTGCC GACCAAGTGC CCGCGCTGTG GCGAGTGCTC CGAGGACGCG 300
 CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCAAG CTGGCGGTGC TCCTTCCCGG CGCCTTCGCG 420
 CGCGCGCGCG CGCTGGCGGA GCTGGCGCGC CTCACCTCA GCGGCAGCGC CCTGGACGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
 CCACTGGCGG ACCTCAGTCC CTTGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600
 AGTCCCTTGG TGAAGCTGAT CCGTGAACCA ATCTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTCG AGGCGATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
 CGCGCGTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 CTGCCCCAGC TCAGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
 TCCTTCGCGA ACCTGACACA TCTAGAAAGC CTCACCTTGG AGGACAATGC CCTCAAGGTC 900
 CTTCACAATG GCACCTTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960
 AACAAATCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCTCTTGG AACCTCAACG TCTGACCTG GACTGTGACC CGATTCTTCC CCAATCCCTG 1140
 CAAACCTCTT ATGTCTTCTT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGGATACA TGGGAAGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320
 AACCTCAGTT CTAACCTGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 TAGATACAAC GGACTTTGAC TAAAGCAGT GAAGGGGATT TGCTTCTTGG TTATGTAAGG 1500
 TTTCTCGGTG TGTCTGTGTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTCTTTTCTT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGCTCTGC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTAACAAAAA GCTGCCTCAA CTTTTCGAG AAAAATACTT TATTATAAAA 1740
 TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAA AATTGCATCC TATAAATGTC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAATAAA CTCCATGGTG CACAGGAGCA CTGTCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGCAT ATTACAAAAA ATAACTTGCA ACTTCATAAC 1920
 TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAAATG ACTGATTTTT 1980
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAATAAAG 2040
 ATTCCTAAAA GAA

Seq ID NO: 405 Protein sequence
 Protein Accession #: NP_006661

1 11 21 31 41 51
 MPGGCSRGPA AGDGRLLRLAR LALVLLGWVS SSSPTSSASS FSSAPPLAS AVSAQPPLFD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSRD DEVRAGAFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180
 NHVPPEDER QNRSEFGMVV AALLAGRALQ GLRRLLEASN HFLYLPDVL AQLPSLRHLD 240
 LSNNSLVSLT YVSPRNLTSL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVP LDNNPWVDCD 300
 HMADMVTLWK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDCDPLPP SLQTSYVFLG 360
 IVALALGAIF LLLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSNSNDV

Seq ID NO: 406 DNA sequence
 Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

```

1      11      21      31      41      51
5      |      |      |      |      |      |
      ATGCCTGGGG GGTGCTCCCG GGGCCCCGCC GCCGGGGACG GGCGTCTGCG GCTGGCGGGA 60
      CTAGCGCTGG TACTCTCTGG CTGGGTCTCC TCGTCTTCTC CCACCTCTCT GGCATCTCTC 120
      TTCTCTCTCT CGGCGCCGTT CTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCGCGAC 180
      CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
      AATCTGACCG AGGTGCCCCA GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
10     AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
      AGCCTCAGCG ACCTGCACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTCTT 420
      CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
      AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACACATTA GGGTTTTCCT GGACAACAAT 540
      CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
15     TTGCAAGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAG AAATGAGGAA TCGGGTCTCT 660
      TTGGAATCTA ACAGTGTGTA CCTGGACTGT GACCCGATTTC TTCCCCATC CCTGCAAAAC 720
      TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CCTGGTTTGT 780
      TATTTTGAAC GCAAGGGGAT AAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAAGGAT 840
      CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
20     AGTTCTAACT CGGATGTCCT CGAGTGA

```

Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

```

25     1      11      21      31      41      51
      MPGCGSRGPA AGDGRLLRLR LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPPLPD 60
      QCPALCECSE AARTVKVCNR NLTEVPTDLP AYVRNLFITG NQLASNHFLY LPRDVLALQP 120
      SLRHLDLSNN SLVSLTYVSF RNLTHLESIH LEDNALKVLH NGTLAEQLGL PHIRVFLDNN 180
30     PWVCDCHMAD MVTWLKETEV VQGDRLTCA YPEKMRNRVL LELNSADLDC DPILPPLQIT 240
      SYVPLGIVLA LIGAIPLVLV YLNRRGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
      SSNSDVLE

```

Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

```

40     1      11      21      31      41      51
      CAGCACCCAG CTCCCGGCCA CGCCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC 60
      CCTGGCTGCC CTGGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
      GCAGATGCTT CGGGAAGTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
      GCGGCAGCAG GTCAGGGAGA TCACGTTCTC GAAAAACACG GTGATGAGT GTGACGCGTG 240
      CGGGATGCAG CAGTCACTAC GCACCGGCCT ACCCAGCGTG CGGCCCTGCG TCCACTGCGC 300
45     GCGCGGCTTC TGCTTCCCGG GCGTGGCCTG CATCCAGACG GAGAGCGCGG GCCGCTGCGG 360
      CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTGCACTGCG ACCGACGTCA ACGAGTGCAA 420
      CGCCACACCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
      GGCTTGCCCC CGGGGTACAA GCGGCCCCAC CCACCAGGGC GTGGGCTGCG CTTTGCCTCA 540
      GCGCAACAAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAAGTGGCT 600
50     CCCCACCTCC GTGTGCTACA ACACCCGGGG CTCCTTCCAG TGCGGCGCGT GCCAGCCCGG 660
      CTTGCTGGGC GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACGG 720
      CTCGCCACGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
      GTGCGTGTGT CGGTTGGCTT GGGCCGGCAA CGGGATCCTC TGTGGTCCG ACCTGACCT 840
      AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGGCGTA AGGACAACTG 900
55     CGTGACTGTG CCCAAGTCA GGCAGGAGGA TGTGGACGCG GATGGCATCG GAGACGCGTG 960
      CGATCCGGAT GCGACGGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG 1020
      GAACCCAGAC GACCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
      GTCCCAAGAG AAGAGGACAC AAAAGGACAC AGACCAGGAG GGCCGGGGCG ATGCGTGCGA 1140
      CGACGACATC GACGGGACCC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGGTACCCAA 1200
60     CTCAGACGAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
      GAAGAGCAAC CCGGATCAGG CCGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
      CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC 1380
      TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCTGCG ACAGACGAGA 1440
      CGACCAATGAC GGAGTCCCTG ACAGTCCGGA CAACTGCCGC CTGGTGCTTA ACCCGGCCA 1500
65     GGAGGACGCG GACAGGAGCG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
      GGTGGTAGAC AAGATCGAGC TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG 1620
      GGCCTTCCAG ACAGTCTGTC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
      GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
      GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCATGTGA ACACGGTCAC 1800
70     GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGTCCAGCT TCTACGTGGT 1860
      CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCTTCCGTG CTGTGGCGGA 1920
      GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
      CGCTCTGTGG CATAAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
75     AAACGTGGGT TGAAGGACA AGAAGTCTTA TCGTTGGTTC CTGCAGCACC GCGCCCAAGT 2100
      GGGCTACATC AGGGTGCAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
      CTTGGACACA ACCATGCGGG GTGGCCGCTT TGTCTCTCCC AGGAGAACAT 2220
      CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
      TCAGCTGGCG CAAGCTTAGG GACCAGGGTG AGGACCCGCG GGATGACAGC CACCTCACC 2340
80     GCGGCTGGAT GGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400
      AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGG

```

Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

```

85     1      11      21      31      41      51
      MVPDTACVLL LTALALGASG QQSPLGSDL GPQMLRELQE TNAALQDVRE WLRQQVREIT 60

```


FLKNTVMECD ACGMQQSVRT GLPSVRPLH CAPGFCFFGV ACIQTESGGR CGPCPAGPTG 120
 NGSHTCDVNE CNAHPCFPVR RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDDQASG CQRGAQRFCP DGSPSECHEH 240
 ADCVLERDGS RSCVCRVQWA GNGILCGRDT DLDGFPDEKL RCEPQCRKD NCVTVPNSSGQ 300
 EDVDRDGI GD ACDDADGDG VPNEKDNCEPL VRNPDQRNTD EDKWDGACDN CRSQKNDQDK 360
 DTDQDGRGDA CDDDDIDGRI RNQADNCPRV PMSDQKDSGD DGIGDADCNQ PQKSNPDQAD 420
 VDHDVFGDAC DSDQDDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
 RDNCRLVFNP GQEDADRDGV GQVCQDDFDA DKVVDKIDVC PENAEVLTLD FRAFQTVVLD 540
 PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 PGYQDSSSFY VVMWQMEQT YWQANPFRAY AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
 RLGVPCFSQE NIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 410 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

1 11 21 31 41 51
 | | | | | |
 20 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
 AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
 ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGCTCTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 25 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
 TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 30 GGTTAATGTT CATCATCCTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCTCTACTGA GGTGCTATGT TCTTAGTGGG TGTTCTGACC CTGCTTCAAA TATTTCCTCTC 660
 ACCTTTCCCA TCTTCCAAGG GACTAAGGA ATCTTCTGCG TTTGGGGTTT ATCAGAATTC 720
 TCAGAACTCT AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTAAAG AATGCTCTTT 780
 ACTTCATGGA TCTCCACTGC CATCTCTCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
 35 CATACAATTC CAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
 CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATGTT 960
 TTTCAAGTGA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAATA AAAATGAGGT ACTCTCTGG AAATATTAAG

Seq ID NO: 411 Protein sequence
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
 | | | | | |
 45 MNQTALICC LIFLTLGSIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
 EIIATMKKKK EKRLNPEK AIKNLLKAVS KEMSKRSP

Seq ID NO: 412 DNA sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

1 11 21 31 41 51
 | | | | | |
 55 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120
 CGCTGCCCGG CAGCGCGGAG CCATGCGACC CCAGGGCCCC GCGCCTCCCG CGCAGCGGCT 180
 CGCGCGCTCT CTGCTGCTCC TGCTGTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CCGAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 60 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 CATTCCGGGT ACACCTGGGA TCCCAGGTGC GGATGGATTC AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATAT GGCATAGATC TTGGGAAAAT TGGGAGTGT ACATTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG 600
 65 CTGTACGCGT TGGTATTTC CAATCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
 AGCTATAATT TAATTTGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTATCG 720
 CACTTCTCT GTGGAAGGAC TTTGTGAAG AATTGGTGTG GATTAGTGG ATGTTGCTAT 780
 CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATGTAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 70 TTTTATTATT ATGCCTTGA ATGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTAAATCTA GCATTATTCA TTTTGTCTCA ATCAAAAGTG GTTTCATAT TTTTCTTAGT 1080
 TGGTTAGAA ACCTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
 GGTCTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
 75 TGTACAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 413 Protein sequence
 Protein Accession #: XP_057014

80 1 11 21 31 41 51
 | | | | | |
 MRPGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANGIPTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTFTK PIRNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECGSLP PIEAIIYLDQ 180
 85 GSPFMNSTIN IHTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK


```

5      1      11      21      31      41      51
      |      |      |      |      |      |
CTCGTGC CGA ATTCCGCGACG AGACCGCGTG TTCGCGCGCTG GTAGAGATT TCTCGAAGACA 60
CCAGTGGGCC CGTGTGGGAAC CAAACCTGCG CGCGTGGCCG GCGCGTGGGA CAACGAGGCC 120
GGGAGAGCGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC 180
10    TCTCTGT CAC AAATCCCCCT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATGGGGAA TCTGGCATT A TGTTGACTT GGCAATTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
TCAGAAAATT ACTTCAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
15    AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCCAC CATAATCATG 540
CTGCTTCTGG TAAATAAAG CGAAAAGCTC TTTGCCAGA CCACTGACTCA GATAGTTCAG 600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACC ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAATCTTTCC 780
20    CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
GAAACACAAA TGAATACCTC CAGGAGTGTT TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
25    TCAACCAAT TGATGCTAGA TCTTGTTCTG TTCATACAAG TGAAAAGAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCTT GTCTCTGTG GGGGTTATCT TAGTGCCCTC CATGAATCGG GTGTTTTTCA 1200
AATTTCTCTT GAGTTTCTTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCACATTTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACAG 1320
CAATGGAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
30    GTGCCATATT TGATTCCACG TGAAGGGTTC TAACAGCTCT AGGAGGCCCTG TATTTTATGT 1440
TTCTTGTTGA ACATGTCCTC ACATTGTATC AACAATTTAA AGATAAGAG AAAAAGAATC 1500
AGAAGAAACC TGAATAATGAT GATGATGTGG AGATTAAGAA GCAAGTTGTC AAGTATGAAT 1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620
GAGCAGACTC ACAGAGAGCC TCCCACCTTG ATTTCTCAGC GCCTGCAGTC TTGGAAGAAG 1680
35    AAGAGGTGAT GAATGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCACCATC 1860
CTCAGAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCGCGC GTCGCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG 1980
40    GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
AGCAGGCTGT CCTTTAATAT GCATTGTGAG CCAATGCTGGC GTATCTTGA ATGGCAACAG 2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTGCA CTTACTGCTG 2220
45    GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCCG TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTGTGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAATT 2400
TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTGAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT 2520
50    TTGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTAAAT 2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTACAC GGTATTACCA GTTTATTATG 2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAAATGT 2700
TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAAATGT CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
55    AGCAAGAGAA TAAGAGAGAA AAGAGAAGAA TCTGAGAAAT GGGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAGG 2940
CAGAAATAGT ATAGAGTACA TTCATTAAAC ATTTTGTGCA GGATTATTTC CCGTAAAAAC 3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTAAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
60    TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGGTT ACCTGGTTTA 3240
CAAAATATATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAAACT ACACTAAGTA 3300
TCATTGTGAT CGATTAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATGT 3360
GAGCAATGTG CTTTATATAC GGTACTGTAG CCATACTAGG CCGTCTGTG GCATTCTCTA 3420
65    GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

```

Seq ID NO: 415 Protein sequence
Protein Accession #: XP_084007

```

70      1      11      21      31      41      51
      |      |      |      |      |      |
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNW ESGINVDLAI STROYHLQQL 60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDSHS DHEHSDHER HSDHEHSDH 120
EHHSDDHDSH HRNHAASGKN KRKALCPDHD SDSSGKDPN SQKGAGRPE HASGRRNVKD 180
75    SVSASEVTST VYNTVSEGT FLETIETPRP GKLPKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTSHGMGIQV PLNATEFNYL CPAIINQIDA 300
RSCLHTSEK KAETPPKTY S LQIAWVGFI AISIISFLS LGVILVPLN RVFFKFLLSF 360
LVALAVGTLS GDAPLHLLPH SHASHHSHS HEEPAMEMKR GPLFSLSSQ NIEESAYFDS 420
TNKGLTALGG LYPMFLVHV LTLIKQFKDK KKNQKKPEN DDDVEIKKQL SKYESQLSTN 480
80    BEKVDTDRRT EGYLRADSQE PSHFDSQQA VLEEEVMIA HAHPQEVYNE YVPRGCKNKC 540
HSHFHDTLQ SDDLIIHHHD YHHILHHHH ONHHPHSHSQ RYSREELKDA GVATLAWMVI 600
MGDGLHNFSD GLAIGAAFTG GLSSGLSTSV AVFCHPELPE LGDFAVLLKA GMTVQKAVLY 660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDEGCS 720
RWGYFPQLQA GMLLPGGIML LISIFERKIV PRINP

```

85 Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

	1	11	21	31	41	51	
5	ATGCCCAAGC	CGCGGCACTG	GGGGGCCCTC	TCCGTGGTGC	TGATCCTGCT	TTGGGGCCAT	60
	CGCGGAGTGG	CGCTGGCCTG	CCCGCATCCT	TGTGCCTGCT	ACGTCCCCAG	CGAGGTCCAC	120
	TGCACGTTC	GATCCCTGGC	TTCCGTGCCC	GCTGGCATTG	CTAGACACGT	GGAAAGAATC	180
	AATTGGGGT	TAAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTGGCAGG	ACTGACCAAG	240
	TTGGAGTAC	TTATGATTCA	CGGCAATGAG	ATCCCAAGCA	TCCCOGATGG	AGCTTTAAGA	300
10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAGGA	360
	CAGACCCCTC	AGGGTCTCTC	TAACTTAATG	AGGCTGCACA	TTGACCACAA	CAAGATCGAG	420
	TTTATCCACC	CTCAAGCTTT	CAACGGCTTA	ACGTCTCTGA	GGCTACTCCA	TTTGGAAAGGA	480
	AATCTCTCC	ACCAGCTGCA	CCCCAGCACC	TTCTCCACGT	TCACATTTT	GGATTATTTT	540
	AGACTCTCCA	CCATAAGGCA	CCTCTACTTA	GCAGAGAACA	TGGTTAGAAC	TCTTCTGCC	600
15	AGCATGCTTC	GGAAATGACC	GCTTCTGGAG	AATCTTTACT	TGCAGGGAAA	TCCGTGGACC	660
	TGCGATTGTT	AGATGAGATG	GTTTTTGGAA	TGGGATGCAA	AATCCAGAGG	AATTCTGAAG	720
	TGTAATAAGG	ACAAAGCTTA	TGAAGGCGGT	CAGTTGTGTG	CAATGTGCTT	CAGTCCAAAG	780
	AAGTTGTACA	AACATGAGAT	ACACAAGCTG	AAGGACATGA	CTTGTCTGAA	GCCTTCAATA	840
	GAGTCCCCTC	TGAGACAGAA	CAGGAGCAGG	AGTATTGAGG	AGGAGCAAGA	ACAGGAAGAG	900
20	GATGGTGGCA	GCCAGCTCAT	CCTGGAGAAA	TTCCAAGTGC	CCCAAGTGGG	CATCTCTTTG	960
	AATATGACCG	ACGAGCAGCG	GAACATGGTG	AACCTGGTCT	GTGACATCAA	GAACAACATG	1020
	GATGTGTACA	AGATTCACTT	GAACCAACG	GATCCTCCAG	ATATTGACAT	AAATGCAACA	1080
	GTTGCCCTGG	ACTTTGAGTG	TCCAATGACC	CGAGAAAAGT	ATGAAAAGCT	ATGGAATTTG	1140
	ATAGCATACT	ACAGTCAAGT	TCCCGTGAAG	CTACACAGAG	AGCTCATGCT	CAGCAAGAAC	1200
25	CCCAGAGTCA	GCTACCAAGT	CAGGACAGAT	GCTGATGAGG	AAGCTCTTTA	CTACACAGGT	1260
	GTGAGAGCCC	AGATTCTTGC	AGAACCAGAA	TGGGTCATGC	AGCCATCCAT	AGATATCCAG	1320
	CTGAACCCGC	CTCAGAGTAC	GGCCAAGAAG	GTGCTACTTT	CCTACTACAC	CCAGTATTCT	1380
	CAACAATAT	CCACAAGA	TACAAGGCAG	GCTCGGGGCA	GAACTGGGT	AATGATTGAG	1440
	CCTAGTGGAG	CTGTGCAAA	AGATCAGACT	GTCTTGGGAG	GGGTCTCATG	CCAGTTGAGC	1500
30	TGCAACGTGA	AAGCTTCTGA	GAGTCCATCT	ATCTTCTGGG	TGCTTCCAGA	TGGTCCATC	1560
	CTGAAGCGC	CCATGGATGA	CCAGACAGC	AAGTTCTCCA	TTCTCAGCAG	TGGTGGCTG	1620
	AGGATCAAGT	CCATGGAGCC	ATCTGACTCA	GGCTTGTACC	AGTGCATTGC	TCAAGTGAGG	1680
	GATGAAATGG	ACCCGATGGT	ATATAGGGTA	CTTGTGCAGT	CTCCCTCCAC	TCAGCCAGCC	1740
	GAGAAAGACA	CAGTGACAAT	TGGCAAGAAG	CCAGGGGAGT	CGGTGACATT	GCCTTGCAT	1800
35	GCTTTAGCAA	TACCCGAAGC	CCACCTTAGC	TGGATTCTTC	CAACAGAAAG	GATAATTAAT	1860
	GATTTGGCTA	ACACATCACA	TGTATACATG	TTGCCAAATG	GAATCTTTTC	CATCCCAAG	1920
	GTCCAAGTCA	GTGATATGG	TTACTACAGA	TGTGTGGCTG	TCAACCAAGC	AGGGGCAGAC	1980
	CATTTTACGG	TGGGAATCAC	AGTGACCAAG	AAAGGGTCTG	GCTTGCCATC	CAAAAGAGGC	2040
	AGACGCCCGC	GTGCAAGGCG	TCTTTCAGAG	GTGAGAGAG	ACATCGTGGG	GGATGAAGGG	2100
40	GGCTCGGGCA	TGGGAGATGA	AGAGAACACT	TCAAGGAGAC	TTCTGCATCC	AAAGGACCAA	2160
	GAGGTGTTCC	TCAAAACAAA	GGATGATGCC	ATCAATGGAG	ACAAGAAAGC	CAAGAAAGGG	2220
	AGAAGAAAGC	TGAAACTCTG	GAAGCATTCG	GAAGAAAGAC	CAGAGACCAA	TGTTGCAGAA	2280
	GGTTCGAGAG	TGTTTGAATC	TAGACGAAGG	ATAAACATGG	CAAAACAAAC	GATTAAATCC	2340
	GAGCGCTGGG	CTGATATTTT	AGCCAAAGTC	CGTGGGAAAA	ATCTCCCTAA	GGGCACAGAA	2400
45	GTACCCCGCT	TGATTAAAC	CACAAGTCTC	CCATCCTTGA	GCCTAGAAGT	CACACCACT	2460
	TTTCTGTGCT	TTTCTCCCC	CTCAGCATCT	CCTGTGCAGA	CAGTAACCAG	TGCTGAAGAA	2520
	TCTCAGCAG	ATGTACCTCT	ACTTGGTGAA	GAAGAGCAGC	TTTTGGGTAC	CATTTCTCTA	2580
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	GGAGTTATTC	TTGTTGAACC	TGAAGTAACA	2640
	AGCACACCTC	TGGAGGAAGT	TGTTGATGAC	CTTCTGAGAG	AGACTGAGGA	GATAACTTCC	2700
50	ACTGAAGGAG	ACCTGAAGGG	GACAGCAGCC	CCTACACTTA	TATCTGAGCC	TTATGAACCA	2760
	TCTCTACTC	TGATACACT	AGACACAGTC	TATGAAAGGC	CCACCCATGA	AGAGACGGCA	2820
	ACAGAGGGTT	GGTCTGCAGC	AGATGTTGGA	TCGTCAACAG	AGCCACATC	CAGTGAGTAT	2880
	GAGCCTCCAT	TGGATGCTGT	CTCCTTGGCT	GAGTCTGAGC	CCATGCAATA	CTTTGACCCA	2940
	GATTTGGAGA	CATGATGACA	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
55	CTTACTCCAA	CCCCACCAT	CTGGGTTAAT	GACTCCAGTA	CATCAGATT	ATTGAGGAT	3060
	TCTACTATAG	GGGAACCCAG	TGTCACAGGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AATATGCTAG	AGGGAGACCC	CACACACTCC	3240
	AGAAGTTCTG	AGAGTGAGGG	CCAAGAGAGC	AAATCCATCA	CTTTGCTTGA	CTCCACACTG	3300
60	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCACAGT	TGGTACCCTC	3360
	CTAGACAAAG	ACACCACAAC	AGTAACAACA	ACACCAGGC	AAAAAGTTGC	TCCGTCTATC	3420
	ACCATGAGCA	CTCACCTTTC	TGGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCCGCC	ACCGGCACAA	GCAAAACCCA	CCCACAACCT	TTGCCCATC	AGAGACTTTT	3540
	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGG	GAGTTCTCTG	3600
65	GTTCTCTACG	CTTGGGTGGA	TACACAGTT	AATACCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCTTCTTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCAGTTTCTG	AAACTATACT	TTTGCCTAGA	3840
	ACTGTTTCTC	TGAAAACCTG	GGGCCCTTAT	GATTCTTTAG	ATTACATGAC	AACCACCAAG	3900
70	AAAATATATT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	TCAGATGGAA	AAGAAATTAA	GGATGATGTT	GCCACAAATG	TTGACAAACA	TAAAGTGAC	4020
	ATTTTAGTCA	CTGGTGAATC	AATTAATAAT	GCCATACCAA	CTTCTGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AATTTAAGGA	AGAATCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
	AATCCCTCAA	GGACGGCCCA	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCCTTCT	4200
75	GGGGAAATC	TTACAGACCC	TCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTTTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTCACC	AGGAAGAAGC	TGGTTCTTCC	4320
	ACAACTCTCT	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTTT	4380
	GATCAAGATC	ATCTTGAAC	CACGTGGGCT	ATTCTCCTTT	CTGAAACTAG	ACCACAGAA	4440
	CACACCCCTA	CTGCTGCCCG	GATGAAGGAG	CCAGCATCCT	CGTCCCCATC	CACAATCTC	4500
80	ATGCTTTTGG	GACAAACAC	CACCACTAAG	CCAGCACTTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTT	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCAG	TCAACATGA	AGGAACACAG	CATATGTCAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGATGTC	ATTTAACTTG	TCTACAAAGC	TGGAATTGGA	AAAGCAAGTA	4740
	TTTGGTAGTA	GGAGTCTACC	AGCTGGCCCA	GATAGCCAAC	GCCAGGATGG	AAGAGTTCAT	4800
85	GCTTCTCATC	AACCAACAG	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
	CTACCTGAAA	TGTCCACACA	AAGCGCTTCC	AGATACTTTG	TAACTTCCCA	GTACCTCGT	4920
	CACCTGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAAATTCCT	TCCCATTGCA	CATGTCCAAA	5040

	CCCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTCATG	TTACTCCAAA	5100
	GTGTTTGGA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCCAGTCCA	5160
	AGAATTCCTC	ATTATTCCAA	TGGAAGACTC	CCTTTCTTTA	CCAACAAGAC	TCTTTCTTTT	5220
5	CCACAGTTGG	GAGTCACCCG	GAGACCCGAG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTTCCAGG	TTCTTACAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
	GACTTTTGCC	CTCCGGGACC	TCCGTTGTG	CACACTCCGC	AGACCAAGG	ATCACCTCA	5400
	ACTAACTTAC	AGAAATATCCC	TATGGTCTCT	TCCACCCAGA	GTTCATCTC	CTTTATAACA	5460
	TCTTCTGTCC	AGTCCTCAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAGTTCTT	TGCAGGAGGA	5520
10	CCTCCTGCAT	CCAAATTTCTG	GTCTCTTGGG	GAAAAGCCCC	AAATCCTCAC	CAAGTCCCCA	5580
	CAGACTGTGT	CCGTCACCGC	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
	CCAAAGCCTT	TGCTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAAATACC	5700
	AGGATACAAC	GGTTTGAAGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCAGTATAT	GTGCACCGCC	AGCAACCTGC	ACGGCCTGGA	CAGGATGGTG	5820
15	GTCTTGCTTT	CGGTACCCGT	GCAGCAACCT	CAAATCCTAG	CCTCCCACTA	CCAGGACGTC	5880
	ACTGTCTACC	TGGGAGACAT	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
	CAAAATTTCT	GGATCTTTCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGCACGAAAA	CCGGACCCCT	TCCATCAAGG	AGGCGTCTT	CTCAGACAGA	6060
20	GGCGTCTATA	AGTGCGTGGC	CAGCAATGCA	GCCGGGGCGG	ACAGCCTGGC	CATCCGCTGT	6120
	CACGTGGCGG	CAGTGCCTCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGCTGCCC	6180
	CCGGGGCTCA	GCAATTCACAT	TCACTGCAC	GCCAAAGGCTG	CGCCCCCTGC	CAGCGTGGCG	6240
	TGGGTGCTCG	GGGACGGTAC	CCAGATCCGC	CCCTCGCAGT	TCTTCCAAGG	GAACCTGTGT	6300
	GTTTTCCCCA	ACGGGACGCT	CTACATCCGC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGCCTGG	CCGCAACACT	GTGAGGCTCC	GCGCGCAGGA	CGGTGCAGCT	GAACGTGCAG	6420
25	CGTGCAGCAG	CCAAACGCGC	CATCACGGGC	ACCTCCCGCG	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TCCGGGGACC	CCTGGCCGCG	CATCTCTGTG	6540
	AGGCTGCGGT	CCAAAGGAGT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTG	6600
	TTTGCCAAATG	GGACCCCTGGT	GGTGAAATCA	GTGACGGACA	AAGATGCGCG	AGATTACCTG	6660
	TGCGTAGCTC	GAATAAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGG	TGTGGTGATG	6720
30	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AACGACCACA	AAGTCTTCTA	CGGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCC	AGATCTCCTG	GAGCCTCCCA	6840
	GACGGGAGTC	TGGTGAATCT	CTTCATGCAG	TCCGATGACA	GCGGTGGACG	CACCAAGGCG	6900
	TATGTGCTCT	TCAACAATGG	GACACTCTAC	TTTAACGAAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
35	GTGTGTGACG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTC	GGTGCCTTAT	7080
	GGAGACGTGG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
	TTGTCCCAAA	CCAAACAAGT	GATCCCCACC	TCCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTAGCAA	AGCCACGCGT	TCTGACAGCG	GCAACTACAC	CTGCCCTGTC	7260
	AGGAACAGCG	CGGAGAGGGA	TAGGAAGACG	GTGTGGATTG	ACGTCAACGT	CCAGCCACCC	7320
40	AAGATCAACG	GTAACCCCAA	CCCCATCACC	ACCGTGCGGG	AGATAGCAGC	CGGGGGCAGT	7380
	CGGAAACTGA	TGAGTGTCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGTGT	ATGGGCTTTT	7440
	CCCGAGGGTG	TGGTTCTGCG	AGCTCCATAC	TATGGAAACC	GGATCACTGT	CCATGGCAAC	7500
	GGTTCCCTGG	ACATCAGGAG	TTTGAGGAAG	AGCGACTCCG	TCCAGCTGGT	ATGCATGGCA	7560
	CGCAACAGGG	GAGGGGAGGC	GAGGTTGATC	GTGCAGTCA	CTGTCTTGA	GCCCCATGGG	7620
45	AAACCCATCT	TCCACGACCC	GATCAGCGAG	AAGATCAACG	CCATGGCGGG	CCACACCATC	7680
	AGCCTCAACT	GCTCTGCCCG	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
	GGCACCGATC	TGCAGATGG	ACAGCAGCTG	CAGCGCTTCT	ACCACAAGGC	TGACGGCATG	7800
	CTACACATTA	GCGGTCTCTC	CTCGGTGGAC	GCTGGGGCCT	ACCGCTGCGT	GGCCCGCAAT	7860
	GCCGCTGGCC	ACACGGAGAG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAGCC	AGAAGCAAAC	7920
50	AAGCAGTATC	ATAACCTGGT	CAGCATCATC	AATGGTGAGA	CCCTGAAGCT	CCCCTGACCC	7980
	ACTCCCGGGG	TCCGGCAGGG	ACGTTTCTCC	TGGACGCTCC	CCAATGGCAT	GCATCTGGAG	8040
	GGCCCCCAAA	CCCTGGGAAG	CGTTTCTCTT	CTGGACAATG	GCACCTCAC	GGTTCGTGAG	8100
	GCCTCGGTGT	TTGACAGGGG	TACCTATGTA	TGCAGGATGG	AGACGGAGTA	CGGCCCTTCG	8160
	GTCAACGACA	TCCCGGTGAT	TGTGATCGCC	TATCCTCCCC	GGATCACCAG	CGAGCCCACC	8220
55	CCGGTCACTC	ACACCCGGCC	CGGGAACACC	GTGAAACTGA	ACTGCATGGC	TATGGGGATT	8280
	CCCAAGAGCTG	ACATCAGCTG	GGAGTTACCG	GATAAGTGGC	ATCTGAAGGC	AGGGGTTTCA	8340
	GCTCGTCTGT	ATGGAAACAG	ATTTCTTAC	CCCCAGGGAT	CACTGACCAT	CCAGCATGCC	8400
	ACACAGAGAG	ATGCCCGGCT	CTACAGTGC	ATGGCAAAAA	ACATTCTCGG	CAGTGACTCC	8460
	AAACAACCTT	ACATCCACCT	TTCTGAAAT	GTGGATTCCA	GAATGATTGC	TTAGGAAGCTG	8520
60	ACAACAAAGC	GGGGTTTGTA	AGGGAAGCCA	GGTTGGGGAA	TAGGAGCTCT	TAAATAATGT	8580
	GTCAAGTGC	ATGTTGGCCT	CTGGTGGGTT	TCAAGTTGAG	GTTGATCTTG	ATCTACAATT	8640
	GTTGGGAAAA	GGAAGCAATG	GAGACACGAG	AAGGAGGGCT	CAGCCTTGCT	GAGACACTTT	8700
	CTTTTGTGTT	TACATCATGC	CAGGGGCTTC	ATTGAGGGTG	TCTGTGCTCT	GACTGCAATT	8760
	TTTCTTTCTT	TGCAAAATGCC	ACTCGACTGC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
65	ACATTATACA	AAAATAAGCC	ATAGACATGA	ACAACACCTC	ACTACCCCAT	TGAAGACGCA	8880
	TCACCTAGTT	AACCTGTGTC	AGTTTTTACA	TGATAGACTT	TGTTCCAGAT	TGACAGTCA	8940
	TCTTTCACTT	ATTTCTCTGT	TCACTTCAAA	ACTCCAGCTT	GCCCAATAAG	GATTTAGAAC	9000
	CAGAGTGACT	GATATATATA	TATATATTTT	AATTCAGAGT	TACATACATA	CAGCTACCAT	9060
	TTTATATGAA	AAAAGAAAAA	CATTTCTTCC	TGGAACCTAC	TTTTATATA	ATGTTTATA	9120
70	TATATATTTT	TTCTTTTCAA	ATCAGACGAT	GAGACTAGAA	GGAGAAATAC	TTTCTGTCTT	9180
	ATTAATAATTA	ATAAATTATT	GGTCTTTACA	AGACTTGGAT	ACATTACAGC	AGACATGGAA	9240
	ATATAATTTT	AAAAAATTC	TCTCCAACCT	CCTTCAAATT	CAGTCACCAC	TGTTATATTA	9300
	CCTTCTCCAG	GAACCTTCCA	GTGGGAAGG	CTGCGATATT	AGATTTCCTT	GTATGCAAG	9360
	TTTTTGTGTA	AAGCTGTGCT	CAGAGGAGGT	GAGAGGAGAG	GAAGGAGAAA	ACTGCATCAT	9420
75	AACTTTACAG	AATTGAATCT	AGAGTCTTCC	CGAAAAAGCC	CAGAAACTTC	TCTGCAGTAT	9480
	CTGGCTGTGC	CATCTGTGCT	AAGGTGGCTG	CTTCTTCCCC	AGCCATGAGT	CAGTTTGTGC	9540
	CCATGAATAA	TACACGACCT	GTTATTTCCT	TGACTGCTTT	ACTGTATTTT	TAAGGTCAAT	9600
	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		

Seq ID NO: 417 Protein sequence
Protein Accession #: NP_056234.1

	1	11	21	31	41	51	
85	MPKRAHWGAL	SVVLLILLWGH	PRVALACPHP	CACYVPSEVH	CTFRSLASVP	AGIARHVERI	60
	NLGFNSIQAL	SETSPAGLTK	LELLMIHNGE	IPSIPDGALR	DLSSLQVFKP	SYNKLKRVITG	120
	QTLQGLSLNL	RLHIDHNKIE	FIHPQAFNGL	TSRLRLHLEG	NLLHQLHPST	FSTFTFLDYF	180
	RLSTIRHLVL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCEMRWFLE	WDAKSRGILK	240

CKDKAYEYGG QLCAMCFSPK KLYKHEIHLK KDMTCLKPSI ESPLRQNRSR SIEEBEQEER 300
 DGGSQLILEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360
 VALDFECFMT RENYERLWKL IAYYSEVPVK LHRELMLSKD PRVSYYQYRD ADEALYYTG 420
 VRAQLAEPE WVMQPSIDIQ IARRQSTAKK VLLSYTYQYS QTISTKOTRQ ARGSRWMIIE 480
 PSGAVQRDQT VLBGGPCQLS CNVKASESPS IFWVLPDSSI LRAPMDDPDS KPSILSSGWL 540
 RIKSMEPSDS GLYQCIQAVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600
 ALAIPEAHLS WILPNRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQQGAD 660
 HFTVGITVTK KSGGLPSKRK RRFAGAKLSR VREDIVEDEG GSGMGDEENT SRLLHPKDKQ 720
 EVFLKTKDDA INGDKKAKKG RRLKLLWKHS EKEPETNVAE GRRVFESRRR INMANKQINP 780
 ERWADILAKV RGNLPLKGT E VPPLIKTTSP PSLSLEVTPP FPAVSPSPAS PVQVTSAEB 840
 SSADVPLLGE EEHLVGTISS ASMGLEHNNH GVILVEPEVT STPLEEVDD LSEKTEEITS 900
 TEGDLKGTA PTLISEPYEP SPTLHLDTV YEKPTHEETA TEGNSAADVG SSPEPTSSEY 960
 EPPLDAVSLA ESEPMQYFDP DLETKSQDPE DKMKEDTFAH LTPTPTIWNV DSSTSOLFED 1020
 STIGEPVPGV QSHLQGLTND IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHSS 1080
 RSSESEGGES KSITLPDSTL GIMSSMSPVK KPAETTGTGL LDKDPTTITV TPRQKVAPSS 1140
 TMSHTPSRRR PNRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVESSL 1200
 VPTAWVNTV NTKPQLEMEK NAEPTSKGTP RRGKHKRPNK HRYTPTSTVSS RASGSKPSPS 1260
 PENKHNIVT PSETILLR PVSLEKTEGY DSDLYMTTTR KIYSSYPKVQ ETLPTVKYPT 1320
 SDGKEIKDDV ATNVDKHKS D ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFPPTPTW 1380
 NPSRTAQPR LQTDIPVTS GENLTDPLL KELEDVDFTS EFLSSLTST PFHQEEAGSS 1440
 TTLSSIRVEV ASSQAETTL DQDHLTTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500
 MSLGQTITTK PALPSRISQ ASRDSKENVF LNYVGNPETE ATPVNNETQ BMGSPNELST 1560
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620
 LPEMSTQSAS RYFVTSQSPR HWTNKPEITT YPSGALPENK QFTTPTLSST TIPLPLHMSK 1680
 PSIPSKPTDR RTDQFNGYSK VPGNNIPEA RNFVGKPPSP RIPHYSNGRL PFPTNKTLSE 1740
 PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPPL HTPQTGSPS 1800
 TNLQINPMVS STQSSISFPT SSVQSSGFSH QSSSKFPAGG PPASKFWSLG EKQPIILTKSP 1860
 QTVSVTAETD TVFPCEATGK PKPFVTWTKV STGALMTPNT RIQRFEVLKN GTLVIRKQVQ 1920
 QDRGQYMCTA SNLHGLDRMV VLLSVTVQPP QILASHYQDV TVYLGDTIAM ECLAKGTPAP 1980
 QISWIFPDRR WQTVSPVES RITLHENRTL SIKEASFSDR GYKCVASNA AGADSLAIRL 2040
 HVAALPVIH QEKLENIISL PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100
 VFPNGTLYIR NLAPKDSGRY ECVAAANLVS ARRTVQLAVQ RAAANARITG TSPRTDVRV 2160
 GGTLKLDCA SDGPWPRIILW RLPSKRMIDA LFSFDSRIKV FANGTLVVK SVDKADAGDYL 2220
 CVARNKVGDD YVVLKVDVVM KPAKIEHKEE NDHKVFGYGD LKVDCAVATGL PNPEISWSLP 2280
 DGLSVNSFMQ SDDSGGRTRK YVVFNGTLY FNEVGMREEG DYTCEAENQV GKDEMVRVK 2340
 VVTAPATIRN KTYLAVQVQY GDVTVACEA KGEPMKVTW LSPTNKVIPT SSEKYQIYQD 2400
 GTLLIQAKR SDGNYTCLV RNSAGEDRKT VWHVNVQPP KINGNPNPT TVREIAAGSS 2460
 RKLIDCKAEG IPTFRLWAF PEGVVLPAFY YGNRITVHGN GSLDIRSLR SDSVQLVMA 2520
 RNEGGEARLI VQLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TPSLVVWVLPN 2580
 GTDLQSGQQL QRFYHKADGM LHSIGLSSVD AGAYRCVARN AAGHTERLVS LKVLKPEAN 2640
 KQYHNVLIS II NGETLKLPCP PFGAGQGRFS WTLFNGMHLE GPQTLGRVSL LDNGTLTVRE 2700
 ASVFRDGTIV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820
 KTTYIHVF

Seq ID NO: 418 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

1 11 21 31 41 51
 | | | | |
 ATGCCAGGCA CAAACTAAC CCGAACAGGC GCCCCAGCAG ACTACAGAGT GATATTGAAG 60
 ACCTCTCAAG AGGACGAAT GGATGTACCT GACGACATCA GCGTCGGGT TATGTATCT 120
 CAGTCTGTGC TTGTGCTCTG GGTGGATCCT GTTCTGGAAG AACAGAAGAA AGTGTGTGCA 180
 TCAAGACAGT ACACCGTGC CTATCGAGAG AAGGGGGAAT TGGCCAGGTG GGATTATAAG 240
 CAGATCGCTA ACAGGGCTGT GCTGATTGAG AACCTGATTC CAGACACTGT GTATGAATTT 300
 GCAGTCCGTA TTTCACAGGG TGAAAGAGAT GGCAAAATGGA GTACGTCAGT CTTCCAAAGA 360
 ACACCAAGAT TCACCCCTAC CACAGCTCCT GAAAACTTGA ACGTCTGGCC AGTCAATGGC 420
 AAACCTACAG TTGTCTGTGC ATCTTGGGAT GCGCTACCAG AGACTGAGGG GAAAGTGAAA 480
 GTCTGTCTGC TGGACACAGG ACTGTTTCA GTTCTCTCCT TCCACCATC TGCCAAATCA 540
 TTTCAAGAATA CATTCTTCA TACGCCCGCG CTCTCAAACC ATTGGAGCA AAGTCCCTCA 600
 CCTATCTCTG AGACACTACT TCTGCCCTGG TGGATGTCT GCAGCTGGG GAACGCTATC 660
 TTTTCAAAT CCGGGCCACA AACAGGAGAG GCCTGGGACC TCACTCCAAA GCCTTCATTG 720
 TCGCTATGCC AACACGAATG CAGCTGTACC CAGAAGGATT TCACTGTCT AGCTTACCTG 780
 ATCGATATCC AAACCAACA AGTTAATAAA GATCCACAAC TGAAGGGGAG TGTTTTGGGA 840
 CCATGTTTTT TTTTCTACTT CCTCACATTT ATGCTGGATA TTGGCGGCTT TTCTTTCATT 900
 ATGTGCTATG AAGACCCANN TGTCTCTCT TTGACAGGCA ATCTTTTAAA ATCTGTTGCA 960
 GCCAGTAAGG CGGATGTTCA GCAGAACAGG GAGGACAATG GGAACCCGGA AAAACCTGAG 1020
 CCTTCTCTAC CTCTCTCCAG AGCTCCAGCT TCTTCCCAAC ACCCTCTGT GCCTGCTTCT 1080
 CCCCAAGGGA GAAATGCCAA GACCTTCTT CTGACTTGA AGAACAAAT ATTGGCTAAT 1140
 GGTGGGGGCG CCCGAAAACC CCAGCTTCGC GCCAAGAAGG CAGAGGAGCT GGATCTTCAG 1200
 TCGACAGAAA TCACTGGGGA GGAGGAGCTG GGTTCCTGGG AGGACTCGCC CATGTCAACC 1260
 TCAGACACCC AAGACAGAA ACGGACCTG AGGCCGCCAA GTAGACACGG CCACTCGGTG 1320
 GTTGCTCCCG GCAGGACTGC AGTGAGGGCC CGGATGCCAG CGCTGCCCCG AAGGGAAGGC 1380
 GTAGATAAGC CTGGCTTTTC CTTGGCCAGC CAGCCCGGCC CAGGGGCGCC CCCCTCGGCT 1440
 TCGGCTCTC CTGCCACCA CCGCTCCACC CAGGGCACCT CTCATCGTCC TTCCCTGCCT 1500
 GCCAGCTTGA ATGACAAACA CTGTGTGGAC TCAGACGAAG ATGAGCGCGC TGTGGGCTCC 1560
 CTCACCCCA AGGGCGCCTT CGGCCAGCCC CGGCCAGCCC TGTCCCCAG CCGCCAGTCC 1620
 CCGTCCAGCG TTCTCCGCGA CAGAAGCTCT GTGCACCCCG CGCAGAGCC AGCCTCGCCG 1680
 GCGCGGAGGA CCCCCATTC AGGGGCGCA GAGGAAGATT CCACTGCTCT AGCCCCACCC 1740
 TCAAGACTTT CTGCGGATCA TCTCGGCTGC TGCCCCCA GGCACACCTG 1800
 AGCTCTCCAC TTTCAGAGG CGGGAAGGAT GGTGAGGAG CCCCAGCCAC CAATCCCAAT 1860
 GCGCCATCAC GTTCCACCAT GTCTCTCTC GTCTCTCTC ATCTCTCTG CAGGACGCG 1920
 GTCTCTGAGG GAGCGGAGGC TTCTGATGGT GAAAGCCACG GTGACGGCGA TAGGGAAGAC 1980
 GCGGGAAGGC AGCGGAGGC CACGGCCAG ACGCTGCGGG CCGGCGCTGC CTCTGGACAC 2040
 TTCCATTTC TCAGACACAA ACCCTTGTCT GCCAACGGGA GGTCTCCAAG CAGGTTTCAG 2100
 ATGGGCGGG GACCTCGGCT CGAGCCCTCC AGCTCCCAAC AGTCCACTGT GCCCTCCGCA 2160

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

342

ARAKEAAASL PKHQVESPST GAGAGGDHRS QRGHAASPAR PSRPGGPQSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQSVSA EDEEEDAGF FKGGKEDLLS SSVKWPSSS TPRGGKDADG 1080
 SLAKEERSPA IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFSTTPMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 SNGKPNQRI INGPQGTQWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLG DGRTIVDLEG 1260
 TFWVSPDGLP LFGQGRHGTB LANAQDKPIL SLGGKPLVGL EVIKKTTTHP TTTMQPTTTT 1320
 TPLPTTTTPR PTTATTMQPT TTTTLPPTTT PRPTTATRR TTTTRPTTV RTTTTRTTT 1380
 TPKPTTPIPT CPPGTLEHHD DDGNLIMSSN GIPECYAEED EFGSLETDTA VPTEEAYVIY 1440
 DEDYEFETSR PPTTTEPSTT ATTPRVIPEE GAISFPPEEE FDLAGRKRFRV APYVTVLNKD 1500
 PSAPCSLTD A LDHFQVDSL EIIPNDLKKS DLPPQHAERN ITVVAVEGCH SFVIVDWDKA 1560
 TPGDLVTGYL VYSASYEDFI RNKPFSTQASS VTHLPIENLK PNTRYVFKVQ AQNPHGYGPI 1620
 SPSVSFVTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 420 DNA sequence
 Nucleic Acid Accession #: NM_022743
 Coding sequence: 128..1237

1 11 21 31 41 51
 GTGGATTMTA GAGATACCTC CCTCCTCTCT GCTCAGCTGC CTTGCAGTAA TTAACCTCTT 60
 TCTCTGCTGC AACACCCCTA CTGTTCTCCG TGTATTGGCT TTTCTGGGCA GCAGGAAGGA 120
 AAAGCTGATG CGATGCTCTC AGTGCCGCGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
 AAAAGCTTGG CCAGACCACA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCCAGATA 240
 TCCTCCAGAC TCCGTTGCAG TTCTTGGCAG AGTTGTCTTC AAACCTTAGG ATGGAGCACC 300
 TTCAGAAATCA GAGAAGCTTT ACTCATTTTA TGATCTGGAG TCAAAATATTA ACAAACTGAC 360
 TGAAGATAAG AAAGAGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
 AGAAATACAG GATGCTCTC AGCTGCCACC TGCCCTTGAC CTTTGTGAAG CCTTTGCAAA 480
 AGTGATCTGC AACTCTTTCA CCATCTGTAA TGCGGAGATG CAGGAAGTTG GTGTGGCCTT 540
 ATATCCCACT ATCTCTTTCG TCAATCACAG CTGTGACCCC AACTGTTTCA TGTGTTCAA 600
 TGGGCCCCAC CTCTTACCTG GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
 CTGCTACTCG GATATGCTGA TGACCACTGA GGAGCGCCGG AAGCAGCTGA GGGACCAGTA 720
 TGGTCTTGA TGTGACTGTT TCCGTTGCCA AACCCAGGAC AAGGATGCTG ATATGCTAAC 780
 TGGTGATGAG CAAGATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840
 GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATA GCAGCAATTC 900
 TGAACGGCTT CCGCATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960
 CTGCATCAAC CTCGGCTCTG TGGAGGAAGC CTTGTTCTAT GGTACTCGGA CCATGGAGCC 1020
 ATACAGGATT TTTTCCCAAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAGTTGG 1080
 CAAACCTGCG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140
 TGATATTATG AGAGTGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200
 TTTAGAAGAA TGGCAGGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAATA 1260
 CGGCGTGTGT CTTTGTGTA TGCCTTATG AGGTCACACA CTCTATGCTT TGTAGCTGT 1320
 GTGAACCTCT CTATTGGAA ATTCTGTTCC GTGTTTGTGT AGGTAATAA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
 MRCSQCRVAK YCSAKCQKKA WPDHKRECKC LKSCKPRYPF DSVRLLRV FKLMDGAPSE 60
 SEKLYSPFDL ESNINKLTED KKEGLRQLVM TFQHFMRBEE QDASQLPPAF DLFEAFKVI 120
 CNSFTICNAE MQEYGVGLYP SISLLNHSCD PNCISIVFNGP HLLLRVRDI EVGEELTICY 180
 LDMLMTSEER RKQLRDYQCF ECDRCFRQTO DKDADMLTGD EQVWKEVQES LKKIEELKAH 240
 WKWEQVLAMC QAISSNSER LPDINIYQLK VLDCAAMDACI NLGLLEALP YGTRTMEPYR 300
 IFPPGSHVPR GVQVMKVGKL QLEHGMFFQA MXNLRLAFDI MRVTHGREHS LIEDLILILLE 360
 ECDANIRAS

Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

1 11 21 31 41 51
 GGCGGGTTCC CGCCCCGAAG GCTGAGAGCT GGCGCTGCTC GTGCCCTGTG TGCCAGACGG 60
 CGGAGCTCCG CGGCGCGACC CCGCGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120
 AAATCTCTCT GCGCCCGAGA AGATTTCTTC CTCGGCGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
 TTCTCTCCA TCCTAGTGGC GCTGTGCTGC TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
 CGGCGCTGCG AGGCGGTGCG CATCCCTATG TGCCGCGACA TGCCCTGGAA CATCAAGCGG 360
 ATGCCCAACC ACCTGCACCA CAGCAGCGAG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCCCTGA GTTCCTGCAC GACCTATCA AGCCGTGCAA GTGCGGTGTC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTCT ATGAAGATGT ACAACCAAG CTGGCCCGAA 600
 AGCCTGGCCT GCGACGAGCT GCTGTCTAT GACCGTGGCG TGTGCATTTC GCCTGAAGCC 660
 ATCGTCACGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAGGCC CTCTGTATGT TGAATGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGATAA 780
 AAGGTGAAGC CAATTTTGGC AACGTATCTC AGCAAAAAC ACAGCTATGT TATTCATGCC 840
 AAAATAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCTCATC ACCCATCCCT CGAATCAAG TCCCGCTCAT TACAAATTCT 960
 TCTTGCCAGT GTCCACACAT CCTGCCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAAACAG CGGCGCGCAC CAGTCGTAGT AATCCCCCA AACCAAAAGG AAAGCCTCCT 1200
 GCTCCCAAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCCA GAAGAGAACA 1260
 AACCAGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGGA GACTTCCGAC TTCCTTACAG 1320
 GATGAGGCTG GGCATTGCCT GGCAGAGCCT ATGTAAGGCC ATGTGCCCTT TGCCTAACCA 1380

ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAGG CTATGCTTCA 1440
 GTTTTCTTTT GTAAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500
 GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
 CTAGAAGAGT AGGGAATAA ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAAT 1620
 AAATGCCATA TTTCACAAAC AACACGTAAT TTTTTCACAG TATGTTTTAT TACCTTTTGA 1680
 TATCTGTGTG TGCATGTGTA GTGATGTTTT AAAATGTGAT GAAAAATATAA TGTTTTTTAA 1740
 AAGGAACAGT AGTGGAAATGA ATGTTAAAAA ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800
 TTTTGTGTAT GAAAGGGGAT TTTTGA AAAA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATAGT AGAAACTTAA AAACAAAAAT 1920
 AATAATAAAG AAAAATAAAT AAAAAGGAGA GGCAGACAAT GTCGGATTG CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040
 ACAGTGAGTT TGCTGTGACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCCAGGACAT CCACCCTGAG 2160
 AATAATTGGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220
 TTAAATATTT TCTTTGCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAAGTTGAGT TCCACTCTCG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAACT TATTTCGAGC ATTTTATCAA CAAATTTTCT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAAT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA AGCCCAAG GAAATAAAT CCTACTCTCT CCTACTCTCC 2520
 ACTACACAGA GGTAACTACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACTTATAA AATGATTGGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCCTCT TGCTTGGCCC TTTATTGAGA TAAGTTTTCG TGTCAGAAA GCAGAAACCA 2700
 TCTCATTCTT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGGTGGTT TCTTCACTGA CAAACTGGA TAAACATCTC ACCGGAATTG

Seq ID NO: 423 Protein sequence
 Protein Accession #: NP_003005.1.

1 11 21 31 41 51
 MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHST QENAILAIEQ 60
 YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPKSV CQRARDCEP LMKMYNHSWP 120
 ESLACDELFP YDRGVCSPE AIVTDLPELV KWIDITPDM VQERPLDVDC KRLSPDRCK 180
 KKVKPTLATY LSKNYSVVIH AKIKAVQRSG CNEVTTVDV KEIFKSSSPI PRTQVPLITN 240
 SSCQCPLHP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRTTVQD 300
 KKKTAGRTSR SNFPKPKGP PAKPASPKK NIKTRSAQKR TNPKRV

Seq ID NO: 424 DNA sequence
 Nucleic Acid Accession #: BC010423
 Coding sequence: 248..1780

1 11 21 31 41 51
 CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCAGCGCT TCTTGGGGGT 60
 AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGGTCCCCT AGTGGAGACC 120
 CAAGTGCAGG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGTGAGTTC CTTATTCAAG 180
 TCTGCAGCCG GCTCCAGGGG AGATCTCGGT GGAACCTCAG AAACGCTGGG CAGTCTGCCT 240
 TTCAACCATG CCCCTGTCCC TGGGAGCCGA GATGTGGGGG CCTGAGGCCT GGCTGTGTCT 300
 GCTGTCTACT CTGGCATCAT TTACAGGCCG GTGCCCGCGG GGTGAGCTGG AGACCTCAGA 360
 CGTGGTAACT GTGGTCTGG GCCAGGACGC AAAACTGCCG TGCTCTTACC GAGGGGACTC 420
 CGGCGAGCAA GTGGGCGAAG TGGCATGGGC TCGGGTGGAC GCGGGCGAAG GCGCCAGGA 480
 ACTAGCGCTA CTGCATCTCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCGCGT 540
 GGAGCAGCCG GCGCCGCCAC CCGACCCCTT GGACGGCTCA GTGCTCTGCG GCAACGCAGT 600
 GCAGGCGGAT GAGGCGGAGT ACGAGTGCCG GGTGAGCACC TTCCCGCCCG GCAGCTTCCA 660
 GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCCTGCCG TCACTGAATC CTGGTCCAGC 720
 ACTAGAAGAG GGCAGGAGCC TGACCTTGGC AGCCTCTGCG ACAGCTGAGG GCAGCCAGC 780
 CCCAGCGGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCAGGCGGTT CCTTCAAGCA 840
 CTCCCGCTCT GCTGCCGTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG 900
 GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCTGTCTC CAGGACCAA GGATCACCCA 960
 CATCTCTCAC GTGTCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
 GTGGCACATT GGCAGAGAAG GAGCTATGCT CAAGTGCTG AGTGAAGGGC AGCCCTCC 1080
 CTCATACAACT TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAG TGGATGGGGA 1140
 CACTTTGGGC TTTCCGCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTGAG 1200
 CAATGAGTTT TCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
 CTCTGGGAAG CAGGTGGACC TAGTGTGAGC CTCGGTGGTG GTGGTGGTG TGATCGCCGC 1320
 ACTCTTGTTC TGCTTCTGCG TGGTGTGTGT GGTGCTCATG TCCCGATACC ATCGCGGCAA 1380
 GGCCGAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCAGGG AGAACTCCAT 1440
 CGGAGGCTG CATTCCTATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500
 GAGAGCCGAG GGCACCCCTG ATAGTCTCAA GGACAACAGT AGCTGCTCTG TGATGAGTGA 1560
 AGAGCCCGAG GGCAGCAGTT ACTCCACGCT GACCACGGTG AGGGAGATAG AAACACAGAC 1620
 TGAAGTGTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT 1680
 CAAACAGGCC ATGAACCAAT TTGTTCAAGG GAATGGGACC CTACGGGCCA AGCCACCGGG 1740
 CAATGGCATC TACATCAATG GCGGGGGACA CCTGCTCTGA CCCAGGCGCT CCTCCCTTCC 1800
 CTAGGCCTGG CTCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCCTTA 1860
 ACACCCCATC TTCTTGGGGA AGATGCTCCC CATCCACTG ACTGCTTGAC CTTTACCTCC 1920
 AACCTTCTG TTCAATCGGA GGGCTCCACC AATTGAGTCT CTCCACCAT GCATGCAGGT 1980
 CACTGTGTGT GTGCATGTGT GCTGTGTGTA GTGTGACTG ACTGTGTGTG TGTGAGGGG 2040
 TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGATC 2100
 AAGTGAACCT TGGTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTGAGG 2160
 GTTGGCGGTG TGTGTATGT GGTGTGTGT GACCTCTGCC TGAATAAGCA GGTATTTTCT 2220
 CAGACCCAG AGCAGTATTA ATGATGCAGA GGTGGAGGA GAGAGGTGGA GACTGTGGCT 2280
 CAGACCCAGG TGTGCGGGA TAGCTGGAGC TGGAACTGTC CTCGGGTGTG AGGGAACCTG 2340
 TCTCTACCA CTTCGAGGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400
 GAGGCTTGA CTGTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT 2460
 ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC 2520
 ACTTTTAAAT TTTTCTTTT TTTTCTCTG CCCTTCCAT TAGTGTGATT TTTTATTTAT 2580
 TTTTATTTT ATTTTCTTT AGAGTTTGTG TCCAGCCTGG ACGATATAGC CAGACCCCTG 2640

CTGTAAAAAA ACCAAAACCC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence
Protein Accession #: AAH10423

1 11 21 31 41 51

MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDDV TVVLGQDAKL PCFYRGDSGE 60

QVQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPRNPLDG SVLLRNAVQA 120

DEGEYECRV TFPAGSFQAR LRLRVLPPL PSNLNPGPALE EGQGLTLAAS CTAEGSPAPS 180

VTWDTVEKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPLG LQDQRITHIL 240

HVSFLAEASV RGLDEDNLWH IREGAMLKLC LSEGQPPPSY NWRTRLDGFLP SGVRVDGDTL 300

GFPLLTTEHS GIYYCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVASV VVVGIAALL 360

FCLLVVVVVL MSRYHRRKAQ QMTQKYESEL TLTRENSIRL LSHHTDPRS QPEESVGLRA 420

EGHPDSLKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIQ 480

AMNHFVQENG TLRAPKTGNG IYINGRHLV

Seq ID NO: 426 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

1 11 21 31 41 51

CACTAACGCT CTTCTAGTC CCCGGGCCAA CTCGGACAGT TTGCTCATT ATTGCAACGG 60

TCAAGGCTGG CTTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA 120

CTTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGGCGGC GCGGGCCGTG CGCGAGGGCT 180

CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCGGTTCGC GACGCCCGGC CCGCTCGGC 240

GCCCGCGTGG GATGGTCAG CGCTCGCCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCCG 300

GCGACGATGG CAGCGCGCCC GCTGCCCGTG TCCCCCGCCC GCGCCCTCCT GCTCGCCCTG 360

GCCGGTGTCT TGCTCGCGCC CTCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA 420

GCTGATGAAG TTGTCACTGC CTCTGTTCGG AGTGGGGACC TCTGGATCCC AGTGAAGAGC 480

TTGACTCCA AGAATCATCC AGAAGTGCTG AATATTCGAC TACAACGGGA AAGCAAAGAA 540

CTGATCATAA ATCTGGAAGA AATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC 600

TATCTGCAAG ACGTACTGTA TGCTCCCTC GCTCGAAATT ACACGGTAAT TCTGGGTGAC 660

TGTTACTACC ATGGACATGT ACGGGGATAT TCTGATTGAG CAGTCAGTCT CAGCAGTGT 720

TCTGGTCTCA GGGGACTTAT TGTGTTTGA AATGAAAGCT ATGCTTAGA ACCAATGAAA 780

AGTGCAACCA ACAGATCAAA ACTCTTCCCA GCGAAGAAGC TGAAGAAGCG CCGGGGATCA 840

TGTGGATCAC ATCAACACAC ACCAAACCTC GCTGCAAGA ATGTGTTCC ACCACCTCT 900

CAGACATGGG CAGAAAGGCA TAAAGAGAG ACCCTCAAGG CAACTAAGTA TGTGGAGCTG 960

GTGATCGTGG CAGACAAACG AGAGTTTCAG AGGCAAGGAA AAGATCTGGA AAAAGTTAAG 1020

CAGCGATTAA TAGAGATTGC TAATCAGTTC GACAAGTTT ACAGACCACT GAACATTGCG 1080

ATCGTGTGG TAGGCGTGGG AGTGTGGAAT GACATGGACA AATGCTCTGT AAGTCAGGAC 1140

CCATTACCA GCCTCCATGA ATTTCTGGAC TGGAGGAAGA TGAAGCTTCT ACCTCGCAA 1200

TCCCATGACA ATGCGCAGCT TGTCACTGGG GTTTATTTCC AAGGGACCAC CATCGGCTG 1260

GCCCCAATCA TGAGCATGTG CACGGCAGAC CAGTCTGGGG GAATTGTCAT GGACCATTC 1320

GACAAATCCC TTGGTGGAGC CGTGACCTTG GCACATGAGC TGGGCCACAA TTTCCGGATG 1380

AATCATGACA CACTGTGACG GGGCTGTAGC TGTCAAATGG CGGTGAGAA AGGAGGCTG 1440

ATCATGAACG CTTCCACCGG GTACCCATT CCATGCTGT TCAAGCAGTT CAGCAGGAAG 1500

GACTTGGAGA CCAGCCTGGA GAAAGGAATG GGGGTGTGCC TGTTTAACCT GCCGGAAGTC 1560

AGGAGTCTTT TCGGGGGCCA GAAAGTGTGG AACAGATTGG TGGAAAGAAG AGAGGAGTGT 1620

GACTGTGGGG AGCCAGAGGA ATGTATGAAT CGTCTGCTCA ATGCCACCAC CTGTACCCTG 1680

AAGCCGGAGC CTGTGTGCGC ACATGGGCTG TGCTGTGAAG ACTGCCAGCT GAAGCCTGCA 1740

GGAAACAGCG TCGGGGACTC CAGCAACTCC TGTGACCTCC CAGAGTTCTG CACAGGGGCC 1800

AGCCCTCACT GCCCAGCAA CGTGTACCTG CACGATGGGC ACTCATGTCA GGATGTGGAC 1860

GGCTACTGCT ACAATGGCAT CTGCCAGACT CACGAGCAGC AGTGTGTGAC ACTCTGGGGA 1920

CCAGGTGCTA AACCTGCCCC TGGGATCTGC TTTGAGAGAG TCAATTCTGC AGGTGATCCT 1980

TATGGCAACT GTGGCAAGT CTGGAAGAGT TCCTTTGCCA AATGCGAGAT GAGAGATGCT 2040

AAATGTGAAA AATCTCAGT TCAAGGAGGT GCCAGCCGGC CAGTCATTGG TACCAATGCC 2100

GTTTCCATAG AAACAAACAT CCCCCTGCAG CAAGGAGGCC GGATTCTGTG CCGGGGGACC 2160

CACGTGTACT TGGGCGATGA CATGCCGGAC CCAGGGCTTG TGCTTGCAGG CACAAAGTGT 2220

GCAGATGGAA AATCTGCTCT GAATCGTCAA TGTCAAATA TTAGTGTCTT TGGGGTTCAC 2280

GAGTGTGCAA TGCACTGCCA CGGCAGAGGG GTGTGCAACA ACAGGAAGAA CTGCCACTGC 2340

GAGGCCACTC GGGCACTTCC CTCTGTGAC AAGTTTGCTT TGGAGGAAG CACAGACAGC 2400

GGCCCCATCC GGCAGTGA TAACCAAGGT TTAACCATAG GAATCTGGT GACCATCTG 2460

TGCTCTCTTG CTGCCGATT TGTGTTTAT CTCAAAGGA AGACCTGAT ACGACTGCTG 2520

TTTACAAATA AGAAGACCAC CATTGAAAA CTAAGGTGTG TGGCCCTTC CCGGCCACCC 2580

CGTGGCTTCC AACCTGTGCA GGCTCACCTC GGCCACCTTG GAAAAGCCCT GATGAGGAAG 2640

CGCCAGATT CCTACCCACC GAAGACAAT CCCAGGAGAT TGCTGCAGTG TCAGAAATGT 2700

GACATCAGCA GACCCCTCAA CGGCCTGAAT GTCCCTCAGC CCCAGTCAAC TCAGCGAGTG 2760

CTTCTTCCCC TCCACCGGGC CCGACGTGCA CCTAGCGTCC CTGCCAGACC CTGCCAGCC 2820

AAGCCTGCAC TTAGGCGAGC CCAGGGGACC TGTAAGCCAA ACCCCCTCA GAAGCCTCTG 2880

CCTGCAGATC CTCTGGCCAG AACAACTCGG CTCACTCATG CCTTGGCCAG GACCCAGGA 2940

CAATGGGAGA CTGGGCTCGG CCTGGCACCC CTCAGACCTG CTCCACAATA TCCACACCA 3000

GTGCCCAGAT CCACCCACAC CGCCTATATT AAGTGAAGAG CCGACACCTT TTTTCAACAG 3060

TGAAGACAGA AGTTGCTACT ATCTTTCAGC TCCAGTTGGA GTTTTTTGA CCAACTTTTA 3120

GGATTTTTTT TAATGTTTAA AACATCATTA CTATAAGAAC TTTGAGCTAC TGCCGTCACT 3180

GCTGTGCTGT GCTATGTGTC TCTGTCTACT TGCAAGGTA CTGTAAAT ATTAAATTTAT 3240

GCAGAAATGT GATTACAGTG CAGTGGCTG TATTAGGCAT TTTTACCATC ACTGAGTTT 3300

CCATGGCAGG AAGGCTTGTG GTGCTTTTAG TATTTTAGTG AACTTGAAAT ATCTGCTTG 3360

ATGGGATTCG GGACAGAGAT TGTTTGCTTT CTGATCAAGG CCTTATTGGA AAGCAGTCCC 3420

CCAACTACCC CACGCTGTGC TTATGGTACC AGATGCAGCT CAAGAGATCC CAAGTAGAAT 3480

CTCAGTTGAT TTTCTGAGAT CCCCATCTCA GGCACAGCC AAGGGGCTTC AGGTCCAGGC 3540

TGTGTTTGGG TTTCAAGGAG GCCTGTGACC CCTTGACAAC TGGCAGGCAG GCTCCAGGG 3600

ACACCTGGGA GAAATCTGSC TTTCTGCCAG GAAGCTTTGG TGAGAACCTG GGTTCAGAC 3660

AGGAATCTTA AGGTGTAGCC ACACCAGGAT AGAGACTGGA ACCTAGACA AGCCAGAACT 3720

TGACCTGAG CTGACCAACC GTGAGCATGT TTGGAAGGG TCTGTAGTGT CACTCAAGGC 3780

GGTGCTTGAT AGAAATGCCA AGCACTTCTT TTCTCGCTG TCCTTCTAG AGCACTGCCA 3840

	CCAGTAGGTT	ATTAGCTTGT	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
	CAATGATCCT	GTATTCCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTTCAATG	4020
5	TGAACCAITA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTC	ACTTATTAA	4080
	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTTCA	GTCTGCTATC	ATTATTTCGA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAA	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
10	CTCTTTCATC	TTCAAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCTTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAAC	GCATTTCACT	TTCCCGGTGT	4680
15	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGAAC	CCAGCTCTAA	TACATTTCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAAT	TCTTTAAAA	GTAAAGCCAT	GCTGGAAAAT	AATACTGCTG	4860
	AGATACATAC	AGAATTACTG	TAACTGATTA	CACCTGGTAA	TTGTACTAAA	GCCAAACATA	4920
20	TATATACTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAA	AA				

Seq ID NO: 427 Protein sequence
Protein Accession #: NP_003465

25	1	11	21	31	41	51	
	MAARPLPVSP	ARALLLALAG	ALLAPCEARG	VSLWNEGRAD	EVVSASVRSG	DLWIPVKSFD	60
	SKNHPEVLNI	RLQRESKELI	INLERNELGI	ASSFTETHYL	QDGTDVSLAR	NYTVILGHY	120
30	YHGHVRGYSD	SAVLSYTCSG	LRGLIVFENE	SYVLEPMKSA	TNRYKLFPAK	KLKSVRGSCG	180
	SHHNTPNLAA	KNVFPFSPQT	WARRHKRETL	KATKYVELVI	VADNREFRQ	GKDLKVKQR	240
	LLEIANHVOK	FYRPLNIRIV	LVGVEVWDM	DKCSVSQDPF	TSLHEFLDWR	KMKLLPRKSH	300
	DNAQLVSGVY	FQGTITGMAP	IMSMCTADQS	GGIVMDHSDN	PLGAAVTLAH	ELGHNFGMNH	360
35	DTLDRGCSCQ	MAVEKGGCIM	NASTGYPPFM	VFSSCSRKDL	ETSLEKGMGV	CLFNLPEVRE	420
	SPFGQKCGNR	FVEBGEBCDC	GEPEECMNRC	CNATTCTLKP	DAVCAHGLCC	EDCQLKPAGT	480
	ACRDSNSCD	LPEFTCGASP	HCPANVYLHD	GHSCQDVG	CYNGICQTHE	QOCVTLWPG	540
	AKPAPGICFE	RVNSAGDPYG	NGCKVSKSSF	AKCEMRDAKC	GKIQCQGGAS	RPVIGTNAV	600
	IETNIPLQGG	GRILCRGTHV	YLDDMPDPG	LVLAGTKCAD	GKICLNRCQ	NISVFGVHEC	660
40	AMQCHRGVVC	NMRKNCHCEA	HWAPPFCDF	GFPGSTDSGP	IRQADNQLT	IGILVTILCL	720
	LAAGFVVYLK	RKTLIRLLFT	NKKTIEKLR	CVRPSRPPRG	FQPCQAHLG	LKGLMRKPP	780
	DSYPPKDNPR	RLLCQCNVDI	SRPLNGLNVP	QPQSTQRLVP	PLHRAPRAPS	VPARPLPAKP	840
	ALRQAQGTCK	PNPPQKPLPA	DPLARTTRLT	HALARTPGQW	ETGLRLAPLR	PAPQYPHQVP	900
	RSTHTAYIK						

Seq ID NO: 428 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

50	1	11	21	31	41	51	
	GAGGAGGAGG	GAAGAGGCGA	GCAAAAAGGA	AGAGTGGGAG	GAGGAGGGGA	AGCGGCGAAG	60
	GAGGAAGAGG	AGGAGGAGGA	AGAGGGGAGC	ACAAAGGATC	CAGTCTCCC	GACGGGAGGT	120
	TAATACCAAG	AACCATGTGT	GCCGAGCGGC	TGGGCCAGTT	CATGACCCCTG	GCTTTGGTGT	180
55	TGGCCACCTT	TGACCOCGCG	CGGGGACCGC	ACGCCACCAA	CCCACCCGAG	GGTCCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCCGCCTGT	CCCTGCAGAA	TACAGCGGAG	ATCCAGCACT	300
	GTTTGTGCAA	CGCTGGCGAT	GTGGGGTGTG	GCCTGTTTGA	ATGTTTCGAG	AACAACTCTT	360
	GTGAGATTGG	GGGCTTACAT	GGGATTGCA	TGACTTTTCT	GCACAACTCT	GGAAAATTG	420
	ATGCCCAGGG	CAAGTCATTC	ATCAAAGACG	CCTTGAAATG	TAAGGCCAC	GCTCTGCGGC	480
60	ACAGGTTCGG	CTGCATAAGC	CGGAAGTGCC	CGGCCATCAG	GGAAATGGTG	TCCAGTTGTC	540
	AGCGGGAATG	CTACCTCAAG	CAGCACTGT	GCGCGCTG	CCAGGAGAAC	ACCCGGGTGA	600
	TAGTGGAGAT	GATCCATTTC	AAGGACTTGC	TGCTGCACGA	ACCCTACGTG	GACCTGTGA	660
	ACTTGCTGCT	GACCTGTGGG	GAGGAGGTGA	AGGAGGCCAT	CACCCACAGC	GTGCAGGTTT	720
	AGTGTGAGCA	GAACCTGGCC	AGCCTGTGCT	CCATCTTGAG	CTTCTGCACC	TCCGCCATCC	780
65	AGAAGCTTCC	CACGGCGCCC	CCCGAGCGCC	AGCCCCAGGT	GGACAGAAC	AAGCTCTCCA	840
	GGGCCACCA	CGGGGAAGCA	GGACATCACC	TCCAGAGCC	CAGCAGTAGG	GAGACTGGCC	900
	GAGGTGCCAA	GGGTGAGCGA	GGTAGCAAGA	GCCACCCAAA	CGCCCATGCC	CGAGGCAGAG	960
	TGGGGGCGCT	TGGGGCTCAG	GGACCTTCCG	GAAGCAGCGA	GTGGGAAGAC	GAACAGTCTG	1020
	AGTATTCTGA	TATCCGGAGG	TGAAATGAAA	GGCCTGGCCA	CGAAATCTTT	CCTCCACGCC	1080
70	GTCCATTTTC	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTCAC	1140
	ACGCAGGATT	CTGTGGGGAC	TGTGGACTTC	ATCGAGGTGT	GTGTTCCCGG	AACGGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	CCGTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCACCTAC	1260
	ACGTACTCAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
	AGTCAGTGGG	TGTGGCGCGC	TCTGTTGTGG	GGGAGGTGAA	CCAGGGAGGG	GCAGGGCAAG	1380
75	GCAGGGCCCC	CAGAGCTGGG	CCACACAGTG	GGTGTGGGCG	CTCGCCCGGA	AGCTTCTGGT	1440
	GCAGCAGCCT	CTGGTGTGCT	CTCCGCGGAA	GTCAGGGCGG	CTGGATTCCA	GGACAGGAGT	1500
	GAATGTAAAA	ATAAATATCG	CTTAGAATGC	AGGAGAAGGG	TGGAGAGGAG	GCAGGGGCGG	1560
	AGGGGGTGCT	TGGTGCCAAA	CTGAAATTC	GTTTCTGTGT	TGGGGCCTTG	CGGTTTCAGAG	1620
	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
80	TGCTGGGCT	GGGGGGGACA	CTGTCCAAAG	GAGTGGCCCC	TATGAGTTTA	TATTTTAAAC	1740
	ACTGCTTCAA	ATCTCGATT	CACCTTTTTT	ATTATCCAG	TTATATCTAC	ATATCTGTCA	1800
	TCTAAATAAA	TGGCTTTCAA	ACAAAGCAAC	TGGGTCTATTA	AAACCACTC	AAAGGGGGTT	1860
	TAAAAAATAA	AAAAACAGCC	CATCCTTTGA	GGCTGATTTT	TCTTTTTTTT	AAGTTCTATT	1920
	TTAAAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCTGTCC	1980
85	CACCTGGGGG	AAACCTTATA	CCAGAGGAA	AATACACACC	TGGGGAGTAC	ATTGTACAAA	2040
	TTTCCCTTAG	GATTTGTTTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	2100
	CTGGCGATTC	CAGGAGACCC	AGCTGGAAC	CTGGCTTCTC	CATGTGAGGG	GATGGGAAAG	2160
	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CTTTTACATA	2220

AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC

5 Seq ID NO: 429 Protein sequence
 Protein Accession #: NP_003705

1 11 21 31 41 51
 10 MCAERLGQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRLSLQNT AEIQHCLVNA 60
 GDVGGCVFEC FENNNSCIRG LHGICMTFLH NAGKFDAQGK SPIKDALKCK AHALRHRFGC 120
 ISRKCPAIRE MVSQIQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKEAIT HSVQVQCEQN WGSLSLSLSF CTSAIQKPPT APPERQPOVD RTKLSRAHHG 240
 15 EAGHHLPEPS SRETGRGAKG ERGSKSHPNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300
 RR

Seq ID NO: 430 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

20 1 11 21 31 41 51
 AAGCCCAGCA GCCCCGGGGC GGATGGCTCC GGCCGCCCTGG CTCGCAGCG CGGCCGCGCG 60
 CGCCCTCCTG CCCCCTGATG TGCTGCTGCT GCTCCAGCCG CCGCCGCTGC TGGCCCGGGC 120
 25 TCTGCCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCC GGCCGCGCAG 240
 CAGCCCTCAG CCTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
 CGACACAGAA AGGTTCTGTC TTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
 GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
 30 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC 480
 TGACATCATG ATCGACTTCG CCAGGTAAGT GCATGGGAGC GACCTGCCGT TTGATGGGCG 540
 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGCG ACAGACCTGC TGCAGGTGGC 660
 AGCCCATGAA TTTGGCCAGG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
 35 GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
 TCAACACCTA TATGGCCAGC CCTGGCCAC TGTCACTCC AGGACCCAG CCTGGGCC 840
 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC 900
 CTGTGAGGCC TCCTTTGAGC CGTCTCCAC CATCGAGGC GAGCTCTTTT TCTTCAAAGC 960
 40 GGGCTTTGTG TGGCGCTCC GTGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC 1020
 TCGCCACTGG CAGGACTGCG CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080
 CATTTGGTTC TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTGGG 1140
 CCCCACACCC CTCACCGAGC TGGGCTGCTG GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACACC 1260
 45 CAGCACCCGG CGTAGAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GACGCTGCTT TCAGGATGTC TGATGGCTAT GCCTACTTCC TGCAGGGCCG 1380
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGCTCTCGT 1440
 GGGTCTTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACACT TTCTCTGAC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTGAC CCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560
 50 ATCTTTGTGG CTGTGGGCAC CAGGCAATGG ACTGAGCCCA TGCTCTCTGC AGGGGGATGG 1620
 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCGTG GTCACCTGCC 1680
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740
 GGGACCGGCT ATGCAGGTCC TGGCAAACCT GGTGCCCCG TCTCATCCCT GTCCCTCAGG 1800
 GTAGACCATG GGCAGGACTG GGGGAAGTGG AGTGTCTTGG CTGTATCCCT GTTGTGAGGT 1860
 55 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
 TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTCTG 1980
 ATCTGTCTGC CTCTGGCTG ACAATCCTGG AAATCTGTTT TCCAGAATCC AGGCCAAAAA 2040
 GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCAGGGCC CTGGAGGCTG 2100
 CAACATACCT CAATCTCTGC CAGGCCCGGA TCCTCTGTA GGCCTTTTTC CAGCACTGCT 2160
 60 ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT

Seq ID NO: 431 Protein sequence
 Protein Accession #: NP_005931

65 1 11 21 31 41 51
 MAPAAWLRS AARALLPPML LLLLPPLP ARALPPDVH LHAERRGPQ WHAALPSSPA 60
 PAPATQEA PR PASSLRPPRC GVPDPSDGLS ARNRQKRFLV SGRWEKTDL TYRILRFPWQ 120
 70 LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DGPGGILAHA 180
 FFPKTHREGD VHFYDEDTWT IGDDQGTDL LQVAHEBFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLVQGP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELEF PKAGFVWRLR GGLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA 360
 QYWVYDGEKP VLGPAPLTEL GLVRFVPHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420
 75 PVPERRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDL VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL

Seq ID NO: 432 DNA sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

80 1 11 21 31 41 51
 ACCGGGCACC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACAGTGTGGC CTACTATCTC TTCCGTGGTG 120
 85 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCTCT AAATATTCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTCTGTGC ACCAGATGCA 300

5	GATGCTGTTG	CTGCACAGAT	CCTGTCAGTG	CTGCCATTGA	AGTTTTTTTC	AATCATCGTC	360
	ATTGGGATCA	TTCGATTGAT	ATTAGCACTG	GCCATTGGTC	TGGGCATCCA	CTTCGACTGC	420
	TCAGGGAAGT	ACAGATGTGC	CTCATCCTTT	AAGTGTATCG	AGCTGATAGC	TCGATGTGAC	480
	GGAGTCTCGG	ATTGCAAAAG	CGGGGAGGAC	GAGTACCGCT	GTGTCCGGGT	GGGTGGTCAG	540
	AATGCCGTGC	TCCAGGTGTT	CACAGCTGCT	TCGTGGAAGA	CCATGTGCTC	CGATGACTGG	600
	AAGGGTCACT	AOCGAAATGT	TGCCTGTGCC	CAACTGGGTT	TCCCAAGCTA	TGTGAGTTCA	660
	GATAACCTCA	GAGTGAGCTC	GCTGGAGGGG	CAGTTCGGGG	AGGAGTTTGT	GTCCATCGAT	720
	CACCTCTTGC	CAGATGACAA	GGTGACTGCA	TTACACCACT	CAGTATATGT	GAGGGAGGGA	780
10	TGTGCCTCTG	GCCACGTGGT	TACCTTGCA	TGCACAGCCT	GTGGTCATAG	AAGGGGCTAC	840
	AGCTCACGCA	TCGTGGGTGG	AAACATGTCC	TTGCTCTCGC	AGTGGCCCTG	GCAGGCCAGC	900
	CTTCAGTTCC	AGGGCTACCA	CCTGTGCGGG	GGCTCTGTCA	TCACGCCCTT	GTGGATCCTC	960
	ACTGCTGCAC	ACTGTGTTTA	TGACTTGTAC	CTCCCCAAGT	CATGGAACAT	CCAGGTGGGT	1020
	CTAGTTTCCC	TGTTGGACAA	TCCAGCCCCA	TCCCCTTGG	TGGAGAAGAT	TGTCTACCAC	1080
	AGCAAGTACA	AGCCAAAGAG	GCTGGGCAAT	GACATGCCCC	TTATGAAGCT	GGCCGGGCCA	1140
15	CTCACGTTCA	ATGAAATGAT	CCAGCCTGTG	TGCTGCCCCA	ACTCTGAAGA	GAACCTCCCC	1200
	GATGGAAGAA	TGTGCTGGAC	GTGAGGATGG	GGGGCCACAG	AGGATGGAGG	TGACGCCTCC	1260
	CCTGTCTTGA	ACCAGCGGCG	CGTCCCTTTG	ATTTCACAA	AGATCTGCAA	CCACAGGGAC	1320
	GTGTACGGTG	GCATCATCTC	CCCTCCATG	CTCTGCGCGG	GCTACCTGAC	GGGTGGCGTG	1380
20	GACAGCTGCC	AGGGGGACAG	CGGGGGGCCC	CTGGTGTGTC	AAGAGAGGAG	GCTGTGGAAG	1440
	TTAGTGGGAG	CGACAGCTTT	TGGCATCGGC	TGCGCAGAGG	TGAACAAGCC	TGGGGTGTAC	1500
	ACCCGTGTCA	CCTCCTTCTT	GGACTGGATC	CACGAGCAGA	TGGAGAGAGA	CCTAAAAAAC	1560
	TGAAGAGGAA	GGGACAAAGT	AGCCACCTGA	GTTCCTGAGG	TGATGAAGAC	AGCCCCGATC	1620
	TCCCTTGGAC	TCCCGTGTAG	GAACCTGCAC	ACGAGCAGAC	ACCCCTGGAG	CTCTGAGTTC	1680
25	CGGCACCACT	AGCAGGCCCG	AAAGAGGCAC	CCTTCCATCT	GATTCCAGCA	CAACCTTCAA	1740
	GCTGCTTTTT	GTTTTTTGTT	TTTTTGAGGT	GGAGTCTCGC	TCTGTTGCCC	AGGCTGGAGT	1800
	GCACTGGCGA	AATCCCTGCT	CACTGCAGCC	TCCGCTTCCC	TGGTTCAGGC	GATTCTCTTG	1860
	CCTCAGCTTC	CCAGTAGCT	GGGACCAACAG	GTGCGGCCCA	CCACACCCAA	CTAATTTTTG	1920
	TATTTTTAGT	AGAGACAGGG	TTTACCATG	TTGGCCAGGC	TGCTCTCAA	CCCTGACCT	1980
30	CAATAGTGT	GCCTGCTTCA	GCCTCCACA	GTGCTGGGAT	TACAGGCATG	GGCCACCACG	2040
	CCTAGCCTCA	CGCTCCTTTC	TGATCTTCAC	TAAGAACAAA	AGAAGCAGCA	ACTTGCAGG	2100
	CGGGCCTTTC	CCACTGGTCC	ATCTGGTTTT	CTCTCCAGGG	GTCTTGCAA	ATCTCTGACG	2160
	AGATAAGCAG	TTATGTGACC	TCACGTGCAA	AGCCACCAAC	AGCCACTCAG	AAAAGACGCA	2220
	CCAGCCCAAG	AGTGACGAAC	TGCAGTCACT	GCACGTTTTC	ATCTCTAGGG	ACCAGAACCA	2280
35	AACCCACCTT	TCTACTTCC	AAGACTTATT	TTACATGTG	GGGAGGTTAA	TCTAGGAATG	2340
	ACTCGTTTAA	GGCTFTNEMI	CATGATTCTT	TTGTAGCATT	TGGTGGCTGA	CGTATTATTG	2400
	TCCTTTGATT	CCAAATAATA	TGTTTCCTTC	CCTCAAAAAA	AAAAAATAAA	AAAAAATAAA	2460
	AAAAA						

Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

45	1	11	21	31	41	51	
	MGENDPPAVE	APFSFRSLFG	LDDLKISPVA	PDADAVAAQI	LSLLPLKFFP	IIVIGIIALI	60
	LALAIGLGH	FDCSGKYRRC	SSFKCIELIA	RCDGVSDCKD	GEDEYRCVRV	GGQNAVQLVP	120
	TAASWKTMS	DDWKHYANV	ACQLGFPSY	VSDNLRVSS	LEGQFREEFV	SIDHLLPDDK	180
	VTALHHSVY	REGCASGHVV	TLQCTACGHR	RGYSSRIVGG	NMSLLSQWPW	QASLQPGQYH	240
	LCGGSVITPL	WIITAAHCVY	DLXLPKSWTI	QVGLVSLLDN	PAPSHLVEKI	VYHSKYKPKR	300
50	LGNIALMKL	AGPLTFNEMI	QPVCLPNSSE	NFPDGVKVCWT	SGWGATEDGG	DASPLVNHAA	360
	VPLISNKICN	HRDVYGGIIS	PSMLCAGYLT	GGVDSQCGDS	GGPLVCQERR	LWKLVGATSF	420
	GIGCAEVNKP	GVYTRVTSFL	DWHEQMERD	LKT			

Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

60	1	11	21	31	41	51	
	CACCTTCTGC	ACTGCTCATC	TGGCAGAGG	AAGCTTCAGA	AAGCTGCCAA	GGCACCATCT	60
	CCAGGAATCT	CCAGCAGCA	GAATCCATCT	GAGAATATGC	TGCCACAAAT	ACCTTTTGTG	120
	CTGCTAGTAT	CCTTGAACCT	GGTTCATGGA	GTGTTTACG	CTGAACGATA	CCAAATGCCC	180
	ACAGGCATAA	AAGGCCCACT	ACCAACACCC	AAGACACAGT	TCTTCATTC	CTACACCATA	240
	AAGAGTAAAG	GTATAGCAGT	AAGAGGAGAG	CAAGGTACTC	CTGGTCCACC	AGGCCCTGCT	300
65	GGACCTCGAG	GGCACCCAGG	TCCTTCTGGA	CCACCAGGAA	AACCAGGCTA	CGGAAGTCTC	360
	GGACTCCAAG	GAGAGCCAGG	GTGGCCAGGA	CCACCCGGAC	CATCAGCTGT	AGGGAAACCA	420
	GGTGTGCCAG	GACTCCACAG	AAAAACAGGA	GAGAGAGGAC	CATATGGACC	AAAAGGAGAT	480
	GTGGACCACT	TGCGCCTACC	AGGACCCCGG	GGCCACCCAG	GACCACTGG	AATCCCTGGA	540
	CCGGCTGGAA	TTTCTGTGCC	AGGAAAACTT	GGACAACAGG	GACCCACAGG	AGCCCCAGGA	600
70	CCAGGGGCTT	TTCTGTGAGA	AAAGGGTGCA	CCAGGAGTCC	CTGGTATGAA	TGGACAGAAA	660
	GGGGAAATGG	GATATGGTGC	TCCTGGTCTG	CCAGGTGAGA	GGGGTCTTCC	AGGCCCTCAG	720
	GGTCCACAG	GACCATCTGG	CCCTCCTGGA	GTGGGAAAAA	GAGGTGAAAA	TGGGGTTCCA	780
	GGACAGCCAG	GCATCAAAGG	TGATAGAGGT	TTTCCGGGAG	AAATGGGACC	AATTGGCCCA	840
	CCAGGTCCCC	AAGGCCCTCC	TGGGGAACGA	GGGCCAGAA	GCATTGGAAA	GCCAGGAGCT	900
75	GCTGGAGCCC	CAGGCCAGCC	AGGGATTCCA	GGAAACAAAG	GTCTCCCTGG	GGCTCCAGGA	960
	ATAGCTGGGC	CCCCAGGGCC	TCCTGGCTTT	GGGAAACCA	GCTTGGCCAG	CCTGAAGGGA	1020
	GAAAGAGGAC	CTGTGGGCTT	TCCTGGGGGT	CCAGGTGCCA	AAGGGGAACA	AGGGCCAGCA	1080
	GGTCTTCTTG	GGAGGCCAGG	TCTGACTGGA	CCCCCTGGGA	ATATGGGACC	CCAAGGACCA	1140
80	AAAGGCATCC	GGGGTAGCCA	TGGTCTCCCA	GGCCCTAAAG	GTGAGACAGG	GCCAGCTGGG	1200
	CCTGCAGGAT	ACCTTGGGGC	TAAGGGTGAA	AGGGGTTCCT	CTGGGTGAGA	TGGAAAAACA	1260
	GGGTACCCAG	AAAAACAGG	TCTCGATGGT	CCTAAGGGTA	ACCCAGGGTT	ACCAGGTCCA	1320
	AAAGGTGATC	CTGGAGTTGG	AGGACCTCCT	GGTCTCCAG	GCCCTGTGGG	CCCAGCAGGA	1380
	GCAAAGGGAA	TGCCCGGACA	CAATGGAGAG	GCTGGCCCAA	GAGGTGCCCC	TGGAATACCA	1440
	GGTACTAGAG	GGCTTATTGG	GCCACAGGAC	ATTCAGGAT	TCCCTGGGTC	TAAAGGGGAT	1500
85	CCAGGAAGTC	COGTTCTTCC	TGGCCAGCT	GGCATAGCAA	CTAAGGGCCT	CAATGGACCC	1560
	ACCGGGCCAC	CAGGGCCCTCC	AGGTCCAAGA	GGCCACTCTG	GAGAGCCTGG	TCTTCCAGGG	1620
	CCCTCTGGGC	CTCCAGGGCC	ACCAGTCAA	GCAGTCATGC	CTGAGGGTTT	TATAAGGGCA	1680
	GGCCAAAGGC	CCAGTCTTTC	TGGGACCCCT	CTTGTTAGTG	CCAACAGGGG	GGTAACAGGA	1740

ATGCCTGTGT CTGCTTTTAC TGTATTCTC TCCAAGCTT ACCCAGCAAT AGGAACTCCC 1800
ATACCATTTG ATAAAAATTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860
TTTACTTTGC AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
CATGTTTGGG TAGGGCTGTA TAAGAAATGG ACCCCTGTAA TGTACACCTA TGATGAATAC 1980
5 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAAATGAC 2040
CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC 2100
CACTCCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160
TAAATCTGT GCTGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
10 AGGTAGGCTG AAAAGAATGT AATTTTATT TTCTGAAATA CAGATTGAG CTATCAGACC 2280
AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAA CGTATGTGAA GCCTCTCTTG 2340
AATTTCTAGT TAGCAATCTT AAGGCTCTT AAGGTTTTCT CCAATATTA AAAATATCAC 2400
CAAGAAGTC CTGCTATGTT AAAACAACAA AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTGA GAAACTCGGC 2520
15 ATTTCTTTT TAAAAAGGCC TGTTTCTAAC TATGAATATG AGAATCTCTA GGAAACATCC 2580
AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TAITCAAAT TAAAGACAC 2640
TGTATCCCCT AAAATATTTT TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700
CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAGC 2760
CCCAAAATAT TGAAGTTTCT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
CTTTCTATG ATTGCAGAGA AGCTTTTAT ATACCCAGCA TAACTTGGAA ACAGGTATCT 2880
20 GACCTATTCT TATTAGTGA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCCTTATTG 2940
AATCTTATGT GATATGATT TCTGGATTGA CAGAACATTA GCACATGTAC CTGTGCCTC 3000
CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAA ATTCGACTAG AAGTGGAGAT 3060
ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAC TTTTAAGCTG 3120
25 TGCCCTCACT ATTAAGCAC AAAATGTTTT ACCTACTCCT TATTTACGAC ACAATAAAAT 3180
AACATCAATA GATTTTATAG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTTCAACCA 3240
TTCTTTCAAG GCTTTTCTAT CGACACAATA AAATAACATC AATAG

Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

1 11 21 31 41 51
MLPQIPFLLL VSLNLVHGVF YAERYQMPGT IKGPLPNTKT QFFIPYTIKS KGIIVRGEQG 60
35 TPGPFGPAGP RGHPPGSPGP GKPGYGSPL QGEPGLPGPP GPSAVGKPGV PGLPGKPGER 120
GPGYFGKDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GPGKEKGAPG 180
VPGMNGQKGE MGYGAPGRPG ERLPGPQGP TGPSGPPGVG KRGENGVPQO PGIKGDRGFP 240
GEMPIGPPG PQQPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300
PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPKG IPGSHGLPGP 360
40 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLGDGPK GNPGLPGPKG DPGVGGPPGL 420
PGPVGPAGAK GMPGNGEAG PRGAPGIPGT RGPIGPPGIP GFPGSKGDPG SPGPPGPGAI 480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
SANQGVGTMP VSAFTVILSK AYPAGTPIP FDKILYNRQO HYDPRTGIFT CQIPGIYYFS 600
YHVHVKGTHV WVGLYKNGPT VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
45 GLYSSEYVHS SFSGLVAPM

Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

1 11 21 31 41 51
ATGTGGGGCG CTCGCGCTCTC GTCGCTCTCC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG 60
CTGCTGCTGG CTGCGCTGCT GCGCGCGGGG GCGAGGGCCA GCGCGAGTA CTGCCACGGC 120
55 TGGCTGGACG CGCAGGGCGT CTGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 240
GCGGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGGCTGG CGAGCCTGGC 300
CGGGCGGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTAGTGCC GTTCCTCATT 360
60 GTTGGCTCCG TGTGTGTCG CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTTGCTGC 420
AGATGTCTCC GGCTTAAGCA GGATCCCGAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
ATGGAGACCA TCCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCTG CTCACGCCAG 540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAACTCAG GGGCCCGGGC GCCCCCAACA 600
AGGTACAGCA CCAACTGTTG CTTGCCGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
CCCACGAATT TCTCTGTGCT GAACTGTGAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
65 CAGTATCTGC ATCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
GCTGTGCCAC CTTTATGGA CGGCCTCGAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

1 11 21 31 41 51
MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
75 GDATICGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI 120
VGSFVVARII LGLSLVAACC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCLLPE GTMNNVYVNM PTNFSVLNCQ QATQIVPHQG 240
QYLHPPYVGY TVQHSVPMPT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 438 DNA sequence
Nucleic Acid Accession #: NM_004004.1
Coding sequence: 1..681

1 11 21 31 41 51
ATGGATTGGG GCAAGCTGCA GACGATCCTG GGGGGTGTGA ACAAACTC CACCAGCATT 60
85 GGAAAGATCT GGGTCACCGT CCTCTTCATT TTTGCAATTA TGATCCTOGT TGTGGCTGCA 120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180

AAGAACTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGCCCTGCAG 240
 CTGATCTTGG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
 GAGAAAGAGA GGAAGTTTCA CAAGGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
 ATCAAAACCC AGAAGGTCGG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
 TTCTTCCGGG TCATCTTCTGA AGCCGCTTTC ATGTAGCTCT TCTATGTCAT GTACGACGGC 480
 TTCTCCATGC AGCGGCTGGT GAAGTGCAC GCCTGGCCTT GTCCCAACAC TGTGGAGTGC 540
 TTGTGTCCG GGCCCAAGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
 ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTATTC TAATTAGATA TGTCTCTGGG 660
 AAGTCAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 MDWGTLLQTL GGVNKHSTSI GKIWLTVLFI FRIMILVVAA KEVNGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
 IKTKQVRIDG SLWWTYTSSI FFRVIFEAAP MYVFPVMDYG FSMQRLVKCN ANPCPNTVDC 180
 FVSRPTEKTV FTVFMIASVG ICILLNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
 ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60
 CACCGAGCGC TGGTCCGCGC TCTCCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG 120
 CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGTCCCGAT GATTGGAGGT 180
 CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTFA 240
 GTTGGGAAGC CTCCTTTTGA GGCAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
 AATTACAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCCTGTTA 360
 GATGGGTCTA ACACGCTCGG GAAGGGGAGC TTGAAAGGT CCAAGCACTT TGCCATCACA 420
 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCAAT CCAGTTCAGT 480
 TCCACTCCTC ATCTGGAAAT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
 AGAATCAAGA GGAATGGTTT CAAGAGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
 CTCTCTGACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
 GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
 GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCACAGGT GGGAGGAGCT GCATGCACTG 780
 GCCAGCGAGC CTAGAGGACA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
 GGCTCTTTCA GCACCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
 CCCGAGCTTG TCTTCATGGA CGCGTTAATG GGCACTCTCT TGATAGGCCC CTGTGACTCG 960
 CAGCCCTGCG AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTCCTCT 1020
 TGCCCCGTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
 GTCGACCTCC TCTTCTCTGT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTGCGG 1140
 GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
 GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCCTGTGGG GGAGTACCAG 1260
 GATGTGCCTG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCACCCCTG 1320
 ACGGGCAGTG CTTTCCGCGA GCGGGCAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
 CAGGACCGGC CAGCTAGAGT GGTGGTTTTC CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
 GCGGGCCCGC CGCTGCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
 GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
 GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG 1620
 CGGCCAGGGT GCGGACACA AGCCCTGGAC CTGCTCTTCA TGTGGACAC CTCTGCCTCA 1680
 GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
 GAGGTGAACC CTGACGTGAC ACAGGTCCGG CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
 GCCTTCGGGC TGGACACCAA ACCACCCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
 CCTACCTAG TGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG 1920
 ATGACCGTCC AGAGGGGTGC CCGGCCCTGG GTCCCAAGG CTGTGGTGGT GCTCAAGGC 1980
 GGGAGAGGCG CAGAGGATGC AGCCGTTCCCT GCCAGAAAGC TGAGGAACAA TGGCATCTCT 2040
 GTCTTGGTGC TGGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC 2100
 CGGGATTCCC TGATCCAGCT GGCAGCTTAC GCGCACTGC GGTACCAACA GGACGTGCTC 2160
 ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAAGTCAACC TCTGCAAAAC CAGCCCGTGC 2220
 ATGAATGAGG GCAGCTGCGT CCTGCAGAA GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
 TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
 GGATGGATTG TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAAGGAGG CAGCAGCCGT 2400
 ACCCTCCCA GCAACTACAG AGAAGGCCTG GGCACGAAA TGGTGCCTAC CTCTCTGGAAT 2460
 GTCGTGCCCC CAGGTCTTGA G

Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 MPNTSGTTRI EIWLLEPPG HRLVAALLP VSPSPALALA PGYPPVPAAD DRPTLPMIGG 60
 QMHGEKVDLW SLGVLCEYFL VGGKPPFEANE VHVSKETIGK ISAASKMMMC SAAVDIMPLL 120
 DGSNSVKGGS PERSKHFAIT VCDGLDISPE RVRVGAQFQS STPHLEFPLD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALKY LLHRLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTVPVAVGR FPRWEELHAL ASEPRGQHVLA LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGGAN CALKLSLECR 360
 VDLLFLDSS AGTTLDGFLR AKVFKRFVR AVLSSESRAR VGVATYSREL LVAVPVGEYQ 420
 DVPLDVLWSD GIPFRGGPTL TGSALRQAAE RFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRALEEIT GSPKHMVYS DPQDLFNQIP ELQKLCRSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAPV AQKLRNNGIS VLVVGVGPVL SEGLRLRAGP RDSLIHVAAY ADLRYHQDVL 720

IEWLCEGAQK PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSO 780
GWILETFLRH MAPVQEGSSR TPPSNYREGI GTEMVPTFWN VCAPGP

Seq ID NO: 442 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

10 1 11 21 31 41 51
| | | | | |
ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TCTGTGTTAGA TGGGTCTAAC 180
AGCGTCGGGA AAGGAGGCTT TGAAGGTCC AAGCACTTTC CCATCAGAGT CTGTGACGGT 240
CTGGACATCA GCCCGAGAGG GGTCAAGATG GGAGCATTCC AGTTCAAGTTC CACTCCTCAT 300
15 CTGGAATTCC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGGTTTTCA AAGGAGGGCG CAGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA 420
GGGTGCGCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
AAGTCCCAGG GGGATGTGCG ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGCTACTGTG 540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
20 AGAGGGCAGC ACGTGTCTGT GGTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
ACCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
CCCTGTGAGC ACAGGAGCCT GGAGATGGTC CGGGAGTTCC CTGGCAATGC CCCATGCTGG 780
AGAGGATCGC GGGCAGCCTT TGGCGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTC TAAACCAACC TGCCACCTGC TACAGGACCA CCGTCCCGAG CCCCTGTGAC 900
25 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCGTGAATGC 1020
AGGGTGCAGC TCCTCTTCTT TCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCTGT 1080
CGGGCCAAAG TCTTCTGTAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGGAGTAC 1200
30 CAGGATGTGC CTGACTGGT CTGGAGCCTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCCCTTGG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
GGCCAGGACC GGGCAGCTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
35 TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCCGAGC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTC TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
40 ACTGCCCTCG GGTGAGACAC CAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
GCCCTTACC TAGTGCGGCT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCAGT 1980
TCTGTCTTGG TCGTGGGCGT GGGGCCCTGT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
45 CCGCGGATT CCGTGTATCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGCAATGATG AGGCAGCTG CGTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
GGCTGGGAGG GCCCCACTG CGAAGACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGCAGGA GGCAGCAGC 2340
50 CGTACCCCTC CCAGCACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
AATGTCTGTG CCCAGGTCC TTAG

Seq ID NO: 443 Protein sequence
Protein Accession #: Eos sequence

55 1 11 21 31 41 51
| | | | | |
MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEPLDSFST QQEVKARIKR 120
60 MVFKGGRTEI ELALKYLLHR GLPGRNASV PQILIIVTDG KSQGDVALPS KQLKERVTV 180
FAVGVRFPFW EBLHALSEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHC PFYSWK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSARTT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLVGVS 480
65 EAVRAELEBI TGSPKHMVY SDPQDLFNQI PELQKLCRSR QRPGRCTQAL DLVFMILDTSA 540
SVGPENFAQM QSFVRSCALQ FEVNPVDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGS A GTALLHIYDK VMTVQRGARP GVPKAVVULT GGRGAEDAAV PAQKLNNNGI 660
SVLVVGVGPV LSEGLRLRAG PRDSLHVAA YADLRVHODV LIENLCEAK QPVNLCKPSP 720
70 CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 444 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

75 1 11 21 31 41 51
| | | | | |
GCCCCCTGGC CCGAGCCGCG CCCGGGTCTG TGAGTAGAGC CGCCCGGGCA CCGAGCGCTG 60
80 GTGCGCGCTC TCCTTCGGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGTCTG 120
TGTTTTCTCT TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA 180
AGAAACCATC GGGAGATTT CAGCTGCCAG CAAATGATG TGGTGTCTCG CTGCAGTGGG 240
CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA 300
GCACTTTGCC ATCAGACTCT GTGACGGTCT GGACATCAGC CCCGAGAGGG TCAGAGTGGG 360
85 AGCATTCAGT TCACTTCCA CTCTCATCT GGAATCCCC TTGGAATCAT TTTCAACCCA 420
ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA 480
ACTTGCTCTC AAATACCTTC TGCACAGAGG GTTGCCCTGGA GGCAGAAATG CTTCTGTGGC 540
CCAGATCCTC ATCATCTGCA CTGATGGGAA GTCCCGGGG GATGTGGCAC TGCCATCCAA 600

	GCAGCTGAAG	GAAAGGGGTG	TCACCTGTGT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTGCGT	GGCAATGCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCTTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCCAGAAGGA	CTGGACGGCT	ACCAGTGCCT	CTGCCGCTTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTTCTGTC	TGGACAGCTC	1140
10	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCGTGAAGC	GGTTTGTGCG	1200
	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGTGGG	GTGCTGTGGG	GGGAGTACCA	GGATGTGCCT	GACCTGTGCT	GGAGCCTCGA	1320
	TGGCATTCCT	TTCGTGGTGT	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
15	GCGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACTACTCG	AGGATGAGGT	TGCGGGCCCA	GCGCGTCAAG	CAAGGGCGCG	1500
	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTCTA	ACCAATATCC	1620
	TGAGCTGCAG	GGGAGGCTGT	GACGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
20	CCTCGTCTTC	ATGTTGGACG	CCTTCGCTTC	AGTAGGGCCC	GAGAAATTTT	CTCAGATGCA	1740
	GAGCTTTGTG	AGAACTGTGT	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTGGG	1800
	CCTGTGTGGT	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCCACCTTA	GGTGGGTGGG	GCTCAGCCGG	1920
	CACCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGGCCCTG	1980
25	TGTCGCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTC	2040
	TGCCCAGAA	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	TGTGGCGTGG	GGCCTGTCTC	2100
	AAGTGAGGGT	CTGCGGAGGC	TTGCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCCTGCAGAA	2280
30	TGGGAGCTAC	CGCTGCAAGT	GTGCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCGG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCCCT	AGAATGTCTG	CTTCCCGCCG	TGGCCAGGAC	CACATATCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCAACCAC	2580
35	AAACGATGTT	GTGAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGTCTG	2640
	GCCTTGTGTA	GGCTATGTCA	CTCGCCACCT	TTCCCTTGAG	GATAAACAA	GGGTCTCGAA	2700
	GACTTAAATT	TAGCGGCTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVNGKSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QDEVKARIKR	120
	MYFKGGRTE	ELAKLYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRPPRW	EELHALASEP	RQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCFPGCD	300
50	SQPCQNGGTC	VPEGLDGYOC	LCPLAFGGEA	NCALKSLEEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVVFVKRF	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGFSGSATR	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEBI	TGSPKHMVMY	SPQDLEFNQI	PELQGLKCSR	QRPGCRTQAL	DLVFMLD TSA	540
	SVGPENFAQM	QSFVRSALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
55	APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAQKLNNNGI	660
	SVLVVGVGPF	LSEGLRLRLG	PRDSLHVA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

	1	11	21	31	41	51	
65	CCCGAGCCCC	GCCCCCTCCG	GCCCCGGTCG	GCGCGCCAG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCCTCCT	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
	CGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCGCAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTCAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCAGTTCGGG	AAGGCTGTAG	GACCCGACGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACCTCCGAT	CAGAAGATGA	AAGTGAATG	480
	AATTTTGTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAAACTC	540
	ATGTCTGAAT	TAGAAAGCTT	CCTGGCTCG	TTCCGTGGAA	GACATCCCCT	CCCAGGCTCC	600
75	GACTCACAAT	CAAGGAGACC	GCGAAGGCGT	ACATTCCCGG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCCAGAA	GCCGTCGCTC	CAGATCATCC	840
	GTGACCCCTC	CGCATATAAT	TGCCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTGGAGAAAC	900
80	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTTAC	TGGGCTCTAC	TTGTCTATCA	960
	TGCCGTCAGA	AGACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGCCCC	CTGCCTTCGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTCGCA	TGCCCCGCTT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGACCGGTG	TGCGACTGGG	GTCCCTTGTT	ATTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCATGCCTA	CTTGAAAAGC	CTGAAACAGG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGGAAA	ATTTGCTGCC	TGCTCTCTAC	TTCTCAATTC	TTTCTGTGTA	AAGTTTCCAA	1320
	TTTTTTCAC	GAAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCTGCGAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC 1500
TCTATTTCCA ATGCTCTCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
5 GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
CTTGTTTACA CAAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTAATAGAA 1740
TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
CTCCTAATTT CTCTGCCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
AAGGTTGGTG GGCATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
10 ATGAGTAAGC TGATTGTAAT TTTCAGTATA AACCTTTAGT ATAATTGTAG TTTGCAAAAGT 2040
TTATTTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCIT GGACAATTTT GTATGGAAAC 2100
TTGATATTAA AAACTAGTCT GTGGTCTTT GCAGTTTCTT GTAAATTTAT AAACCAGGCA 2160
CAAGGTTCAA GTTAGATT TTAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT 2220
GTAACTTTTA GCAGTTTGT AACTTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
15 CTGTGTCACT ATCCCCCTC CTCTTTCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
AAGTGTGTGT ATGTCCAATT TACTTGATA TGTAAACCAT TGCTGTGCCA TTCAATGTTT 2400
GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTTGATCT GTAATGCTTT 2460
TATACAAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAAATA

Seq ID NO: 447 Protein sequence
Protein Accession #: NP_114148.1

1 11 21 31 41 51
MDARRVPQKD LRVKQNLKPF RYVKLISMET SSSSDSDSCDS FASDNFANTR LQSVREGCRT 60
RSQCRHSGPL RVAMKFPARS TRGATNKKAB SRQPSSESVT DSNDSSEDES GMNFLEKRAL 120
25 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRFR RRTFPGVASR RNPERRARPL 180
TRSRSRILGS LDALPMEEEE EEDKMYLVRK RKTVDGYMNE DDLPRSRRSR SVVTLPHIR 240
PVEEITEEEL ENVCSNSREK IYNRLSGSTC HQCRQKIDT KTCNRPDCW GVRGQPCGPC 300
30 LRNRYGEEVR DALLDPNWHC PPCRGICNCS PCRQDRGCA TGVLVYLAKY HGFNGVHAYL 360
KSLKQEFEMQ A

Seq ID NO: 448 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

1 11 21 31 41 51
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120
40 CTGAGCCTGG CGAGTATCAT CATGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCACTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
45 GGGAACTGGT TCTCTGCTGT TTTGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAACCCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
50 AGCATCCAGT ACGCAAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCACGGCAG CCCACTGTCT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCAATTGA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
55 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GCGTACCAGG GGGAAAGTCA CGAGAAGATG ATGTGTGCAG GCATCCCCGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
60 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
Protein Accession #: NP_063947.1

1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60
YFLCGQLPHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
70 GNWFSACFDN FTEALAEATAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNSS 180
GPCLSGSLVS LHCLACGKSL KTPRVVGEE ASVDSWPWQV SIQYDKQHC GGSILDPHV 240
LTAHCFRKH TDVFNKVRRA GSKLGSFPS LAVAKIIIE FNPMPKND IALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIWG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAIGPEGV DTCQDGGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420

Seq ID NO: 450 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 52..3042

1 11 21 31 41 51
GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60
GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAG 120
80 GACCGGGCA GAGCCTGGCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAG 180
CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTGGAGGAT 240
AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCATTG CCAGTACTGA TTACTCCATG 300
85 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCAA CCAGGTCAAA 360

	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GGGGAGGAGA	TAGACGGCGT	GGACATGCGG	420
	GCGGAGGTTG	GGCTTCTGAG	CCGGAACATC	ATAGTGATGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAACCCACAT	CTGCAATTTT	TTTGACTTCC	ATACCTTTGG	GGGCCACATC	540
5	AAGTTTGCTC	TGGGATTTAA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCAAGT	CCCGATTAC	TTCCACCTGG	CCGGTGATGT	AGACGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTCGC	720
	TGCGTCACAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTCAC	GGGAAGATGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
10	CTTGGCCTCC	TTGTCAAGTC	TGGAAACCTC	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCCA	AGCCCAGGCA	AGACTGCAAT	960
	GCTGTGTCCA	GCTTCTTCAC	GGCCAATCCC	AACAACAACC	TCATCAACTG	TGCCGTGTGA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTCAACACG	TACCAACGGG	CCCTCCGTG	1080
	GGAAATGTACT	CCCCAGGTTA	TTCAGAGCAC	ATTCCACTGG	GAATAATCTA	TAACAACCGA	1140
15	GCACATTCCA	GTACACGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCCTGCCAAG	ACAAGCGGCC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAAG	1260
	GACGCGGACC	CGCTGAAGCC	CCGGAGCGCG	GCCATCATCA	GACACTTCAT	TGCTTACAAG	1320
	AACCAGGACC	ACGGGGCCCTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGGTTT	1380
	GCTGACAATG	GCATTGGGCT	GACCTTGGCC	AGTGTGGGAA	CCTTCCCGTA	TGACGACGGC	1440
20	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTC	GTGGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCCGGC	GGCTTGGACC	ATAGCGGAAG	GACCTCCCT	1560
	ATAGGCCACA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACCT	TCCGAAGTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	CGCCTGAATA	ATGCTTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCTTTGAG	1740
25	GACGTTCCGA	TTACTTCCAG	ATGTTCTTTC	GGAGAGCCCTG	GGCCCTGGTT	CAACGAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTT	CATGACGTCT	ACGGCTCCGT	GTCCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCCAGA	CTGCATCAAT	1920
	GTTCGCCACT	GGAGAGGGGC	CATTTGCACT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
30	TACAAGACCA	GTAACTCCG	AATGAAGATC	ATCAAGAATG	ACTTCCCGAG	CCACCTCTTT	2040
	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCAAC	2100
	CTGCAGAAGG	GCTACACCAT	CCACTGGGAC	CAGACGGCCC	CCGCCGAACT	CGCCATCTGG	2160
	CTCATCAACT	TCAACAAGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGCACC	2220
	ACATTTCTCA	TCTTCTCGGA	TGTTCACAAT	CGCCTGCTGA	AGCAAAACGTC	CAAGACGGGC	2280
35	GTCTTCGTGA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTTGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCTGAAGC	TGAAAGCTCA	GAACGAGAGA	2400
	GAGAAAGTTG	CTTTCTGCTC	CATGAAGAGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
	CCAAAGAAAG	CAGCGCTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTGCTAG	ACGTGCCGAT	GCCCAAGAAG	CTCTTTGGTT	CTCAGCTGAA	AACAAGGAC	2580
40	CATTTCTTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
	TTGCTTACA	TTGAAGTGA	TGGGAAGAAG	TACCCAGTT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAATCTCATT	2760
	CTGCAGGACA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCTAA	2820
	GTGCTTATGG	CATCAAGGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGTGGAAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTCTG	TGGCTTCAAA	2940
45	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCACAAGGC	CAAAATCTTC	3000
	CAAGTTGTGC	CATGCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
	GCCACCTCGT	GGTAGACTAT	GACGCTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCACC	AGCTGCCTGG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCAGACAGCC	TGGTGCTGCC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
50	CCCTGGGGGC	GGTGCTGGCC	AATGCTGGAA	ACATTCACCT	TCTGTCAGCC	TCTTGGGTGC	3300
	TTCTCTCTTA	TCTGTGCTCT	TTTCTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
	GTGCTGACAG	CAAGATGTCA	TTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
	GGGCTGGTCA	TTTCAAGATC	CCCATGGTCT	TCAGCAGACA	AGTGAGGGTG	GTAATGTAG	3480
	GAGAAAGAGC	CTTGGCCTTA	AGGAAATCTT	TACTCCTGTA	AGCAAGAGCC	AACCTCACAG	3540
55	GATTAGGAGC	TGGGGTAGAA	CTGGCTATCC	TTGGGGAAGA	GGCAAGCCCT	GCCTCTGGCC	3600
	GTGTCCACCT	TTTCAAGAGC	TTTGAGTGGC	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
	AGGCCCTTTT	AGTTCTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAACCC	3720
	AACAGTTTAT	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
	GAGAGGTGAG	AACTAATGCC	TAGCTTGAGG	GGTCTGCAGT	CCAGTAGGGC	AGGCAGTCAG	3840
60	GTCCATGTGC	ACTGCAATGC	CAGGTGGAGA	AATCACAGAG	AGGTAAATG	GAGGCCAGTG	3900
	CCATTTTACA	GGGGAGGCTC	AGGAAGGCTT	CTTGCTTACA	GGAAATGAAG	CTGGGGGCAT	3960
	TTTGCTGGGG	GGAGATGAGG	CAGCCTCTGG	AATGGCTCAG	GGATTTCAGC	CTCCCTGCCG	4020
	CTGCTGTCTG	AAGCTGTGTA	CTACGGGGTC	GCCCTTTGCT	CAGCTCTCTC	TGGGCCACTC	4080
	ATGATGGAGA	AGTGTGTCTA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
65	ATTCAGTCCC	CAGGCAGCCC	TGCTCTGAC	TCCAGAGGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TCCTGCCTTA	GGGCTCATTT	TGCTCTTCAT	CCAGGGAAC	GAGCACAGGG	GGCCTCCAGG	4260
	AGACCTTAGA	TGTGCTCGTA	CTCCCTCGGC	CTGGGATTTT	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAGT	GAGCCCCCAA	GATGGGAAAG	4380
	AACCAACAG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCTTA	GCCTTGTGCT	CCACACCACA	4440
70	TTGCTCTAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
	CCCTCCTGCT	CCACAGCCAC	ACAAACCCGC	CCTCCCTTTG	GTGTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCACTACCT	GTCAGCCGAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGAC	CTCTACAGGT	GAGGCCAGC	AGAGGGAGTA	4740
75	GGGCTCGCCA	TGTTTCTGGT	GAGCCAAATT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGTGCTG	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
	ATAGAGAGCC	CTGTAAGAGG	CTGTAAGAGG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTTC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACCTAC	ATTTATCCCC	TTTCTGCCCC	4980
	CAACCAACAA	CTCTTTCTCT	CAAGAGGGGC	CTGCTGGGCT	CCCTCCACCC	AACTGCACCC	5040
80	ATGAGACTGC	TGCCAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTCAGG	GAGGCTTTTC	5100
	CCACCAACAA	TCCTTTCAGT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCAG	GGAGATTAGT	GGTGATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCTTCTT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
	CTAATGCAAG	GGTCTCACAC	TGTGAACCA	TTAGGATGTG	ATCACTTTCA	GGTGCCAGG	5340
85	AATGTTGAAT	GTCTTTGGCT	CAGTTTCAAT	AAAAAAGATA	TCTATTGGA	AGTTCTCAGA	5400
	GTGTACATA	GTGTTCACAG	TACAGGATCT	GTACATAAAA	GTCTTCTTCC	TAAACCATTC	5460
	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TGTCTCTCT	TGTTATTCTT	GTTTGTGAAG	CTTAAGTGAG	TTAGGTCTTT	AAGGAAAGCA	5580

ACGCTCCTCT GAAATGCTTG TCTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTCGGGA 5640
 GTTAGATGTA TAGAGTGTTT GTATGTAAAC ATTTCTTGTA GGCATCACC TGAACAAAGA 5700
 TATATTTTCT ATTTATTAT TATATGTGCA CTCAAGAAG TCACTGTCCAG AGAAATAAAG 5760
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

1 11 21 31 41 51
 MDGVNLSTEV VYKQGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN 60
 LEDNVQSWKP GDTLVIASDT YSMYQAEFQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120
 DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFPALGPK AAHLEGTELK 180
 HMQQLVGGY PIHFLAGDV DERGGYDPPT YIRDLSEIHT FSRCTVTHGS NGLLIKDVVG 240
 YNSLGHCFPT EDGPEERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
 DCNAVSTFWM ANPNNNLINC AAAGSEETGF WPIFHHVPTG PSVGMYSPPY SEHIPLGKFI 360
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSIISARYS PHQDADPLKP REPAIRRHFI 420
 AYKNQDHGAW LRGGDVWLDS CRPADNGIGL TLASGGTFPY DDGSKQBIKN SLEFVGESGNV 480
 GTEMMDNRIW GPGLDHSRGR TLPIGQNFPPI RGIQLYDGPNI NIQNTCTFRKF VALEGRHTSA 540
 LAERLNAWQ SCPIHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGVS 600
 SEYPGSYLTK NDNWLVRHPD CINVDPWRGA ICSGCAQMY IQAYKTSNLR MKIINKDFPS 660
 HPLYLEGLAT RSTHYQYQP VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DNIRVGLCYP 720
 RGTTFSLSD VHNRLKQTS KTVFVRTLQ MDKVEQSYFG RSHYYWDEDS GLLPLKKAQ 780
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFGSQLK 840
 TKDHFLEVEM ESSKHQFPHL WNDPAYIEVD GKYPSESDG IQVVIDGNQ GRVVSHTSFR 900
 NSLQGIWQ LFNYVATIPD NSVLMASKR RYVSRGPWTR VLEKLGDADR LKLKEQMAFV 960
 GFKGSFRPIW VTLDTEDHKA KIPQVPIPV VKKKKL

Seq ID NO: 452 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 261..2861

1 11 21 31 41 51
 GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60
 CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCAGACT 120
 AGCTACCACT CGCTTGCCC ACGCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCAAG 180
 ACGTCCGGGG CGGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240
 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA 300
 TGCTGACCAT CAGCTGGCTG ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG 360
 CTGGGTGCCC TGACCAGAGC CTTGAGTTGC AACCTGGAA CCCTGGCCAT GACCAAGACC 420
 ACCATGTGCA TATCGGCCAG GGCAGAGCAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT 480
 CCATCCACAT CTCAGAGGGA GGCAGAGCTG TCATTAAAGA CCACGACGAG CCGATTGTTT 540
 TGGCAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCTCT 600
 GCCCTTTCCA GGGCAATTTT ACCATCATT TGTATGGAAG GGCTGATGAA GGTATTACGC 660
 CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTGAGTTGC 720
 ATGGACAGAA AAAAGCTCTCC TGGACATTTG TGAACAAGAC CCTTCACCCA GGTGGCATGG 780
 CAGAAGGAGG CTATTTTTTT GAAAGAGAGT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840
 TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900
 AAGAGAGTGA ACGTCTGGTC CAGTATTGGA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG 960
 TTGCAGTGA TGAAGAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020
 AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCCTTGGAGT TTTCTAACTG 1080
 TGAAGAGAAA TCCATCATCT TCAAGTGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140
 CTGCTGCTGC CGGGTATGAT AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200
 CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTGAT CATGATAAAG 1260
 TATCTCAGAC TAAAGGTGGG GAGAAAAATT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320
 TATGCAATCG TCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG 1380
 AGGTTGTCTA CAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440
 GCGGAGAGTA CCGTGTACGG TTCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA 1500
 CCATTGACAC CAATGTGAAC AGCACCATTC TGAACCTGGA GGATAATGTA CAGTCATGGA 1560
 AACCTGGAGA TACCTGTGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620
 TCCAGGTGCT TCCCTGCAGA TCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA 1680
 TGTACTGCA CATCGGGGAG GAGATAGACG CGCTGGACAT CGCGGCGGAG GTTGGGCTTC 1740
 TGAGCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800
 ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGAT 1860
 TTAAGGCAGC ACACCTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC 1920
 AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980
 CCACATACAT CAGGACCTTC TCCATCCATC ATACATTCTC TCGCTGCTC ACAGTCCATG 2040
 GCTCCAATGG CTGTGTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT 2100
 TCACGGAAGA TGGGCGGAG GAACGCAACA CTTTGAACA CTGTCTTGGC CTCTTGTCTA 2160
 AGTCTGGAAC TCCCTCTCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220
 ACTCCTACCC AGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280
 GGATGGCCAA TCCCAACAAC AAACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG 2340
 GATTTTGGTT TATTTTTCAC CAGTACCAA CGGGCCCTC CGTGGGAATG TACTCCCCAG 2400
 GTTATTGAGA GCACATTCCA CTGGGAAAT TCTATAACAA CCGAGCATAT TCCAACTACC 2460
 GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC 2520
 GGCCTTCTCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
 AGCCCGGGA GCCGCCATC ATCAGACACT TCATTGCTTA CAAGAACCAG GACCACGGGG 2640
 CCTGGCTGCG CGGCGGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAGAGGG GAGGCTCAGG 2700
 AAGGCTTCTT GCTTACAGGA ATGAAGGCTG GGGGCATTTT GCTGGGGGGA GATGAGGCAG 2760
 CCTCTGGAAT GGCTCAGGGA TTCAGCCCTC CTGCGGCTG CCTGCTGAAG CTGGTGAATA 2820
 CGGGGTCGCC CTTTGCTCAC GTCTCTCTGG CCCACTCATG ATGAGAGAGT GTGGTCAGAG 2880
 GGGAGCAATG GCGCTTGTCT CTTATGAGCA CAGAGGAATT CAGTCCCCAG GCAGCCCTGC 2940
 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCCTTAGGG CCTCATTTGC 3000
 TCTTCATCCA GGGAACTGAG CACAGGGGGC CTCAGGAGA CCCTAGATGT GCTCGTACTC 3060
 CCTCGGCTCG GGATTCAGGA GCTGGAATA TAGAAATAT CTAGCCCAAA GCCTTCATT 3120

TAAACAGATGG GGAAGAGTGG CCCCCAAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC 3180
 TGGGGAGCCC CACCTAGGCC CTGTCTGCCA CACCACATTC CCTCAACAAC CGGCCCCAGA 3240
 GTGCCCAGGC ACTCCTGAGG TAGCTTCTGG AAATGGGGAC AAGTCCCCTC GAAGGAAAGG 3300
 AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGTCTCC AGCGCACACA 3360
 AACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTC ACTACCTGTC 3420
 AGCCAGCCTT GGGTGACAG TAGCTGCAAC TCCCATTGG TGCTACCTGG CTCTCCTGTC 3480
 TCTGCAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATGT TTCTGGTGAG 3540
 CCAATTGGC TGATCTTGGG TGCTGAAACA GCTATTGGGT CCACCCCACT CCCTTTTCAGC 3600
 TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG 3660
 TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGACAG AGGCACCAGA GTCTCCCTGG 3720
 GTCTTGTGAT GAATACATTT TATCCCTTTT CCTGCCCAA CCACAAATC TTCTCTTCAA 3780
 AGAGGGCCTG CCTGGCTCCC TCACCCCAAC TGCACCCATG AGACTCGGTG CAAGAGTCCA 3840
 TTCCCCAGGT GGGAGCCAAC TGTCAGGGAG GTCTTTCCCA CCAACATCTT TTCAGCTGCT 3900
 GGGAGGTGAC CATAGGGCTC TGCTTTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960
 GGAAGGACTT CTTCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG 4020
 TCCTTCTTGT CCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGGT CTCACACTGT 4080
 GAACCACTTA GGATGTGATC ACTTTTCAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140
 TTCAATTAAA AAGATATCTT ATTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC 4200
 AGGATCTGTA CATAAAAGTT TCTTCTCTAA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260
 TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAATTG TCCCTCCTGT TATTCTGTGT 4320
 TGTAAAGACT AAGTGAAGTT GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATCTCTGTCT 4380
 TTTTCTGTGT GCGGAAATAG CTGGTCTTTT TTCGGGAGTT AGATGTATAG AGTGTITGTA 4440
 TGTAAACATT TCTTGTAGGC ATCACCATGA ACAAAGATAT ATTTTCTATT TATTATTAT 4500
 ATGTGCACTT CAAGAAGTCA CTGTACAGAG AATAAAGAAAT TGTCTTAAAT GTCATGATTG 4560
 GAGATGTCTT TTGCATTGCT TGAAGGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620
 TTGGAAAAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680
 AAAAAAATAA AAAAAAATAA AA

Seq ID NO: 453 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPNWPGH DQDHHVHIGQ 60
 GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFPQGNF 120
 TIILYGRADE GIQDPDYYGL KYIGVGKGGG LELHGQKKLS WFLNKLTHLP GMAEGGYFF 180
 ERSWGHGVI VHVDPKSGT VIHSDRFDY RSKKESERLV QYLNAPVDPGR ILSVAVNDEG 240
 SRNLDDMARK AMTLGSKHF LHLGFRHPWS FLTUVKGNPSS SVEDHIEYHG HRGSAARVVF 300
 KLFQTEHGEY FNVLSSEWV QDVWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
 IQATMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVPRK LTVTIDTNVN 420
 STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPKR SCAPNQKVA GKPMYHLIGE 480
 EIDGVDMRAE VGLLSRNIIV MGEMEDKCYF YRNHICNFFD FDTFGGHIKF ALGFKAHLE 540
 GTELKHMGGQ LVGQYPIHFF LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
 KDVVGYNSLG HCFPTEDGCG ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI 660
 PKPRQDCNAV STFWMANFNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720
 LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSRQDA DPLKPREPAI 780
 IRHFIAVKNQ DHGAWLRGGD VWLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAAAGMAQG 840
 FSPPCRLKLV LVTGSPFAH VSLAHS

Seq ID NO: 454 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

1 11 21 31 41 51
 CGACTCCTTA GAGCATGGCA TGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60
 GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTC GGACCATGGA CGGGAGGCAG 120
 ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG CGCGAAGATC 180
 CAGGAGCTGT TCCACGTGGA GCCAGGCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
 GAGGACGGCC ATCCCTCTT CGACTACGAG GTCCGCTTGA ATGACACCAT CCAGCTCCTG 300
 GTCCGCCAGA GCTCGTCTCT CCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC 360
 ACCGACTCCG GCTGCTGCTT GGGCCAGAGT GAGTCAGACA AGTCTCCAC CCACGGCGAG 420
 GCGGCCGCCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480
 GGGCTGTACA AGGTCAATGA GTACGTGAT GCTCGGGA CAACATGAGG GGCCTGGTTT 540
 GAGGCGCAGG TGGTCAGGGT GAGCGGAAG GCCCCTCCCC GGGACGAGCC CTGCAGCTCC 600
 ACGTCCAGGC CGGCTCTGGA GGAGGACGTC ATTTACCAG TGAAATACGA CGACTACCCG 660
 GAGAACGGCG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CGCGCGCCCG CACCATCATC 720
 AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780
 AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGGG 840
 CGGGAACCTT ACGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC 900
 TTCGTGGACG AAGTCTTCAA GATTGAGCG CCGGTGAAG GGAGCCCCAT GGTTGACAAC 960
 CCGATGAGAC GGAAGAGCGG CCGTCTCTGC AAGCACTGCA AGGACGACGT GAACAGACTC 1020
 TGCCGGGTCT GCGCTGCCA CCGTGCCTGG GCGCGCAGG ACCCGACAA GCAGCTCATG 1080
 TGGATGAGT GCGACATGGC CTTCACATC TACTGCTGG ACCCGCCCTC CAGCAGTGT 1140
 CCGAGCGAGG ACGTGTGTA CTGCTCTGAG TGCCGGAATG ATGCCAGCGA GGTGGTACTG 1200
 GCGGAGAGGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCTCGGC CACATCGTCC 1260
 TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC 1320
 GTCCCGTCCA ACCACTACGG ACCCATCCCG GGGATCCCCG TGGGCACCAT GTGGCGGTTT 1380
 CGAGTCCAGG TCAGCGAGTC GGTGTCCAT CCGCCCCACG TGGCTGGCAT ACACGGCCGG 1440
 AGCAACGAGC GAGCGTACTC CTTAGTCTTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
 GGGAAATTTT TCACATACAC GGTGAGTGGT GGTGAGATC TTTCCGGCAA CAAGAGGACC 1560
 GCGGAACAGT CTTGTGATCA GAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC 1620
 TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCG 1680
 GTACGGGTGG TCGCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
 AACCGTACG ATGGCATCTA CAAGGTTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG 1800
 TTTCTCGTGT GCGCGTACTT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
 GAGGGGAAGG ACCGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACTCG 1920

GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACGACA AGAGGGAGGA GGAGGAGCAG 1980
 CAGGAGGGGG GCTTCGCGTC CCCACGAGCG GGCAAGGGCA AGTGGAAAGC GAAGTCGGCA 2040
 GGAGGTGGCC CGAGCAGGGC CGGGTCCCGG CGCCGGACAT CCAAGAAAAC CAAGGTGGAG 2100
 CCTACAGTC TCACGGGCCA GCAGAGCAGC CTCATCAGAG AGGACAAAGC CAACGCCAAG 2160
 CTGTGGAATG AGGTCTCTGC GTCACTCAAG GACCGGCCGG CGAGCGGCAG CCCGTCCAG 2220
 TTGTTCTGTA GTAAAGTGA GGAGACGTTC CAGTGTATCT GCTGTGAGG GCTGGTGTTC 2280
 CGGCCCATCA CGACCGGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT 2340
 CGGGCACAGG TGTTCAGCTG CCTGCTCTGC CGCTACGACC TGGGCCGCGAG CTATGCCATG 2400
 CAGGTGAACC AGCCTCTGCA GACCGTCTCT AACCAGCTCT TCCCGGCTA CGGCAATGGC 2460
 CGGTGATCTC CAAGCACTTC TCAGCAGGCG TTTTGCTGAA AACGTGTGCG AGGGCTCGTT 2520
 CATCGGCACT GATTTTGTTC TTAGTGGGCT TAACTTAAAC AGGTAGTGTT TCCTCCGTTT 2580
 CCTAAAAAGG TTTGTCTTCC TTTTATTTT TTTTATTTT TCAATCTAT ACATTTTCAG 2640
 GAATTTATGT ATTCGCTGTA AAAGTTGGAC TTCTCAGTAT TGTGTTTGT TCTTTGAAAA 2700
 CATAAAGCC TGCAATTTCT CGACAAAACA ACACAAGATT TTTTAAAGAT GGAATCAGAA 2760
 ACTACGTGGT GTGGAGGCTG TTGATGTTT TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC 2820
 CAATCTTTTA AGAAGGCGAC AGGATCAGTC CTCTCTAGG GTTCTGGCCC CCAAGGTGAG 2880
 AGCAAGCATC TTCCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCGCTGG 2940
 TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTGAAAGT GTTGCAAGGA 3000
 AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTTGCTCT AAAGCCATCC CCCACCAGAC 3060
 TGCTTAGCGT CTGAGATCCG CGTGAAGAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC 3120
 CAGCAGAAAA TGGCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGAAGTGAAG 3180
 TGTCCGACGA AGGCGGCGAC GGACGAGCG CAGCACAGCA AGTCACGTGC AAGTGCCTTT 3240
 GATTGCTTCC TTCTTTCTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAA 3300
 GTCAACACGA TTCTAGAAAC TCGGTCATC CAGTCTCTCC TGACACCGGA TGGGTGCTTG 3360
 GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA 3420
 CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATT TCTAAATGAA 3480
 TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT 3540
 TTGTTTTTGT ATTTTTTTTC TTTTGAAGG GTTTGTTAAT TTTTCTAAT TTACCAAAGT 3600
 TTGCAGCCTA TACCTCAATA AAACAGGAT ATTTTAAAT ACATACCTGC AGACAAACTG 3660
 GAGCAATGTT ATTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT 3720
 AGGGAAGAAAT GAGACAATTT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCCAGATT 3780
 TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAAA AAAAAAAA

Seq ID NO: 455 Protein sequence
 Protein Accession #: NP_037414.2

1 11 21 31 41 51
 MWIQVRTMDG RQHTVDSLS RLTKVEELRR KIQLFHVPEP GLQLFVYRGK QMEDGHTLFD 60
 YEVRLLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAEETDSR 120
 PAEDDMWDET ELGLYKVNVEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
 DVIYHVKYDD YPENGVMQMN SRDVRARART IIKWQDLEVG QVVMNLNYPD NPKERGFWDY 240
 AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGEGSPMV DNPMRKSGP 300
 SCCHKDDVN RLCRVKACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSSEDEWYC 360
 PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTEKC TIVPSNHYGP 420
 IPGIPVGTMW RPRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DGNFFTYTG 480
 SGGRLDSGNK RTAEQSCDQK LNTNRLALAL NCFAPINDQE GAERKDWRSK KPVVRVVRNVK 540
 GGNKSKYAPA EGNRYDGIYK VVKYWEPEKQ SGFLVWRYLL RRDDDEPGPW TKEGKDRICK 600
 LGLTMQYPEG YLEALANRER EKENSKEEEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
 SPRTTSKTKK VEPYSLTAQK SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
 TFCICCCQEL VFRPITTVQC HNVCKDCLDR SFRAQVFSPP ACRYDLGRSY AMQVNPQLQT

Seq ID NO: 456 DNA sequence
 Nucleic Acid Accession #: NM_001200.1
 Coding sequence: 325..1514

1 11 21 31 41 51
 GGGGACTTCT TGAACCTTGCA GGGAGAATAA CTTGCGCACC CCACTTTGCG CCGGTGCCTT 60
 TGCCCCAGCG GAGCCTGCTT CGGCATCTCC GAGCCCCACC GCCCCTCCAC TCCTCGGCCT 120
 TGCCCCAGAC TGAGACGCTG TTCCAGCGT GAAAGAGAG ACTGCGCGCG CGGCACCCGG 180
 GAGAAGGAGG AGGCAAGAA AAGGAACGGA CATTGCGTCC TTGCGCCAGG TCCTTTGACC 240
 AGAGTTTTTC CATGTGGACG CTCTTTCAAT GGACGTGTCC CCGCGTGTCT CTAGACGGA 300
 CTGCGGTCTC CTAAGGTGCG ACCATGGTGG CCGGGACCCG CTGTCTTCTA GCGTTGCTGC 360
 TTCCCCAGGT CCTCTCTGGC GCGCGGCTG GCCTCGTTCG GGAGCTGGGC CGCAGGAAGT 420
 TCGCGCGGCG GTGCTCGGCG CGCCCTCAT CCCAGCCCTC TGACGAGGTC CTGAGCGAGT 480
 TCGAGTTGCG GCTGCTCAGC ATGTTGCGGC TGAAACAGAG ACCCACCCCC AGCAGGGACG 540
 CCGTGTGCC CCCCTACATG CTAGACCTGT ATCGCAGGCA CTCAGGTCAG CCGGGCTCAC 600
 CCGCCCCAGA CACCGCGTTG GAGAGGGCAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660
 ACCATGAAGA ATCTTTGGAA GAACTACCG AAACGAGTGG GAAAAACAAC CGGAGATTCT 720
 TCTTTAATTT AAGTTCTATC CCCACGGAGG AGTTTATCAC CTCAGCAGAG CTTCAGGTTT 780
 TCCGAGAACA GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCCATCAC CGAATTAATA 840
 TTTATGAAAT CATAAAACCT GCAACAGCCA ACTCGAAATT CCCCGTGACC AGACTTTTGG 900
 ACACCAAGTT GGTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGATGTC ACCCCCGCTG 960
 TGATGCGGTG GACTYKACG GACACGCGCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020
 TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080
 ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGGCCAT GATGAAAAAG 1140
 GGCATCCTCT CACACAAAGA GAAAAACGTC AAGCCAAACA CAACACGCGG AAACGCTTTA 1200
 AGTCCAGCTG TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACGTGGGG TGAATGACT 1260
 GGATTGTGGC TCCCCCGGGG TATCACGCCT TTTACTGCCA CGGAGAATGC CCTTTTCTCT 1320
 TGGCTGATCA TCTGAACCTC ACTAATCATG CCATTGTTCG GACGTTGGTC AACTCTGTTA 1380
 ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGCTATC TCGATGCTGT 1440
 ACCTTGACGA GAATGAAAA GTTGTATTAA AGAACTATCA GGACATGTTT GTGGAGGGTT 1500
 GTGGGTGTCG CTAGTACAGC AAAATTAAAT ACATAATAT ATATATA

Seq ID NO: 457 Protein sequence
 Protein Accession #: NP_001191.1

1	11	21	31	41	51	
MVAGTRCLLA	LLLLPQVLLGG	AAGLVPELGR	RKFAAASSGR	PSSQPSDEVL	SEFELRLLSM	60
5	FGILQRPPTPS	RDVVPVPMY	DLVRRHSGQP	GSPAPDHRLE	RAASRANTVR	120
	LPETSGKTR	RFFNLSISIP	TEEPITSDEL	QVFRQMQDA	LGNSSSFHHR	180
	TANSKFPVTR	LLDT				

Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

1	11	21	31	41	51	
15	ATGGGGAGAA	GACGGAGGCT	GTGTCTCCAG	CTCTACTTCC	TGTGGCTGGG	CTGTGTGGTG 60
	CTCTGGGCGC	AGGGCAGCGC	CGGCCAGCCT	CAGCCTCCTC	CGCCCAAGCC	GCCCCGGCCC 120
	CAGCCGCGCG	CGCAACAGGT	TCCGTCGGCT	ACAGCAGGCT	CTGAAGGCGG	GTTTCTAGCG 180
	CCCGAGTATC	GCGAGGAGGG	TGCCGAGTGT	GCCAGCCGCG	TCCGCCGCGG	AGGACAGCAG 240
20	GACGTGCTCC	GAGGGCCCAA	CGTGTGGGCG	TCCAGATTCC	ACTCCTACTG	CTGCCCTGGA 300
	TGGAAGACGC	TCCCTGGAGG	AAACCACTGC	ATTGTCCCGA	TTTGTAGAAA	TAGTTGTGGA 360
	GATGGATTTT	GTTCCTCTCC	TAACATGTGT	ACTTGTTCCT	GTGGGCAAA	ATCATCAACC 420
	TGTGGATCAA	AATCAATTC	GCACTGCAGT	GTGAGATGCA	TGAATGGTGG	GACCTGTGCA 480
	GATGACCACT	GCCAGTGCCA	GAAGGATAT	ATTGGAACCT	ATTGTGGACA	ACCTGTCTGT 540
25	GAAATGGAT	GTGAGATGG	TGGACGTTGC	ATCGCCCAAC	CGTGTGCTTG	TGTTTATGGG 600
	TTCACTGGTC	CACAGTGTGA	AGGAGATTAC	AGGACAGGCC	CGTGTTCAC	TCAGGTCAAC 660
	AACCAAGTGT	GCCAAGGGCA	GCTGACAGGC	ATTGTCTGCA	CGAAGACTCT	GTGCTGTGCC 720
	ACCACTGGAC	GGGCGTGGGG	CCATCCCTGT	GAGATGTGTC	CAGCCAGGCC	TCAGCCCTGC 780
	GCAGCGGGTT	TCATCCCAAA	CATCCGCACT	GGAGCTTGCC	AAGATGTTGA	TGAATGCCAG 840
30	GCTATCCAG	GGATATGCCA	AGGAGGAAAC	TGTATCAATA	CAGTGGGCTC	TTTGAATGCG 900
	AGATGCCCTG	CTGTGTCACA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG 960
	TGCAGCATCA	TTCTCTGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT 1020
	TTTTGTGTTT	GTCCACGTGG	ATATGTAACC	TCAACAGATG	GCTCTCGATG	CATCGATCAG 1080
	AGAACAGGCA	TGTGTTTCTC	GGGCTGTGGT	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG 1140
35	AGAATGACGA	AAATGACAGT	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAAT 1200
	CCTGAAGCCT	GTCCCTGTCA	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT 1260
	CCAATGGGAG	GAATTCACAG	GAGTGTCTGT	TCCAGACCTG	GAGGCACTGG	GGGAAATGGC 1320
	TTTGCCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCAGGAG	GGACAGGCTT	CATCCCCATC 1380
	CCTGGAGGCA	ATGGCTTTTC	TCCTGGCGTT	GGGGGAGCCG	GTGTGGGGCG	CGGGGACAG 1440
40	GGACCTATCA	TCACCTGACT	AACAATCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT 1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC 1560
	AAACATGGTT	ATAAGCAGGA	TGCAAATGGA	GATTGTATAG	ATGTCATCA	ATGCACATCA 1620
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTGAT 1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG 1740
45	AATGGGGTTC	TTTGTAAAAA	CGGTCCGATG	GTGAACTCAG	ATGGAAGTTT	CCAGTGCATT 1800
	TGCAATGCCG	GCTTTGAATT	AACTACAGAT	GGAAAAAAGT	GTGTTGATCA	TGATGAATGT 1860
	ACAACCTACCA	ACATGTGTTT	GATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC 1920
	ATCTGCAAAC	CAGGATTGTT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA 1980
	TGCCAGACCC	CAGGAATCTG	CATGAATGGG	CACTGCATCA	ACAGTGAAGG	GTCCCTCCGC 2040
50	TGTGACTGTG	CCCGAGGCTT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC 2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCCGGT 2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGTTTGTGG	AGAACCCCTG 2220
	CAGCCATGCC	CTGCAAAAAA	TTCACTGAA	TTTACCGGCC	TTTGTAGTAG	TGGAGTAGGT 2280
	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT 2340
55	GGGATTGTTG	AAAACCTTAC	TGTTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA 2400
	GATGCTCTG	GAGGAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT 2460
	GATAACGGAT	TGTGCCGAAA	CAGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT 2520
	GTGTTACAGA	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAAG	CAACCCATGT 2580
	GTCAATGGGG	CCTGACAGAA	CAACCTTGGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC 2640
60	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC 2700
	ATCCAGGACA	GGCGCTGTGA	GGTGAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT 2760
	GCCACCTCG	GAGCCGCTG	GGGGAGCCCC	TGTGAGCGGT	GTGAACTAGA	TACAGTTGTC 2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG 2880
	TTCCCTGGCG	TTTGTCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCAATGCGAG 2940
65	TGCCCTGAAG	GCCTTAGCTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TGCGATGGAG 3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCTCTG	AAAGTTCCGC 3060
	ATGGATGCTC	GCTGCTGTGC	TGTCGGGGCG	GCTTGGGGCA	CCGAGTGTGA	GGAGTGCCCC 3120
	AAACCTGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA 3180
	GGGGATGTTT	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT 3240
70	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAAATCGAA	GCTTCAATG	CCGTTGCAAT 3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACCTGCACG	ACATCGACGA	GTGCAGGATT 3360
	TCTCTGACCC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCAG 3420
	TGCTTGAAG	GCTATGAAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGACGGA 3480
	TGTGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCAGCTTT 3540
75	CAGTGTGACT	GCCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT 3600
	AATGAAATGCT	CTCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA 3660
	ACCTATCAGT	GCTCTGTCAA	TCCTGGATAT	CAGGCTACGC	CAGACCCCCA	GGGCTGTACA 3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCAGTGCAC	AAATTCAGAG 3780
	GGAAAGCTAG	AATGCAGCTG	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT 3840
80	GCAGACATTG	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC 3900
	ATTCCTGGAG	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA 3960
	ACATGCATTG	ATGTCAATGA	ATTGTACCTA	TCTGCATGTT	TGGGGAAATG	TGGGGAAATG 4020
	GAGAACACAA	AGGGATCCTT	CATTGGCCAC	TGTCACTGCG	GTTACTCAGT	GAAGAAGGGG 4080
	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAAATTTGGT	CTCATACTG	CGACATGCAT 4140
85	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	CTGGATTGGA 4200
	AAACGGCATCA	AGTGTATTGA	TCTGGAAGAA	TGTTCTAATG	GAACCCACCA	GTGTAGCATC 4260
	AATGTCTCAGT	GTGTAAATAC	CCCGGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT 4320
	GGTGTATGGCT	TTACCTGTCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG 4380

	AACGGCAGT	GCCTTAATGT	CCCGGGTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
	CCAGCCTCAG	ACAGCAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTGT	4500
	GTCTCTGGAA	CATGTAATAA	CCTGCCCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
5	GAATTGGACA	GAACAGGAGG	GAACGTGTACA	GATATTGATG	AGTGTGACAGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACACGCCCT	GGTCGCTATG	AGTGTAACTG	CCCACCCGAT	4680
	TTTCAGTTGA	ACCCCACTGG	TGTGGGTTGT	GTTGACAACC	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTGAGGAGAG	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGGCTC	4800
	AGTCGCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCCTGGG	GAAACCCCTG	TGAGACATGC	4860
10	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
	CAGGGTGGA	ACTGCATCAA	CACCTTTTGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATACCCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCACCT	5160
15	GAGTACATGC	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
	CGAAGCTATA	ATGGAACCA	TTGTGAGAAT	GAGTTGCCTT	TCAATGTGAC	AAAAAGGATG	5280
	TGCTGCTGCA	CATATAATGT	GGGCRAAGCT	GGGAACAAAC	CTTGTGAACC	ATGCCCAACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGATTTCAC	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTTGA	CATTGATGAA	TGTAAAGAGA	TTCACGGCAT	TTGTGCAAT	5460
20	GGTGTGTGCA	TTAAACAGAT	TGGCAGTTTC	CGCTGTGAAT	GGCCTACAGG	ATTCACTTAC	5520
	AATGACCTGC	TGTTGGTTTG	TGAAGATATA	GATGAGTGCA	GCAATGGTGA	TAATCTCTGC	5580
	CAGCGGAATG	CAGACTGCAT	CAATAGTCCT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
	TTCAAACCTT	CACCCAATGG	GGCCTGTGTA	GATCGCAATG	AATGTTTAGA	AATCCTAAC	5700
	GTTTGACAGT	ATGGCTTGTG	TGTTGATCTG	CAAGGAAGTT	ACCAGTGCA	CTGCCACAAT	5760
25	GGCTTTAAGG	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
	CCATGTGGAA	ATGGAACCTG	TAAAAACACC	GTTGGATCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	CTACTCATAA	TAATGATTGC	CTGGACATAG	ATTGAGTGCA	TTCTTTTTTT	5940
	GGTCAGGTGT	GCAGGAATGG	ACGTTGTTTT	AATGAAATTG	GTTCTTTCAA	GTGCTATGTG	6000
	AACGAAGGTT	ATGAACCTTAC	CCCAGATGGC	AAAACTGTA	TAGACACTAA	TGAGTGTGTC	6060
30	GGCCTTCCCG	GCTCTTGCTC	TCCTGGTACC	TGTCAGAATT	TGGAGGGATC	CTTCAGATGC	6120
	ATCTGTCCCC	CAGGGATATGA	AGTAAAAAGC	GAGAACTGCA	TTGATATAAA	TGAATGTGAT	6180
	GAAGATCCCA	ACATTTGTCT	TTTTGGTTCC	TGTACTAATA	CTCCAGGGGG	CTTCCAGTGC	6240
	CTCTGCCCCC	CTGGCTTTGT	ACTATCTGAT	AATGGACGGA	GATGCTTTGA	TACTGCCAG	6300
	AGCTTCTGCT	TCACAAATTT	TGAAAAATGA	AAGTGTCTCG	TACCCAAAGC	TTTCAACACC	6360
35	ACAAAGACAA	AATGTGCTG	TAGTAAGATG	CCAGGAGAGG	GCTGGGGGGA	CCCTGTGAG	6420
	CTGTGCCCA	AAGACGATGA	AGTTGCATTT	CAGGATTTGT	GTCATATGG	CCATGGAAT	6480
	GTCCCTAGTC	TTCATGATAC	ACGTGAAGAT	GTCAATGAGT	GTCTTGAGAG	CCCAGGCATT	6540
	TGTTCAAATG	GTCATGTAT	CAACACCGAC	GGATCTTTTC	GCTGTGAATG	TCCAATGGGC	6600
	TACAACCTTG	ACTACACTGG	AGTACGCTGT	GTGGATACTG	ATGAGTGTTC	AATCGGCAAT	6660
40	CCGTGTGGAA	ATGGTACATG	CACCAATGTT	ATTGGGAGTT	TTGAATGCAA	TTGCAATGAA	6720
	GGCTTTGAGC	CAGGGCCCAT	GATGAATTTG	GAAGATATCA	ACGAATGTGC	CCAGAACCCA	6780
	CTGCTGTGTG	CTTTACGCTG	CATGAACACT	TTTGGGTCC	ATGAATGCAC	GTGCCCGATT	6840
	GGCTATGCC	TCAGGGAAGA	TCAAAGATG	TGCAAGATC	TGGATGAATG	TGCTGAAGGG	6900
	TTACACGACT	GTGAATCTAG	GGGCATGATG	TGTAAGAAATC	TAATCGGCAC	CTTCATGTGC	6960
45	ATCTGCCCTC	CTGGAATGGC	CCGAAGGCC	GATGGAGAAG	GCTGTGTAGA	TGAAATGAA	7020
	TGCAGGACCA	AGCCAGGAAT	CTGTGAAAT	GGACGTTGTG	TTAACATTAT	TGGAAGCTAT	7080
	AGATGTGAGT	GTAAATGAAG	ATTCCAGTCA	AGTTCTTCAG	GCATGAAATG	CCTTGACAA	7140
	CGACAGGGTC	TCTGCTTTGC	AGAGGTACTG	CAGACAATAT	GTCAAAATGGC	ATCCAGTAGT	7200
	CGCAATCTCG	TCACTAAGTC	AGAATGCTGC	TGTGATGGTG	GGCGAGGCTG	GGGCCACCA	7260
50	TGCGAGCTTT	GGCCACTTCC	TGGAAGTCC	CAGTACAAAA	AGATATGTCC	TCATGGCCCA	7320
	GGATATACAA	CTGATGGAAG	AGATATTGAT	GAATGTAAGG	TAATGCCAAA	CCTCTGCACC	7380
	AATGTGCTAGT	GCATCAATAC	CATGGGCTCA	TTCCGATGCT	TCTGCAAGGT	TGGCTACACC	7440
	ACAGACATCA	GTGGAACCTC	TTGTATAGAC	CTTGATGAAT	GCTCCAGTC	CCCGAAACCA	7500
	TGCAACTACA	TCTGCAAGAA	CACCTGAGGG	AGTTATCAGT	GTTCATGTCC	GAGGGGGTAT	7560
55	GTCTGCAAG	AGGATGGAAG	GACATGCAAA	GACCTTGATG	AATGTCAAAC	AAAGCAGCAT	7620
	AACTGCCAGT	TCCTCTGTGT	CAACACCTG	GGGGGGTTTA	CCTGTAATG	TCCACCTGGT	7680
	TTACACAGC	ATCACACTGC	TTGTATCGAC	AACAACGAAT	GTGGGTCTCA	ACCTTTGCTT	7740
	TGTGGAGGAA	AGGGAATCTG	TCAAAACACT	CCAGGCAGTT	TCAGCTGTGA	ATGCCAAAGA	7800
	GGGTCTCTC	TTGATGCTGC	CGGACTGAAC	TGTGAAGATG	TTGATGAATG	TGATGGGAAC	7860
60	CACAGGTGCC	AACACGGCTG	CCAGAACATC	CTGGGTGGCT	ACAGATGTGG	CTGCCCCCAA	7920
	GGCTACATCC	AGCACTACCA	GTGGAATCAG	TGTGTGATG	AGAATGAATG	CTCCAAATCCC	7980
	AATGCCCTGTG	GCTCTGTCTC	TGCTTACAAC	ACCCTGGGGA	GTTTACAAGT	CGCCTGCCCC	8040
	TCGGGGTTCT	CCTTCGACCA	GTTCTCCAGT	GCCTGCCACG	ACGTGAATGA	GTGCTCGTCC	8100
	TCCAAGAAC	CTTGCAATTA	CGGCTGCTCT	AACACGGAGG	GGGGCTACCT	CTGTGGCTGC	8160
65	CCCCCTGGGT	ATTGAGAGT	GGGACAAAGC	CACCTGTGCT	CAGGAATGGG	ATTTAAACAG	8220
	GGGCAGTACC	TGTCAGTGG	TACAGAGGTC	GATGAGGAAA	ATGCTCTGTC	CCGAGAAGCA	8280
	TGCTACAGAT	GCAAAATCAA	CGGCTATCCT	AAGAAAGACA	GCAGGCAGAA	GAGAAGTATT	8340
	CATGAACCTG	ATCCCACTGC	TGTTGAACAG	ATCAGCCTAG	AGAGTGTGCA	CATGGACAGC	8400
	CCCGTCAACA	TGAAGTTCAA	CCTCTCCAC	CTCGGCTCTA	AGGAGCACAT	CCTGGAACCTA	8460
70	AGGCCCGCCA	TCCAGCCCTC	CAACAACCAC	ATCCGTTATG	TCATCTCTCA	AGGGAACGAT	8520
	GACAGCGTCT	TCCGCATCCA	CCAAAGGAAT	GGGCTCAGCT	ACTTGACAC	GGCCAAAGAG	8580
	AAGCTCATGC	CCGGCACATA	CACACTGGA	ATCACTAGCA	TCCCTCTCTA	CAAGAAGAAG	8640
	GAGCTTAAGA	AAGTGAAGA	GAGCAATGAG	GATGACTACC	TCCTAGGGGA	GCTTGGGGAG	8700
	GCTCTCAGAA	TGAGGCTGCA	GATTCAAGCT	TATTAACCGT	TCACAGACTT	GGGCCAGGC	8760
75	TCAAATCCTA	GCACAGCCAG	TCTGCAGAAG	CATTTGAAAA	GTCAAGGACT	AATTTTAAAG	8820
	AGGAAAAATA	ATAATAACTC	TGTTTCTCTT	CCTCCCTGTC	TTAGACTTTG	AATGTTGACC	8880
	CTCACAGGGA	GGGATAATTT	AGACTCTGGT	ATGGCCAAAG	ATTTGAGCTC	AAAGGCAACC	8940
	GTGGTTACTG	TATTTTTTAT	ATAAATTCAT	TTTAAAAATAT	ATTTAAAGAA	ACCTAAATGT	9000
	TCAAGATATC	AGCATATGCG	ACTAAATGCA	CAAAATAAT	GTGAGCTTTT	TTTTTTTTTT	9060
80	CCTGTTAGCA	GTCTGTAACA	CTTTGGGTAT	TTTGCTATAG	TTGCTAATTA	AAAAATATA	9120
	GATGTTTATT	TATTTTTTAT	GCAGTAATAT	ATGGAGAAAT	GAACAAACTA	TGTAACAAA	9180
	AAGGAAACT	CACGTGTTTT	TCTTTAGATT	TATAAATTTG	AGCTATTTTT	TTTAGAGGTG	9240
	CTTTTTAAAA	ATCCAATAGA	TACAAGAGAT	GTTTCCTTTG	GTTTCTGCC	AGTCATCCAG	9300
	CTGATACACA	CCTGATCGAT	TTTAAAGAAA	GCCACACAGA	GCTGAATCGG	GCAGTGCTAA	9360
85	TCATAAATTT	AAAAGACATG	AATGTCATTA	GATCCTTTAT	AACGTAGATC	GAAGCCAAAG	9420
	CAGCTCATTT	GTGACAACAT	TTCATATCAC	CAGACACACC	AGGCAACAGA	AGTTGAAGCA	9480
	CAACCACTGT	AGCAAAATAC	CTTGACTGCT	TGTGAGACCA	TTAGCATTTG	AGGCCAAACC	9540
	GTACTGTATT	TCCTTCTCAT	AACCTCAAGG	AACCATATGT	GCTACCCACA	ACACCTCATT	9600

CTTACCCAGG GTGCGCTGCG TCCTCATGGT ACTGTAGGCA GCTGAAGAAC CGCCGTTCCC 9660
 TTGAAAGGGA ACACCTGGCA TTCTGTGGTG TTTCGTGCTG TCTTAAATAA TGGTGCATT 9720
 ATTATGTTCA AGTTATTTTCA GGATTGCCAT ATGTGCAAAAC AAATCATGCA ATGCAGCCAA 9780
 GGAATATATG TTGTGTGGTG TGTFTTAAAC CCATTTTTTT TTTAGAAATT TCATTAATAC 9840
 TGTAGTTATA CACCATATGC CTCAATTTAT CATAGCCTAT TGTGTATGAA AGATGTTTGT 9900
 ACAATGAATT GATGTTTAGT TTGCTTTAGT CATTTAAAAA GATATTGTAC CAGGATGTGC 9960
 TATTAAGAGC ACGTATCCAT TATTCTTCTC AACCCAAGAA CCTGTTTCTT GGACCAAGTA 10020
 CCAAACTCA TATGTGAAAT GGCACAAAGCA CATGCAGGCT CCTGGTTGTT CCTCTCAAAC 10080
 CTGTGCTGAC CAAAGATTAG TAACCAAGTA TACCCAGTAT TTTGAGGTTT TATTGTTTTT 10140
 TTAATAACTA AAAAAAACT CGTGCC

Seq ID NO: 459 Protein sequence
 Protein Accession #: NP_001990.1

1 11 21 31 41 51
 MGRRRRLCLQ LYFLWLGCVV LWAQGTAGQP QPPPKPPRP QPPPOQVRS TAGSEGGFLA 60
 PEYREBGA AVASRVRRRGQQ DVLRGPNVCG SRFHSYCCPG WKTLPQGNQC IVPICRNSCG 120
 DGFCSRPNMC TCSSGGIIST CGSKSIQCCS VRCMNGGTCA DDHCQCCQGY IGTYCQGPVC 180
 ENGCQNGGR IAQPCACVYG FTGPQCERDY RTGPCTQVN NQMCQQLTG IVCTRTLCCA 240
 TTGRAWHGPC EMCAPQPPC RRGFIPNIRT GACQDVDECQ AIPGICQGGN CINTVGSPEC 300
 RCPAGHKQSE TTQKCEDIDE CSIIPIGICET GECSTVGSY FCVCPRGYVT STDGSRCDIQ 360
 RTGMCPSGLV NGRCQAQLPG RMTKMQCCCE PGRCWGIGTI PEACPVRGSE EYRRLCMDGL 420
 PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFIPI PGGNGFSPGV GGAGVGAGGQ 480
 GPIITGLTIL NQITDICKHH ANLCLNGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS 540
 NPCTNDCVNV TFGSYKCKH AGFQRTPTKQ ACIDIDEIQ NGVLCKNGRC VNSDGSFQCI 600
 CNAGFELTTD GKNCVDHDEC TTTNMLNGM CINEDGSPKC ICKPGFVLAP NGRYCTDVDE 660
 CQTPGICMNG HCINSEGSFR CDPCPGLAVG MDGRVCVDTH MRSTCYGGIK KGVCVRPFP 720
 AVTKSECCCA NPDYGFGEPC QPCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN 780
 GICENLRGSY RCNCSGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSTCCPPGY 840
 VFRTETETCE DINECESNPC VNGACRNNLG SFNCECSPGS KLSSTGLICI DSLKGTICWLN 900
 IQDSRCEVNI NGATLKSECC ATLGAAWGSF CERCELDTAC PRGLARIKGV TCEDVNECEV 960
 FPGVCPNRC VNSKGSFHCE CPEGLTLDGT GRVCLDIRME QCYLKWDEDE CIHPVPGKFR 1020
 MDACCACVGA AWGFECEBEP KPGTKEYETL CPRGAGFANR GDVLTGRPFY KDINECKAFP 1080
 GMCTYKCKRN TIGSFYCKRN SGFALDMEER NCTDIDECRI SPDLCGSGIC VNTPGSFCEB 1140
 CFEGYESGFM MMKNCMDIDG CERNPLLCRG GTCVNTGESP QCDCLPHEL SPSREDCVDI 1200
 NECSLSDNLK RNGKCVNMIG TYQCSCNPGY QATPDRQGCT DIDECEMIMNG GCDTQCTNSE 1260
 GSYECSCSEB YALNPDGGRSC ADIDECENNP DICDGGQCTN IPGEYRCLCY DGFMASMDMK 1320
 TCIDVNECDL NSNLCMFGECE ENTKGSFICH CQLGYSVKKG TTGCTDVDEC EIGHNCDMH 1380
 ASCLINPVSF KCSCREGWIG NGIKCIDLDE CSNGTHQCSI NAQCVNTFPG YRCACSEGT 1440
 GDGFTCSVDV ECASNINLCE NGQCLNVPGA YRCECEMGFT PASDSRSCQD IDECSFQNIC 1500
 VSGTCNNLPG MFHICDDGY ELDRGTGNGCT DIDECADPIN CVNGLCVNTP GRYECNCPD 1560
 FQLNPTGVGC VDNRVNGCYL KFGPRGDGSL SCNTEIGVG VSRSSCCSLG KAWGNPCETC 1620
 PPVNSTEYIT LCPGGEGFRP NPITIILEDI DECQELPGLC QGGNCINTFG SPQCECPQGY 1680
 YLSEDRICE DIDECEFAHPG VCGPGTCYNT LGNYTCICPP EYMQVNGGHN CMDMRKSFY 1740
 RSYNGTTCEN ELFPNVTKRM CCTYNVGKA GNKPCEPCPT PGTADEFKIC GNIPGFTFDI 1800
 HTGKAVDIDE KEIPIGICAN GVCINQIGSF RCECPTGPSY NDLLLVCEDI DECSNGDNL 1860
 QRNADCI NSP GSYRCECAAG FKLSPNGACV DRNECLEIPN VCSHGLVDL QGSYQICHN 1920
 GFKAQDQTM CWDVDECEH PCNGTCKNT VGSYNCLCYP GFELTHNND LDIIDECSFF 1980
 GQVCRNGRCF NEIGSFKCL NEGYLETPDG KNCIDTNECV ALPGSCSPGT CQNLEGSFRC 2040
 ICPPGYEVKS ENCIDINECD EDPNICLFPS CTNTPGGFQC LCPGGFVLSD NGRRCFDTRQ 2100
 SFCFTNFENG KCSVPKFA NT TKAACCSKM PGEWGDPCE LCPKDDVAF QDLCPYGHGT 2160
 VPSLHDTRED VNECLESPI CSNGQCINTD GSFRCECPMG YNLDTGVRC VDTDECSIGN 2220
 PCNGTCTNV IGSFECNNE GFEPGPMNC EDINECAQNP LLCALRCMNT FGSYEECTPI 2280
 GYALREDQRM CKDLDECAEG LHDCESRGM CNLIGTFMC ICPPGMARRP DGEQCDVENE 2340
 CRTKPGICEN GRCVNIIGSY RCECNEGFQS SSSGTECLDN RQGLCFAEVL QTICQMASSS 2400
 RNLVTKSECC CDGGRGWGHQ CELCPLPGTA QYKICPHGP GYTIDGRDID ECKVMPNLCT 2460
 NGQCINTMGS TDFPCKVGYT TDISGTSCID LDECSQSPKP CNYICKNTEG SYQCSCPRGY 2520
 VLQEDGKTK DLDEQCTQKH NCQFLCVNTL GGFTCKCPG FTQHHTACID NNECSQPLL 2580
 CGGKGICQNT PGFSFCECQR GFSLDATGLN CEDVDECDGN HRCQHGQNI LGGYRCGCPQ 2640
 GYIHYQWQNV CVDENECNP NACGSASCYN TLGSYKACAP SGFSFDQFSS ACHDVNECSS 2700
 SKNPNYVGS NTEGGYLCGC PPGYRVGQG HCVSGMGFNK GQYLSLDETEV DEENALSPA 2760
 CYECKINGVP KDSRQKRSI HEPTAVEQ ISLESVDMS PVMKFNLSH LGSKEHILEL 2820
 RPAIQPLNNH IRYVISQNGD DSVFRIHQRN GLSYLHTAKK KIMPGTYTLE ITSIPLYKKK 2880
 ELKKLEESNE DDYLLGELGE ALMRLLQIQL Y

Seq ID NO: 460 DNA sequence
 Nucleic Acid Accession #: NM_013372.1
 Coding sequence: 63..617

1 11 21 31 41 51
 GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCGGC CGCACTGACA 60
 GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCTGTCTTCT CCTCTTGGGG ACCCTGCTGC 120
 CGGCTGCTGA AGGGAAGGAG AAGGGTCCC AAGGTGCCAT CCCCCGCCA GACAAGGCC 180
 AGCAATATGA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240
 GGGGCCAAGG GCGGGGCACT GCCATGCCCC GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG 300
 CCTGTCATGT GACGGAGCGC AATACCTGA AGCGAGACTG GTGCAAAACC GACCCGCTTA 360
 AGCAGACCAT CCACAGAGAA GGCTGCAACA GTCGCACCAT CATCAACCGC TTCTGTTAGG 420
 GCCAGTGCAA CTCTTCTACT ATCCCCAGGC ACATCCGGAA GGAGGAAGGT TCCTTTCAGT 480
 CTTGCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACTCTC AACTGCCCTG 540
 AACTACAGCT ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600
 CCATCGATTT AGATTAAAGC AATCCAGGT GCACCCAGCA TGTCTAGGA ATGCAGCCCC 660
 AGGAAGTCCC AGACCTAAAA CAACAGATT CTTACTTGGC TTAACCTAG AGGCCAGAAG 720
 AACCCCGAGC TGCCCTCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG 780
 ATGGGTGCTT TGGGTGTTT TTAGACACCA GAGAAACAC AGTCTCTGCT AGAGAGCACT 840
 CCCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCCGG 900

	CTCACATCTA	AAGGGGCGGG	GCGGTGGTCT	GGTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCAGA	ATCTCCTTTC	GGAAATGAATG	TTTATGGAAG	AGGCTCCTCT	GAGGGCAAGA	1020
	GACCTGTTTT	AGTGCTGCAT	TCGCATGGA	AAAGTCCTTT	TAACCTGTGC	TTGCATCCTC	1080
5	CTTTCCTCCT	CCTCCTCACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGACTA	TGTCAGTCTA	1140
	ATCTCTTGTT	TGCCAAGGTT	CCTAAATTAA	TTCACTTAAC	CATGATGCAA	ATGTTTTTCA	1200
	TTTTGTGAAG	ACCTTCAGAA	CTCTGGGAGA	GGCTGGTGTG	GGCAAGGACA	AGCAGGATAG	1260
	TGGAGTGAGA	AAGGGAGGGT	GGAGGGTGAG	GCCAAATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
	GACATTGCAG	AAGCTTGAAA	GGCCAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
10	TTTTCTAGT	ATTTAACAGA	ACCCAAGTGA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
	ATTAACCTTG	GCCGTGCAAA	TCTGCTCAAA	CCTAACACCA	AACTGAAAAC	ATAAATACTG	1500
	ACCACCTCTA	TGTTGCGACC	CAAGCAAGTT	AGCTAAACCA	AACCAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTG	GAAAAGAGAG	GTAGTTTAGA	ACTCTCTGCA	TAGGGGTGGG	AATTAATCAA	1620
	AAACCKCAGA	GGCTGAAATT	CCTAATACCT	TTCTTTATC	GTGGTTATAG	TCAGCTCATT	1680
15	TCCATTCCAC	TATTTCCCAT	AATGCTTCTG	AGAGCCACTA	ACTTGATTGA	TAAAGATCCT	1740
	GCCTCTGCTG	AGTGACCTG	ACAGTAAGTC	TAAAGATGAR	AGAGTTTAGG	GACTACTCTG	1800
	TTTTAGCAAG	ARATATTKTG	GGGGTCTTTT	TGTTTTAACT	ATTGTGAGGA	GATTGGGCTA	1860
	RAGAGAAAGC	GACGAGAGTA	AGGAAATAAA	GGGRATTGCC	TCTGGCTAGA	GAGTAAGTTA	1920
	GGTGTTAATA	CCTGGTAGAA	ATGTAAGGGA	TATGACCTCC	CTTTCCTTAT	GTGCTCACTG	1980
20	AGGATCTGAG	GGGACCCTGT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTTCACTG	2040
	CTACTGGTGT	GATGGACATA	ACTATTGTAA	CTATTGAGTA	TTTACTGGTA	GGCACTGTCC	2100
	TCTGATTAAA	CTTGGCGTAC	TGCAATGGC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
	AGGGTGGGTG	AACTTTATTG	TACTTTGGAT	TTGGTTAACC	TGTTTTCTTC	AAGCCTGAGG	2220
	TTTTATATAC	AACTCCCTG	AATACTCTTT	TTGCCCTGTA	TCTTCTCAGC	CTCCTAGCCA	2280
25	AGTCCTATGT	AATATGGAAA	ACAAACACTG	CAGACTTGAG	ATTGAGTTGC	CGATCAAGGC	2340
	TCTGGCATTG	AGAGAACCTT	TGCAACTCGA	GAAGCTGTTT	TTATTTCTGT	TTTGTTTTGA	2400
	TCCAGTGCTC	TCCCATCTAA	CAACTAAACA	GGAGCCATTT	CAAGGCGGGA	GATATTTTAA	2460
	ACACCAAAAA	TGTTGGGTCT	GATTTTCAAA	CTTTTAAACT	CACACTGATG	GATTCTCAGC	2520
	CTAGGCGAAT	TTGTCCAAAC	ACATAGTGTG	TGTGTTTTGT	ATACACTGTA	TGACCCACAC	2580
30	CCAAATCTTT	GTATTGTCCA	CATTCTCCAA	CAATAAAGCA	CAGAGTGGAT	TTAATTAAGC	2640
	ACACAAATGC	TAAGGCAGAA	TTTTGAGGGT	GGGAGAGAAG	AAAAGGGAAA	GAAGCTGAAA	2700
	ATGTAAAAAC	ACACCAGGGA	GGAAATGA	CATTGAGAAC	CAGCAACAC	TGAATTTCTC	2760
	TTGTTGTTTT	AACTCTGCCA	CAAGAATGCA	ATTTGTTTAA	TGGAGATGAC	TTAAGTTGGC	2820
	AGCAGTAATC	TTCTTTTAGG	AGCTTGTACC	ACAGTCTTGC	ACATAAGTGC	AGATTGGGCT	2880
35	CAAGTAAAGA	GAATTTCTCT	AACACTAACT	TCACTGGGAT	AATCAGCAGC	GTAACCTACC	2940
	TAAAAGCATA	TCACTAGCCA	AAGAGGGA	TATCTGTTCT	TCTTACTGTG	CCTATATTAA	3000
	GACTAGTACA	AATGTGGTGT	GTCTTCCAAC	TTTCATTGAA	AATGCCATAT	CTATACCATA	3060
	TTTTATTGGA	GTCAGTATG	ATGTAATGAT	ATATTTTTC	ATTATTATAG	TAGAATATTT	3120
	TTATGGCAAG	ATATTGTGGG	CTTGTATCAT	ACCTATTAAA	ATAATGCCAA	ACACCAATA	3180
40	TGAATTTTAT	GATGTACACT	TTGTGCTTGG	CATTAAAAGA	AAAAACACA	CATCCTGGAA	3240
	GTCTGTAAAT	TGTTTTTGTG	TACTGTAGGT	CTTCAAAAGT	AAGAGTGTA	GTGAAAAATC	3300
	TGGAGGAGAG	GATAATTTC	ACTGTGTGGA	ATGTGAATAG	TTAAATGAAA	AGTTATGGTT	3360
	ATTTAATGTA	ATTATTACTT	CAATCCTTT	GGTCACTGTG	ATTCAAGCA	TGTTTTCTTT	3420
	TTCTCCTTTA	TATGACTTTC	TCTGAGTTGG	GCAAGAAGA	AGCTGACACA	CGTATGTTG	3480
45	TTAGAGTCTT	TTATCTGGTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGTCTTCCT	3540
	GAGTCAGTGC	CTGAATCTTT	ATTTTAA	TTGAATGTTT	CTTAAAGGTT	AACATTCTTA	3600
	AAGCAATATT	AAGAAAGACT	TTAAATGTTA	TTTTGGAAGA	CTTACGATGC	ATGTATACAA	3660
	ACGAATAGCA	GATAATGAGT	ACTAGTTCAC	ACATAAAGTC	CTTTAAGGA	GAAATCTTAA	3720
	AATGAAAGT	GGATAAACAG	AACATTATTA	AGTGATCAGT	TAATGCCTAA	GAGTGAAAGT	3780
50	AGTTCTATTG	ACATTCTCTA	AGATATTTAA	TATCAACTGC	ATTATGTATT	ATGCTGCTTT	3840
	AAATCATTTA	AAAACGGCAA	AGAATTATAT	AGACTATGAG	GTACCTTGCT	GTGTAGGAGG	3900
	ATGAAGGGG	AGTTGATAGT	CTCATAAAAC	TAATTTGGCT	TCAAGTTTCA	TGAATCTGTA	3960
	ACTAGAATTT	AAATTTTACC	CCAATAAGT	TCTATATAGC	CTTTGCTAAA	GAGCAACTAA	4020
	TAAATTAAAC	CTATCTTTTC	AAAAA				

Seq ID NO: 461 Protein sequence
Protein Accession #: NP_037504.1

	1	11	21	31	41	51	
60	MSRTAYTVGA	LLLLLGLTLLP	AAEGKKKGSQ	GAIPPPDKAQ	HNDSEQTQSP	QQPGSRNRGR	60
	GQGRGTAMPG	EEVLESSQEA	LHVTERKYLK	RDWCKTQPLK	QTIHEEGCNS	RTIINRFGY	120
	QCNSPYIPRH	IRKEEGSFQS	CSFCKPKKPT	TMMVTLCNPE	LQPPTKKKRV	TRVKQCRCIS	180
	IDLD						

Seq ID NO: 462 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

	1	11	21	31	41	51	
70	ATGAAAGTTG	GAGTGCTGTG	GCTCATTCT	TTCTTCACCT	TCACTGACGG	CCACGGTGGC	60
	TTCTCGGGGA	AAAATGATGG	CATCAAAACA	AAAAAAGAAC	TCATTGTGAA	TAAGAAAAAA	120
	CATCTAGGCC	CAGTCGAAGA	ATATCAGCTG	CTGCTTCAGG	TGACCTATAG	AGATTCCAAG	180
	GAGAAAAGAG	ATTTGAGAAA	TTTTCTGAAG	CTCTTGAAGC	CTCCATTATT	ATGGTCACAT	240
75	GGGCTAATTA	GAATTTCTAG	AGCAAGGCT	ACCAAGAGCT	GCAACAGCCT	GAATGGAGTC	300
	CTGCAGTGTA	CCTGTGAAGA	CAGCTACACC	TGGTTTCCTC	CCTCATGCCT	TGATCCCCAG	360
	AACTGCTACC	TTACACAGGC	TGGAGCACTC	CCAAGCTGTG	AATGTCATCT	CAACAACCTC	420
	AGCCAGAGTG	TCAATTTCTG	TGAGAGAACA	AAGATTGGGG	GCCTTTTCAA	AATTAATGAA	480
80	AGGTTTACAA	ATGACCTTTT	GAATTCATCT	TCTGCTATAT	ACTCCAAATA	TGCAATGGA	540
	ATTGAAATTC	AACTTAAAAA	AGCATATGAA	AGAATTCAAG	GTTTTGAGTC	GGTTCAGGTC	600
	ACCAATTTTC	GAAATGGAAG	CATCGTTGCT	GGGTATGAAG	TTGTTGGCTC	CAGCAGTGCA	660
	TCTGAATGCT	TGTCAGCCAT	TGAACATGTT	GCCGAGAAGG	CTAAGACAGC	CCTTCACAAG	720
	CTGTTTCCAT	TAGAAGACGG	CTCTTTTCTG	GTGTTTCGGA	AAGCCAGTGC	TAATGACATT	780
85	GTCTTTGGAT	TTGGGTCCAA	GGATGATGAA	TATACCTGTC	CCTGCAGCAG	TGGCTACAGG	840
	GGAAACATCA	CAGCAAGTGT	TGAGTCTCTC	GGGTGGCAGG	TCATCAGGGA	GACTTGTGTG	900
	CTCTCTCTGC	TTGAAGAAGT	GAACAAGAA	TTCAATATGA	TTGTAGGCAA	TGCCACTGAG	960
	GCAGCTGTGT	CATCTTCGT	GCAAAATCTT	TCTGTATCA	TTGGGCAAAA	CCCATCAACC	1020

ACAGTGGGGA ATCTGGCTTC GGTGGTGTG ATCTGAGCA ATATTTCATC TCTGTCACTG 1080
 GCCAGCCATT TCAGGGTGTG CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT 1140
 ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGGCGGAAGA AAAGTATGCC 1200
 AGCTCACGGT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCCTCC GACAGCTCTT 1260
 CCTCTGAATT TTTCTCGGAA ATTCAATTGAC TGGAAAGGGA TTCCAGTGAA CAAAAGCCAA 1320
 CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTTCCATC 1380
 AGAGGCCGTG TGTAAATTGG GTCAGACCAA TTCCAGAGAT CCCTTCCAGA AACTATTATC 1440
 AGCATGGCCT CGTGTACTCT GGGGAACATT CTACCCGTTT CCAAAAATGG AAATGCTCAG 1500
 GTCAATGGAC CTGTGATATC CACGGTTATT CAAAATATT CCATAAATGA AGTTTTCCTA 1560
 TTTTITTTCCA AGATAGAGTC AAACCTGAGC CAGCCTCATT GTGTGTTTGG GGATTTTCAGT 1620
 CATTTGCACT GGAACGATGC AGGCTGCCAC CTAGTGAATG AAACCTCAAGA CATCGTGACG 1680
 TGCCAATGTA CTCACTTGAC CTCTTCTCC ATATTGATGT CACCTTTTGT CCCTCTACA 1740
 ATCTTCCCGG TTGTAAATG GATCACCTAT GTGGGACTGG GTATCTCCAT TGGAACTCTC 1800
 ATTTTATGCC TGATCATCGA GGCCTTGTGT TGAAGCAGA TTAATAAAG CCAAACTCT 1860
 CACACACGTC GTTGTTCAT GGTGAACATA GCCCTGTCCC TCTTGATTGC TGATGTCTGG 1920
 TTTATTGTG GTGCCACAGT GGACACCAAG GTGAACCCCT CTGGAGTCTG CACAGCTGCT 1980
 GTGTTCTTTA CACACTTCTT CTACCTCTCT TTGTTCTTCT GGATGCTCAT GCTTGGCATC 2040
 CTGCTGGCTT ACCGGATATC CTCTGGTTC CATCATGCG CCCAGCATTT GATGATGGCT 2100
 GTTGGATTTT GCCTGGGTTA TGGGTGCCCT CTCATTATAT CTGTCTTAC CATGTCTGTC 2160
 ACGCAACCTA GCAATACCTA CAAAAGGAAA GATGTGTGTT GGCCTTAACTG GTCCAATGGA 2220
 AGCAAAACAC TCCTGGCTTT TGTGTCCCT GCACTGGCTA TTGTGGCTGT GAACTTCGTT 2280
 GTGGTGTGCT TAGTCTCTAC AAAGCTCTGG AGGCCGACTG TTGGGGAAG ACTGAGTCGG 2340
 GATGACAAGG CCACCATCAT CCGCGTGGGG AAGAGCTCTC TCATTCTGAC CCCTCTGCTA 2400
 GGGCTCACCT GGGGCTTTGG AATAGGAACA ATAGTGGACA GCCAGAATCT GGCCTGGCAT 2460
 GTTATTTTGG CTTTACTCAA TGCACTCCAG GGATTTTITA TCTTATGCTT TGGAACTCTC 2520
 TTGGACAGTA AGCTGCGACA ACTTCTGTTT AACAAAGTGT CTGCCCTAAG TTCTTGAAG 2580
 CAAACAGAAA AGCAAAACCT ATCAGATTTA TCTGCCAAAC CCAAAATCTC AAAGCTTTTC 2640
 AACCCACTGC AAAACAAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCGACAAC 2700
 ATCATGCTAA CTCAGTTTGT CTCAATGAA TAA

Seq ID NO: 463 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MKVGVLWLIS FFTFTDGHGG FLGKNDGIKT KKLIVNKKK HLGPEVEYQL LLQVITYRDSK 60
 EKRDRLNFIK LLKPPLLWSH GLIRIIRAKA TTDNSLNGV LQCTCEDSYT WFPSPCLDPQ 120
 NCYLHTAGAL PSCECHLNLI SQSVNFCERT KINGTFKINE RPTNDLLNSS SAIYSKYANG 180
 IETQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVSSSA SELLSAIEHV AEKAKTALHK 240
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
 LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360
 ASHFRVSNST MEDVISIADN ILSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPPTAL 420
 PLNFSRKFDI WKGIPIVNSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FORSLPETII 480
 SMASLTGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVEL PPSKIESNLS QPHCVFWDPS 540
 HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPT IFFVVKWITY VGLGISIGSL 600
 ILCLIIIEALF WKQIKKSQTS LTRRIMVNI ALSLLIADVW FIVGATVDTT VNPSSGVCTAA 660
 VFPTHFFYLS LFFWMLMGI LLAYRIILVF HHMAQHLMA VGFCLGYGCP LIISVITIAV 720
 TQPSNTYKKK DVCWLNWSNG SKPLLAFFVP ALAIVAVNEF VVLLVLTKLW RPTVGERLSR 780
 DDKATIIIRVG KSLILITPLL GLTWGFGIGT IVDSONLAWH VIFALLNAFQ GFILFCFGL 840
 LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKHYA PSHTGDSSDN 900
 IMLTQFVSNB

Seq ID NO: 464 DNA sequence
 Nucleic Acid Accession #: AB035089.1
 Coding sequence: 9845..10219

1 11 21 31 41 51
 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAGAAGG 120
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGG CAGAGTAGGA 240
 AGGAGGAAGG GAGGCAAGAG ATAATATCAT TTTCTCTGTG CTCCAACTGT ACTTACATAT 300
 GAGACTATTT CCCTCTCTGC TTTTCAAACC TTACTGGAGT TGTTTTCCCT CATGAAAACC 360
 AAGAAAGGAA AGCTAGTTAG TCTTGTCTG AGGTGTGTCA ATGTATACAT ATCTATATCT 420
 GTAGACAGAA TCCTTGGGAA TACAGTAATT GACATATATT CTGTTATTG ATGCTTGAAA 480
 AATCTCTCC ACTAACCAGT TTCCCTATAG ATTGCCACAA GCACATAATA AGAAACAATA 540
 AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAAACTTTA CAGCCTTCAT 600
 AAGAAAGTGA GGTCCAGGAA AATCTAGGAG ATATTCTTA ACCAATCTAT AAAGGCATTA 660
 GTAATGACAG GATATTTCCT GAAAGTGTA TTTCCCATG AGGATTGTT TTTAATTTCT 720
 GGATTCCTGG AGCCCAATGAA GTTGGTGTAT GTTTATGAAA TATCAAGAGA CATAAGTTGG 780
 CAAGTGTTC TATGCAAAA CTTCTTGGAA TTTCTGAGTT CTCTGTGGCA ATATATGACA 840
 TCAGGATATG TCCAGTCTCA CACACCAGGA TATGTCCCTT CTAGCCTGTC TATCATATGC 900
 TAGGAGAACT ATTTAGGAAC AGAAAAAAT GCCTGAAATG ATTTCTCATT TGAACCTATC 960
 CAGCTTTCT CTAATTTTAA GCAAACTCCT GGTCAATTTT AGTTAGTACC TTTCTTAAG 1020
 TTCACCTTC AGGGCAAAAC TCCGTGCCTC AGACGTTTAG CCATAGTCTG AAATCTCTCT 1080
 CCATAGATTG GTCCCTGTGA ACCCGGTTT GTCTCAGCTT GTTATCCTGT TTTTCTCTT 1140
 CCTCCATTCC CAGGATGAGC TTGTTGCTTC TGTCTATGA GACATTAGAT TCCTTTTCTT 1200
 TGGTACCGGA GTAAATCCAT CCTACTCCAA TAGAGGAAGG TCCATTTTGT TCTTATAGCG 1260
 CTGGATGCAG ACTCAGCTGA GAAGACCAT ATTCAATTTT GGAATTCCTT ATCTCAGATA 1320
 TTTCTCTTC TTCTTTTTC TTCTATCTT GGATTTTATG TCCATCAACG CCCCATTAGT 1380
 CTATTCCCGG ACTTCAATCA GGGAACTTAT ACCTCTTAAA CTCATTGAGA GACTCAAAAC 1440
 ATATATATTG ATACAGGAGA CCTAAGAAGA GCATGCTTGG GGGGTTGAGG AAACAGGCAG 1500
 GTGAGAAAT TCCAGATTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTTCT 1560
 CCTATGTGTT TCTGGCACTT TGTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG 1620
 AAAACAAACT CACGCTGCT GTTAAAAAGG GCCCATGACA ATACCAAGTG TTGGGGAGAA 1680
 TGTGGAGAAA TCAGAACTCT ATTCACGGTC GGTGTGAATG CACACTTGTG CAGAATTCTA 1740

	TGGAGAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTCAT	AGGTTTATAC	TCAAAAAGAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACACATCATAT	TATTCATAAT	AGTAAAAAGGA	TGGAAACAAAC	ACAAATGTCC	1920
5	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCTAGAAA	TGGAAATATTA	TTCCAGCACA	1980
	AAAAGGAATG	ATGTAATGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAAAT	CCATAGAAAAC	AGGAGGTAGA	TTCTCTGGTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAAATTG	TTGTGGAATG	AGATCATGAT	2220
	GATGATAGCA	CAACTTTTGT	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
10	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACTCTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
	AAACAGAAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
	CTTCATTTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
15	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATTGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCCT	CAGAAATACA	GTAGAGGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGATCT	CCTGAGGCTT	2820
	ATTAACTATC	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
20	TGGGTCCCTC	CATAAATCAT	TGGAATTTCT	GGTAGATACA	ATTCAAGTTG	AGATTGGGGT	2940
	GGGAACACAG	CCAAAGCATA	TCATCTAGCA	AGGCAGATAA	CTTCTCACT	GAGCCTATGC	3000
	AAACAGAAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAAGCTGAG	CACCTCAGGAG	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
	ACTGAAGTAC	ACTTCTTAC	TATCTTTTG	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
25	TACAGAAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAAAG	CTTTTTAGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAAGA	ATGGTGGGGT	TTTTGTTTGT	TTGGTTTTGT	TTTTGTTTTA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTTCTA	AACTTATTCT	3420
30	CATTGGCATT	AGAAAAGGAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAAGTGT	AATCCTGTCC	3540
	TTTGTCTATA	ATTTTCTATAT	TCATAAAGGT	GAGTGTATAG	CCGCTTGTA	AATCTGAAGT	3600
	TGAGTAACCT	CAAATACTAA	CCACAGAGGG	AAAGGCGACA	AGAGGAGAGG	CATAAAATTA	3660
	GGATCTCACC	CTTCTATCCA	CAGACACACA	CAGCCTCTCT	GCCACCTCT	GCTTCTCTCA	3720
	GGAAACACAG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAT	3780
35	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
	TATTCTGCCA	GAGCAAAAT	AAAAATACCTA	TTTCACTGTA	TTTGTCTTTT	ATCTAAATTTG	3900
	CTTAGTTCCA	AGTAAACCAA	GGCACTTTTA	GGAAACAGAA	GGGAGAGTGC	CTTGCAGCCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGGACGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
40	AGGTCTCCTG	TTAGCATTTA	TGTAAAGGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
	GAAAGAAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGT	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAAT	CCATTTATTA	AAGTCATTCT	GACAGGAATC	4320
45	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	CGAGTTCAAC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTCATGTTTG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCGTCGG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
50	AGCACAGGGG	GCTGTGCAGG	AATTTCCATA	ACTGTGAGAC	CACTGACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTTGTC	CCGCTTTCATG	TCTCTTCCAG	GTCTCTCACT	TTGATCAAGT	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACCTGATT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGGAAAAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTGGCAT	4920
55	TTATGTCAC	ATAATTATTA	TTCTCATTT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCA	5040
	AAATGATGAA	TAAGAGCAGG	ACACAACCTG	TCGGAGTCCC	AGTGACCTCA	TCCAGAAAA	5100
	CTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATC	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTCTAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC	5220
60	TAATCATAAT	AATGTGAAAA	TAATTTAATT	TTCAATTGAT	CATTAAATGAG	ATTACAGGGA	5280
	ATAAGCACA	GTCCTAAGTAT	ATTTTGGAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCCTTAATAG	GCAAAATGCT	TGCTGGAAAG	GTAGAAAAGT	CTAGATTAA	ACAGGCTTAG	5400
	GTTCAAAACT	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
	TGAGCTTTCT	TGTGTTTCAT	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
65	TTAGCCATGG	ACCTGGCATA	CACCTTCTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCCTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTAAAA	ATATCCAACC	TTCAACATAC	TGATATCCTT	GATGACTGTT	5700
	AGAAGTGAAA	TATGGTCCTT	GCCCATAAAG	AGCTGAGAGT	TTAACTGGGA	AGCTAAACCT	5760
	AACCTTTTAA	ACCAACAAGG	AGAAAACTTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTTCA	5820
70	AAGAGAAAAG	ATTGCAAGTAC	GTTAGAGCAA	GAAGAAATTT	CTGGAAGAA	TCAATATATA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAG	5940
	GTCCTCAATG	AGACTACCA	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
75	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTACAGGT	6180
	AAATTCACCT	GGCCTACCCA	CATTTCATT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AAGCAAGGCA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTCAC	CAACTCTCCC	CCACTGGAGT	GTCCAGAGCC	CCAACGATAC	6360
	ATCACTGAAG	TGTGGATTTA	GGGTAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
80	TGAGTAAGAG	TAATAAGTAA	TAAGATACCA	TCGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGTTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAACAAA	GATCAGAAAC	ATCATGGTTA	AAATTAATCTG	AGAGAAGTCT	GAGAAGCAAT	6660
	GAATCTCTCT	CAGGGAAGCC	TGCTCTGCA	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
85	CTTTTGCCAA	GAGATATTG	ACCTTCAGTG	ACCTCTTCT	TGTGCCAGCC	CACATTTCCC	6780
	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAGGGTC	TGGATTTCAG	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAAAT	ACTCCTAATT	CCTACTTCTT	CCTTCATATC	TCAAGGAAT	ATTTAGATGC	6960

	CATCAAGAAA	TTTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAATG	CTCCAGAAGA	7020
	AAGTCGAAAG	AAGATTTAACT	CCTGGGTGGA	AAGTCAAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACCTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
5	GAACAGGTGT	GGGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAAAATGAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
	GCCAAITTAGA	TGGAAACACA	TCTGGAGAAT	TAITTTGCTTA	TGGCCCTGCA	TGACAAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAAT	TTTTATGATG	AATATTTAAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
10	TTTACTAATT	GGGAAACAAAG	CAGCTCTCTG	GTAAATCACC	CTTTGTCTC	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAAATGTGT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
	ATCAAGGGCA	AAGAGCTTGA	CAAAAGTCTCC	ATTCTACAGA	CATCTTTCTT	ACCTCCACC	7620
	TCTCATTTACA	GGCCAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCGG	7680
	GAAGTAGTGT	CTGACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
15	CTAAAAATGCA	ATCAGGGGCT	CCTTCCCTCG	AATGGGGACC	CGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAATCA	7860
	GTTTATCAGT	ATTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGCTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	AATGCTGAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
20	GTGAGTCTCA	AGCAGGGAT	TGGGTCAATA	ATTAACGATC	AGTCAACGAA	ATTGCAAAAG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAGACT	CTTTTATCT	TTCCCTTGCA	8160
	GAAAAAATTA	AAAACCTATT	TCCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTCTT	8220
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	GAGAAATAAT	TTAAAAAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGCCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
25	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAATAAAAA	8400
	TTGTTTCATGT	CTGTATTATT	GTGTTTTCAT	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
	GAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAATAT	TATCTTTTTT	GTCTTGTGTT	TCACGTGTTA	TTTGTGGAC	8580
	ACATTGATTT	ATTGTCAGAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
30	TTAATTTTGC	CTTGTCTGAG	GATGTACAGG	CCAAGGTCTC	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGGTCTGCAG	AAGGTAAGAA	8760
	CTTGACTCTA	CAACTCTTCC	TTCTACTGCC	GGACATTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCCTC	AAAATGATGA	AAAATCTTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTGTA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
35	GTTTTGTGTT	GTGTTTGTG	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAAGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
	CCATTAATCT	ATCATTTAGC	GTTAGGTATA	TCTCTAATG	CTATCCCTCC	CCCTCCCCC	9120
	CACCCACAA	CAGTCTCAG	AGTGTGATGT	TACCTTCCCT	TGTCCAAGTG	TTCTCATTTG	9180
40	TCAATTCCCA	TCTATGATTT	AATCCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAAATAGGC	GAGTAGAAAA	GGGAATACAA	9360
	ATTAGGAAT	TTAGGGAAT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATGA	CACATGATGT	AGGCTGTTGG	CACAAGAAAT	9480
45	AGTGATACAT	ACAGTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACATACATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
	TTTTACCTAT	TAGAATAATA	ATGTCTATTA	AAGTGAACCT	TCTGTATTTC	ACATTTATTG	9720
	CCAAAAATAC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAAACTCA	CTGCTGAGAA	9840
50	ATTGATGGAA	TGGCAAGATT	TGCAGAAAT	GAGAGAGACA	TGTGTGATT	TACACTTACC	9900
	TCGGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACAG	TTGAGAACCA	TGGGAATGGT	9960
	GAATATCTTC	AATGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CGTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TCGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCGTGTT	10140
55	TAATCACCCCT	TTCTTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCGAATGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTCCACCTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTG	TCTTGGCTCA	TATTTCTTTT	10320
	CTATCTCATC	TTGATGATGA	TAGTCATCAT	CAAGAATTTA	ATGATTAAAA	TAGCATGCCT	10380
60	TTCTCTCTTT	CTCTTAATAA	GCCACATAT	AAATGTACTT	TTCTTCCAG	AAAAATTTCC	10440
	CTTGAGGAAA	AATGTCCAAG	ATAAGATGAA	TCATTTAATA	CCGTGTCTTC	TAAATTTGAA	10500
	ATATAATTCT	GTGTTCTGAC	TGTTTTAAAT	GAACCAAAAC	AAATCATACT	TTCTCTTCAA	10560
	ATTAGCAAC	TAGAGAACAC	ACATTTCTTT	GAATTTAGGT	GATACCTAAA	TCCTTCTTAT	10620
	GTITCTAAAT	TTTGTGATTC	TATAAAACAC	ATCATCAATA	AAATAATGAC	ATAAAAATCAT	10680
65	TTTTGCTTTA	CCTGTTTTCT	CTCTGGAAG	GGCAAGTGTG	CAGTTACACA	TAGGAAGAGT	10740
	AATTTAGAGA	TATATTAAAT	ATATATAAAG	GAAAAATTAA	AACAGAGTAG	TTCATGATGA	10800
	GCCTGGAGTA	GAAGGCATAT	CCCAAGAACAG	GAGGAGCCTT	GTAACACACA	TAGGAACCTC	10860
	CTATTTTATG	CTAAAGGGAT	AAGAAACTCA	TTACAGGCTT	TGATGGTTGT	TTGTCAAAGA	10920
	GGGGCATAAA	ATTATCATAT	CCACATCTAG	AAAATACATC	TCTGGCTACG	CTGATATCAA	10980
	TGGATGCGAG	GAAAGAACAG	TGTGGTTACC	ATATATAAAT	TAGGAATCA	TTAGAGTATT	11040
70	GGGAGTGGAA	ATGGAGAGAA	AGAAAGAGCC	TGGGGGAATT	ATTTAGGAAA	TAATAGTTAC	11100
	AGAAAGACAT	CTAAGTTGCT	GACCTATCTG	ACTGGATGGA	TGGAAGARTA	TCTTGTITCT	11160
	GAGAGAAAAA	AAGACTTTGG	GTTTAAATTT	GTACTTGATG	AATTAAGGTA	CTTTTAAATAT	11220
	TCAAATGGAT	TTGCTGGCA	GGCACTTGAA	GATATTAGTC	TAAATCTCAG	AAACAGAATA	11280
	TGATCTGAAG	CTCTAAATTT	GTGATATTCA	ATATAAATAC	TTTAGAGTCA	TTGGGATAAA	11340
75	TATGGTAGTT	GTAGCTAAAA	GCAAAAAATA	GATACAGGGG	AGAAAGGATA	AAGTTAGAAG	11400
	AAAGAAAGAT	CTAGAAATGA	CCTTGAAGTA	TATCAGCATG	TGTAAGATC	AGGAATTGAT	11460
	CATTTTATT	TTCCAGAAAG	TAGCTTTTCT	TAGGGTTCCA	TATTTACTCC	CATAGATTCT	11520
	TCCC						

Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

	1	11	21	31	41	51	
85	MNSLSEANTK	FMFDLFQQFR	KSKENNIFYS	PISITSALGM	VLLGAKDNTA	QQISKVLHFD	60
	QVTENTTEKA	ATYHYVDRSGN	VHQHFQKLLT	EPNKSTDAYE	LKIANKLFG	KTYQPLQEYL	120
	DAIKKFYQTS	VESTDFANAP	EESRKKINSW	VESQTNKIK	NLFPDGTIGN	DTTLVLVNAI	180
	YFKQGWENRF	KKENTKEEKP	WPNKNYKSV	QMMRQYNSFN	FALLEDDVQAK	VLEIPYKQKD	240

LSMIVLLPNE IDGLQKLEEK LTAELKMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMGMVNIFNG DADLSQMTWS HGLSVSKVLH KAPVEVTEEG VEAAAATAVV VVELSSPSTN 360
 BEPCCNHPFL PFIRQNTNS ILFYGRFSSP

5

Seq ID NO: 466 DNA sequence
 Nucleic Acid Accession #: NM_001910.1
 Coding sequence: 50..1240

10	1	11	21	31	41	51	
	GGAGAGAAGA	AAGGAGGGGG	CAAGGGAGAA	GCTGCTGGTC	GGACTCACAA	TGAAAAACGCT	60
	CCTTCTTTTG	CTGCTGGTGC	TCTTGGAGCT	GGGAGAGGCC	CAAGGATCCC	TTACAGGGGT	120
	GCCCCCTCAGG	AGGCATCCGT	CCCTCAAGAA	GAAGCTGCGG	GCACGGAGCC	AGCTCTCTGA	180
	GTTCTGGAAA	TCCCATTAAT	TGGACATGAT	CCAGTTCAAC	GAGTCCCTGT	CAATGGACCA	240
15	GAGTGCCAAG	GAACCCCTCA	TCAACTACTT	GGATATGGAA	TACTTCGGCA	CTATCTCCAT	300
	TGGCTCCCCA	CCACAGAACT	TCACTGTCTA	CTTCGACACT	GGCTCCTCCA	ACCTCTGGGT	360
	CCCCCTCTGT	TACTGCACTA	GGCCAGCCTG	CAAGACGCAC	AGCAGGTTCC	AGCCTTCCCA	420
	GTCCAGACCA	TACAGCCAGC	CAGGTCAATC	TTTCTCCATT	CAGTATGGAA	CGGGGAGCTT	480
	GTCCGGGATC	ATTGGAGCCG	ACCAAGTCTC	TGTGGAAGGA	CTAACCCTGG	TTGGCCAGCA	540
20	GTTTGGAGAA	AGTGTACAG	AGCCAGGCCA	GACCTTTGTG	GATGCAGAGT	TTGATGGAA	600
	TCGTGGCCTG	GGATACCCCT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAACAT	660
	GATGGCTCAG	AACTGGTGG	ACTTGCCGAT	GTTTCTGTCT	TACATGAGCA	GTAACCCAGA	720
	AGGTGGTGG	GGGAGCCAGC	TGATTTTGG	AGGCTACGAC	CACTCCCAT	TCTCTGGGAG	780
	CCTGAATTGG	GTCCCGATCA	CCAAGCAAGC	TTACTGGCAG	ATTGCATGG	ATAACATCCA	840
25	GGTGGGAGGC	ACTGTTATGT	TCGTCTCCGA	GGGCTGCCAG	GCCATTGTGG	ACACAGGGAC	900
	TTCCCTCATC	ACTGGCCCTT	CCGACAAGAT	TAAGCAGCTG	CAAAACGCCA	TTGGGGCAGC	960
	CCCCGTGGAT	GGAGAAATATG	CTGTGGAGTG	TGCCAACCTT	AACGTCAATG	CGGATGTAC	1020
	CTTCACCAT	AACGGAGTCC	CCTATACCT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
	CGTGGATGGA	ATGCAGTTCT	GCAGCAGTGG	CTTCAAGGA	CTTGACATCC	ACCTTCCAGC	1140
30	TGGGCCCTC	TGGATCCTGG	GGGATGTCTT	CATTGACAG	TTTTACTCAG	TCTTTGACCG	1200
	TGGGAATAAC	CGTGTGGGAC	TGGCCCCAGC	AGTCCCTTAA	GGAGGGGCT	TGTGTCTGTG	1260
	CCTGCTGTCT	TGACAGACCT	TGAATATGTT	AGGCTGGGGC	ATTCTTTACA	CCTACAAAAA	1320
	GTTATTTTCC	AGAGAATGTA	CTGTGTTTCA	GGGTTGCAAC	TTGAATTAAG	ACCAACACAGA	1380
	ACATGAGAA	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
35	ACTCCACCA	CCGTATGAT	GGAGGAATTA	CGTTATACAT	TCATATTTTG	TATTGATTTT	1500
	TGATTATGAA	AATCAAAAAAT	TTTCACATTT	GATTATGAAA	ATCTCCAAAC	ATATGCACAA	1560
	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCCATCCA	1620
	CACACGGCCA	GGCCTGTTTA	TCACACTGCT	TGCCCACTCC	TCTCTCCAGC	TCCACATGCT	1680
	GTACCTGGAT	CATTCTGAAG	CAAAATCCGA	GCATTACATC	ATTTTGTCCA	TAAATATTTC	1740
40	TAAATCCTT	AAATATACAA	TGGGAATTCA	AGCATCTCCC	ATTGTCCAC	AAATGTTTGG	1800
	CTGTTTGTG	AGTTGGATTG	TTTGTATTAG	GATTCAAGCA	AGGCCATAT	ATTGCATTTA	1860
	TTTGAATGT	CTGTAAGTCT	CTTCCATCT	ACAGAGTTTA	GCACATTGGA	ACGTTGCTGG	1920
	TTGAAATCCC	GAGGTGTCTA	TTGACATGGT	TCTCTGAACT	TATCTTTCCT	ATAAAATGGT	1980
	AGTTAGATCT	GGAGGTCCTA	TTTGTGGCA	AAAATACTTC	CTAGGTGGTG	CTGGGTACTT	2040
45	CTTGTGTCAT	CCTGTACGGA	GGCAGATAAT	GCTGGTGCTT	CTCTATTGGT	AATGTTAAGA	2100
	CTGCTGGGTG	GTTTGGAGT	TCTTGGCTTT	AATCATTCAT	TACAAAGTTC	AGCATTTT	

Seq ID NO: 467 Protein sequence
 Protein Accession #: NP_001901.1

50	1	11	21	31	41	51	
	MKTLLLLLLV	LLELGEAQGS	LHRVPLRRHP	SLKKKLRRAS	QLSEFWKSHN	LDMIQFTESC	60
	SMDQSAKEPL	INYLDMIEYFG	TISIGSPPQN	FTVIFDTGSS	NLWVPSVYCT	SPACKTHSRF	120
55	QPSQSSTYSQ	PGQSFSIQVG	TGSLSGIIGA	DQVSVEGLTV	VGQQFGESVT	EPGQTFVDAE	180
	FDGILGLGYP	SLAVGGVTPV	FDNMMAQNLV	DLPMFVSVM	SNPEGAGSE	LIFGGYDHS	240
	FSGSLNWVPE	TQKAYWQIAL	DNIVQVGTVM	FCSEGCQAI	DTGTSITLTP	SDKIKQLQNA	300
	IGAAPVDGEY	AVECANLNMV	PDVPTINGV	PYTLSPYAT	LLDFVDMQMF	CSSGPGGLDI	360
60	HPPAGPLWIL	GDVFIQFYS	VFDGRNNRVG	LAPAVP			

Seq ID NO: 468 DNA sequence
 Nucleic Acid Accession #: NM_018058.1
 Coding sequence: 319..1575

65	1	11	21	31	41	51	
	TACGCGCTGC	GGGACCGGCA	GGGGAACGCC	ATCGGGGTCA	CAGCCTGCGA	CATCGACGGG	60
	GACGGCCGGG	AGGAGATCTA	CTTCTCAAC	ACCAATAATG	CCTTCTCGGG	GGTGGCCACG	120
	TACACGACGA	AGTTGTTCAA	GTTCGCAAT	AACCGGTGGG	AAGACATCCT	GAGCGATGAG	180
70	GTCAACGTGG	CCCGTGGTGT	GGCCAGCCTC	TTTGCCGGAC	GCTCTGTGGC	CTGTGTGGAC	240
	AGAAAGGGCT	CTGGACGCTA	CTCTATCTAC	ATTGCCAATT	ACGCCTACGG	TAATGTGGGC	300
	CCTGATGCC	TCATTGAAAT	GGACCTGAG	GCCAGTGACC	TCTCCGGGG	CATTCTGGCG	360
	CTCAGAGATG	TGGCTGCTGA	GGCTGGGGTC	AGCAAAATATA	CAGGGGGCCG	AGGCGTCAGC	420
	GTGGGCCCCA	TCCTCAGCAG	CAGTGCTCG	GATATCTTCT	GCGACAATGA	GAATGGGCCT	480
75	AACCTCTTTT	TCCACAACCG	GGCGGATGGC	ACCTTTGTGG	ACGCTGCGGC	CAGTGTCTGGT	540
	GTGGACGACC	CCCACACGCA	TGGGCGAGGT	GTGCGCTTGG	CTGACTTCAA	CCGTGATGGC	600
	AAAGTGGACA	TGCTCTATGG	CAACTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAAATGAGC	660
	ACCCATGGGA	AGGTCCGCTT	CCGGACATC	GCCTCACCCA	AGTTCTCCAT	GCCTCCCTCT	720
	GTCCGACCGG	TCATCACCGC	CGACTTTGAC	AATGACCAGG	AGCTGGAGAT	CTTCTTCAAC	780
80	AACATTGCTC	ACCGCAGCTC	CTCAGCCAAC	CGCTCTTCC	CGCTCATCCG	TAGAGAGCAC	840
	GGAGACCCCC	GCTCAATCCC	GGCGACGCTT	TGGAGCCTGA	GGCCCGGGC		900
	ACAGGGGGTG	TGGTGACCGA	CTTCGACCGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
	GGAGAGTCCA	TGGCTCAGCC	GCTGTCCGTC	TTCCGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
	TGGCTGCGAG	TGCTCGACG	CACCCGGGTT	GGGGCCTTTG	CCAGGGGAGC	TAAAGTCTGT	1080
85	CTCTACACCA	AGAAAGATGG	GGCCACCTG	AGGATCATCG	ACGGGGGGCTC	AGGCTACCTG	1140
	TGTGAGATGG	AGCCCGTGGC	ACACTTTGGC	CTGGGGAAGG	ATGAGCCAG	CAGTGTGGAG	1200
	GTGACGTGGC	CAGATGGCAA	GATGGTGAGC	CGGAACGTGG	CCAGCGGGGA	GATGAACCTA	1260

GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
 ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
 ACACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440
 ACGAGGATGG CACAGCCTGC TGCGGGACTC TCGGCCAGTC ACCGGGCCCC CGCCCCACCA 1500
 CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
 CACCGTCTCT CGTAGATGGA GATCTCAATC TGGGGTCCGT GGTAAAGGAG AGCTGCGAGC 1620
 CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCCCTC 1740
 CCCAAGCCCA TCCATGCACA TTAATTAGCT AACAAATTAGG GAGACTCGTA AGGCCAGGCC 1800
 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAAGGA GGTGGTGTCA 1920
 CTGCACAGGA AGTATGAGGA CTTTAGTGTG CTGAGTTCAA ATCCTGATTC AGGAACTCAC 1980
 AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA 2040
 AAATGGGGAT TAAGAAATGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
 GACACTTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAACCAAGT GCCTCTCACT 2160
 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
 Protein Accession #: NP_060528.1

1 11 21 31 41 51
 | | | | |
 MDPEASDLR GILALRDVAA EAGVSKYTGG RGVSVGPILS SSASDIFCDN ENGNPFLFHN 60
 RGDGTFVDAA ASAGGVDPHQ HGRGVALADF NRDGKVDIVY GNMNGPHRLY LQMSTHGKVR 120
 FRDIASPKFS MPSPVRTVIT ADPDNDQELE IFNNIAYRS SSANRLFRVI RREHGDPLIE 180
 ELNPGDALEP EGRGTGGVVT DFDGDMGLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRLVP 240
 RTRVGAFARG AKVVLVYTKKS GAHLRIIDGG SGYLCMEFV AHFLGLKDEA SSVETWPDG 300
 KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETMNAS SSHSCALET S PVVSTPMEAT 360
 GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPLPLLL PLPLLLPLLE LPLLRHS

Seq ID NO: 470 DNA sequence
 Nucleic Acid Accession #: AJ279016
 Coding sequence: 1..1962

1 11 21 31 41 51
 | | | | |
 ATGTCCAGGA TGTTACCGTT CTTGCTGCTG CTCTGGTTTC TGCCCATCAC TGAGGGGTCC 60
 CAGCGGGCTG AACCCATGTT CACTGCAGTC ACCAACTCAG TTCTGCCTCC TGACTATGAC 120
 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180
 TTTGAGATCG TCGTGGCGGG GTACAAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCG 240
 CAGAAGCGGC TGGTGAACAT CGCGGTGCGT GAGCGCAGCT CACCTACTA CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGGTCACT GCCTGCGACA TCGACGGGGA CGGCCGGGAG 360
 GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420
 TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CCAGCCTCTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGGCC TGATGCCCTC 600
 ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
 CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAAATGAGA ATGGGCTTAA CTTCCTTTTC 780
 CACAAACGGG GCGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGAGACCCCC 840
 CACCAGCATG GGCAGAGTGT CGCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
 GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960
 GTCCGCTTCC GGGACATGCG CTCACCCAAG TTCTCCATGC CCTCCCCTGT CCGCAGCGTC 1020
 ATCACGCGCG ACTTTGACAG TGACCCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCCTAC 1080
 CGCAGCTCCT CAGCCAAACG CTTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140
 ATCGAGGAGC TCAATCCCGG CGACGCTTGG GAGCCTGAGG GCCGGGGCAC AGGGGGTGTG 1200
 GTGACGAGCT TCGACGAGGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
 GCTCAGCGCG TGTCCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAATG GCTGCGAGTG 1320
 GTGCCACGCA CCGGGTTTGG GGCCTTTGCG AGGGGAGCTA AGGTCTGTCT CTACACCAAG 1380
 AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
 CCGGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGGAC 1500
 GATGGCAAGA TGGTGAAGCG GAACGTGGCC AGCGGGGAGA TGAATCACT GCTGGAGATC 1560
 CTCTACCCCC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620
 TTCTCCAGC AGGAAATGG CCAATTGCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC 1740
 AACAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCTCCACCG CTGCTGCTGC CACTGCGCT 1860
 GCTGCTGCCG CTGCTGGAGC TGCACTGCTG GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGGTCCG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
 CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT 2040
 AGGGATGTAA AGGCCTGGGA GCTAGACCTT CCCCAGCCC ATCCATGCAC ATTACTTAGC 2100
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CTTGTGCTGG GCACATAGCT GTGATCACAG 2160
 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCAGTGG GGTCTAATGA CCATATCTTA 2220
 GGACACAGAT GTGCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
 CCTGAGTTCA AATCCTGATT CAGGAACCTA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340
 AACTTGTTAG CATCTCATTA TCGCATCTGC AAAATGGGGA TTAAGAAATG AATCTTGGGG 2400
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460
 AAAGGCTCAA TAAAAACAAG TGCTCTCAC TGGGCTTTGT CAACACG

Seq ID NO: 471 Protein sequence
 Protein Accession #: CAC08451

1 11 21 31 41 51
 | | | | |
 MSRLPFLLL LWFPLITEGS QRAEPMPTAV TNSVLPDDYD SNPTQLNYGV AVTDVDHDDG 60
 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQNAIGVT ACDIDGDGRE 120
 EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

GRYSIYIANY AYGNVGPDL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNPLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNDRDGVDI 300
 VYGNMNGPHR LYLMNSTHGX VRFRIASPK FMPSPVVRTV ITADFDNDQE LEIFPNNIAY 360
 RSSSANRLFR VIREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGZSM 420
 5 AQLSVVFRGN QGFNMNMLRV VPTRFPAFA RGAKVVLTK KSGAHLRIID GSGGYLCME 480
 PVAHFLGLKD EASSVEVTWP DGKMSVRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECCQG 540
 FSQENGHCN DTNECIQFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGEYEP NEDGTACVGT 600
 LGQSPGPRPT TPTAAATAA AAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESH
 Coding sequence: 1..4794

15 1 11 21 31 41 51
 | | | | |
 ATGGCGTGTC CGGGAGGACT CCCAGCCCGT TGCTCTGGTT GGATGGGACT GGTGGGGCCC 60
 AGCGGCTCCT CCCAGCATC CCCTCCCAT TCCTCTCCA GGTACAATGG ACCCAACTTG 120
 GTTCTGAAGT ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGGTGCA TGAGCGCAGC 180
 20 TCACTCTACT ACGCGCTGCG GGACCGGCAG GGAACGCCA TCGGGGTGAC AGCCTGCGAC 240
 ATCGACGGGG ACGGCGGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTCTCGGGC 300
 CACAGCAGCT CAGCGCAGGT CCCTCTGGG CTCCACAGAA ACAGGCCTGT GCTGAAGCCT 360
 CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCTCCAC TCAGCGGAAG GCACTTTTCC 420
 TCCTCCCTGG GTACGGCTTC TCGGCAGAGC AGGCAGGAG AGAGGGTGCC GGTTCCTGTC 480
 25 TGTCTGGGTG GACTGAGACC TACCATGAA CCAGAACCAT TTCTCTGAG ACCCAATCA 540
 GGGGTGGCCA CGTACACGA CAAGTTGTTC AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAACGT GGGCCGTGGT GTGGCCAGCC TCTTTGCGCG ACGCTCTGTG 660
 GCCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCTTAC 720
 GGTAAATGTGG GCCCTGATGC CCTCATTGAA ATGGACCTG AGGCCAGTGA CCTCTCCCGG 780
 30 GGCACTTCTG CGCTCAGAGA TGTGGCTGCT GAGGCTGGG TCAGCAAATA TACAGAAGGC 840
 TTCTCCCA CAAGCTCTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA 900
 GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACTG 960
 TGCCGGCTGG GCTGGAAGGA CGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAAGAA 1020
 CAGAGGGAGG CTGGGCGAGC TGGCGTGCCC AGAGGACGTG TTGGAACAGC TCTGCAGACT 1080
 35 TCCAAAGGCC ATTTGGCTGA CAAGAACCCTA TTGGCCAC CATGTTACTA TTCTGTCTGC 1140
 CGGCTTCTC CAGCCCAACC TTTCCCTGCC CGCCAAGCCC CCCAACTA CCTGTAGCC 1200
 CCCTTGTCA CTAGCTAAT GACACATGGA CGTCTGGCTG GAAAACCTAGC CCGGAGTGTC 1260
 CCCACCCCC GAGCCCCAGC AATGGAACCC AAATGTAAGG GCOCGCATGC TGAGCCCGGC 1320
 CTGATGGCTG AGGCTTTGGG CGGCTGGCCA CGCTCAGCA CCACTGTGGT GCCAGGGGCG 1380
 40 CTGAGAAGCT GGGAGGAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG 1440
 GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCAGCTGC CTGCTAGAGA GCTGTATGAC 1500
 CTGGGAGAAC CTCCCACTTT ACAAGAACA GACGGAGATC CAGGAGGAG AAGGGAATCG 1560
 CCCAAGGTCA CACAGGAGTG CCATCTAGTG GCCACCATGC CAGCTCTCGG GGAATCGAG 1620
 GGCCCCGGA GGGTGGCCAA GCGAGAGATT GGGAGAGAGA CTGGGGCAGT AGGAAGACCA 1680
 45 CTCTCCCATC CTCTGCTCCC CAACTTCCCC AGCTGCTTGA GGCTCTTGA AGCCGGGACA 1740
 GTGCCGGGAG CTGCCCTGCC TGGGAATCCT GGGAACTGGG TTCTGGACAT GGCCAAGGCC 1800
 CTGGCTGGA ACCAGATGGA AAAAGAGGAG GGAAGATTC ATGGAGACCA TGAGCCCGA 1860
 TTTAGGCTCA GGAAGCAGC GGAAGCAGAA TTCCCCCAG GCTCCTCTGA GGAGCCTCTG 1920
 CTGCAGTTC CCTCAGGCCT CAGAGGCAGC CTGTCTCTCC AGGTGGGCCT GGGGCTTGCT 1980
 50 TCTGCCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CTGGGGCCCC 2040
 ATCCTCAGCA GCAGTGCTTC GATATCTTTC TGCGACAATG AGAATGGGCC TAACCTCTCT 2100
 TTCCACAACC GGGCGGATGG CACCTTTGTG GACGCTGCGG CCAGTGCTGA ACGTCGTTTA 2160
 GCCTTCATCG TTCACCTCAA ATATCACCTC TGCAGAGATT TTCTCACTC CTGTGCCAC 2220
 CTAGCAGAAA CTGGTCTCTC CTCTCTCTGC TGCCGCTGGC ATGCACGTCT TCTTCAGGCT 2280
 55 CCACATGGC ATCATGTTT GTCTATGAGC TTACAAAGGA CCGGCTCAGG GTTCTATTCA 2340
 TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT 2400
 CAGGGGGCCC CACCTGCTCT TCTGGCAAGA GCTCCTCTGT TCTTGGGGTC TCTGATCCCC 2460
 ACTGCCTATT ACATGTCTCT GTGGTCTGCC ATCCCAGAGA GCCTGATGAC CCACAGCTAT 2520
 60 TTGTCTCTCT AAGAGTCAA CGTGGGTGTG GACGACCCCC ACCAGCATGG GCGAGGTGTC 2580
 GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC 2640
 CCCACCGCC TCTATCTGCA AATGAGCACC CATGGGAAGG TCCGCTTCCG GGACATCGCC 2700
 TCACCCAAGT TCTCCATGCC CTCCCTGTGC CGCACGGTCA TCACCGCCGA CTTTGACAA 2760
 GACCAGGAGC TGGAGATCTT CTCAACAAC ATTGCCTACC GCAGCTCTC AGCCAACCGC 2820
 CTCTTCCGAT GCTCCATCCT GGTCTGTGGC TCTTCATCCT TGACAGCTGG TGGGAGGAAC 2880
 65 GGTCAAGGAG AAGGTTTAA AATCAGAAAG GGAGGTTTCC CAGGGCCAGG GGTCTCAGGC 2940
 AAGGTCAACA CAGGTCCCTT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGAAGGGCA 3000
 AGAGGCTGTG GGAATGCAGG GCAAAGCCTG GCCAAGGAGC CGGCTCTGCT TATTGCAGGG 3060
 AAAGGGGAAG GAAATGTGGC CCAAGTGTG CCCAGAACC AAGCGCCACA AGATACAAAG 3120
 CCACACTACC ACAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAG GGGCTACGGG 3180
 70 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC ACTACAGGA AAAGGGGCTA 3240
 CGGGGTCCAA TCACTAACAG GAAAAGGGG TACGGGTGCC AATCACTACC AGGAAAAGGG 3300
 GCTACGGGCT CCAATCACTA CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA 3360
 AGGGGCTACG GGCTCCAATC ACTACAGGA AAAGGGGCTA CAGGGTCCAA TCACTACCAC 3420
 75 AGAAAAGGGG TACGGGCTCC AATCACTACC AGGAAAAGGG GCTACGGGT CCAATCACTA 3480
 CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC 3540
 ACTACAGGA AAAGGGGCTA CGGGCTCAA TCACTACCAG GAAAAGGGG TACGGGTGCC 3600
 AATCACTACC AGGAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACAGG 3660
 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC ACTACAGGA AAAGGGGCTA 3720
 80 CGGGGTCCAA TCACTACAG GAAAGGGG TACGGGCTCC AATCACTACC AGGAAAAGGG 3780
 GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA 3840
 AGGGGCTATG GGGTCCAATC ACTACAGGAA AAGGGGCTA CGGGGTCCAA CGTCATCCGT 3900
 AGAGAGCAGG GAGACCCCTC CTACGAGGAG CTCAATCCCG GCGACGCTTT GGAGCCTGAG 3960
 GGCCGGGGCA CAGGGGGTGT GGTGACCGAC TTGACGGAG ACGGATGCT GGACCTCATC 4020
 TTGTCCCATG GAGAGTCCAT GGCTCAGCG CTGTCCGTCT TCCGGGGCAA TCAGGGCTTC 4080
 85 AACAACACT GAGTCCGAGT GGTGCCACGC ACCCGTTTG GGGCTTTGC CAGGGGAGCT 4140
 AAGGTCTGTC TCTACACCAA GAAGAGTGGG GCCCACTGA GGATCATCGA CCGGGGCTCA 4200
 GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGAAGGA TGAAGCCAGC 4260
 AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG 4320

ATGAACTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC 4380
 CCACTGGAGT GTGGCCAAAGG ATTCTCCCGAG CAGGAAAAATG GCCATTGCAT GGACACCAAT 4440
 GAATGCATCC AGTTCCCATTT CGTGTGCCCT CGAGACAAAGC CCGTATGTGT CAACACCTAT 4500
 GGAAGCTACA GGTGCCGGAC CAACAAGAAG TGCAGTCCGG GCTACGAGCC CAACGAGGAT 4560
 GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGCTG GAAACCAAGG 4620
 CCAAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTCTCTG 4680
 CCGGGTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCAG CACCCTTCTC 4740
 CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 473 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 15 MACPGGLPAR CSGMGLGPP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
 SPYYALRDRQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
 PPTTPAGLLG LPPLSGRDFS SSLGQASPDG RQGERVPVPC CRGGLRPTHE PEPFLLRPKS 180
 GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKSGSR YSIYIANYAY 240
 20 GNVGPDALIE MDPEASDLR GILALRDVAE EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
 GGDPEEADDE HSGDGSTSQL CRLGWKDGQF KEEAALVEE QREAGAAGVP RGRVRTALQT 360
 SKSHLADKNL FGPPCYYSVC APSPAHFFPA RQAPQHYPA PLVTQLMTHG RLAGKLARSV 420
 PHPRAPGMDP KCKGRHAEFG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCLAR 480
 ELGGPWSQAT QHLPALEYLD LGPEPILQRT DGDPRRRRDS PKVTQECHLV ATMPALGGLE 540
 25 GPCRVAKREI GRETGAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600
 LAWNQMEKEE GKIHGDEHPR FRLRKAREAE FPPGSSEEP LQFPSSGLRGS PVLQVGLGLA 660
 SATHCGSMGF LGGRGVSVGP ILSSASDIF CDNENGPNFL FHNRGDGTFFV DAAASAERRL 720
 AFIVHLKYHL CRDPFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS 780
 FLTQGLASSA HRRTLISLQGS QGAPPCILLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
 30 LSSERVNVGV DDPHQHGGRV ALADFNDRDG VDIVYGNWNG PHRLYLQMS T HGKVRFRDIA 900
 SPKFSMPSPV RTVITADFND DQELIIFNN IAYRSSANR LFRCSILARG SSSLTAGGRN 960
 GQEGELRIRR GGFPGPGQQA KVNTPGLMKK QKGRKDEDAW RGCGNAGQSL AKEPASAIAG 1020
 KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGYV VQSLPGKGAT GSNHYQEKGL 1080
 RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGVGLQSLPG KGATGSNHYH 1140
 35 RKGLRAPITT RKRGYGVQSL PGKGATGSNH YQEKGLRGP TTRKRGYGLQ SLPGKGATGS 1200
 NHYQEKGLQG PITTRKRGYR VQSLPGKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
 AMGSNHYQEK GLRAPITTRK RGVGVQSLPG KGATGSNVIR REHGDPLIEE LNPGDALPEE 1320
 GRGTGGVVD FDDGDMGLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVR TRFGAFARGA 1380
 KVVLYTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRRNVASGE 1440
 40 MNSVLEILYP RDEDLQDPA FLECGGQFSQ QENGHCMDTN ECIQFPFVCP RDKPVCVNTY 1500
 GSYRCRTNKK CSRGYEPNED GTACVGTTELG SRHTMTWKP PKKELQLSQG ICTPVWSPFL 1560
 PGCRLLLKRA QLQAPSTLL QKAPGPEAQ VYEQDQE

Seq ID NO: 474 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

1 11 21 31 41 51
 | | | | |
 50 ATGAGTGCAC TTTTCTTGG TGTGGGAGTG AGGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60
 CAAAACGTTT CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCCT CGGTGACTGG 120
 GCTGTGGGCA CCATGGAGCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180
 AAGGAAAAAG TAGACACACA CTAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240
 GGATTCTGTG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
 55 GACAACTCTG CAAGACAAAT GATCATGAAA GACAAAACT GGCACGATAA AGGCCAGCAG 360
 TACAGAAACT GGTTCCTGAA AGAGTTTCTT CGGTGAAAA GTGAGCTTGA GGATAACATA 420
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
 AATGTGGTGT CTGGCTCTCT CAGCATTTC TCTGGCATCC TGACCTCTCGT CGGCATGGGT 540
 CTGGCACCC TACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
 60 ATCAGAGCCG CTTTGACCGG GATTACACAG AGTACCATGG ACTACGGAAA GAAGTGGTGG 660
 ACACAAGCCC AAGCCCACGA CCTGGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
 GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
 GTACCGCATG CCTCAGCTC ACGCCCCCGG GTCACGAGC CAATCTCAGC TGAAAGCGGT 900
 65 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC 960
 ACGGATGTGG CCCCTGTAA GTCCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
 TCAAAGCACT TACATGAGGG GGCAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
 CAGGAGCTGG AGGAGAAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC 1140
 CAAGAATCTG GA

Seq ID NO: 475 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
 | | | | |
 75 MSALFLGVGV RAEEAGARVQ QNVPSGTDGT DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60
 KEKVSTQNL LLLTNEAWN GFVAAELPR NEADELRKAL DNLARQIMX DKNWHDKGQ 120
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTLVGMG 180
 LAPFTEGGSL VLEPMEELG ITAALTGITS STMDYGGKWW TQAQADLVI KSLDKLKEVR 240
 80 EFLGENISNF LSLAGNTYQL TRIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
 EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVE SKHLHEGAKS ETAELKKVA 360
 QELEEKLNL NNNYKILQAD QEL

Seq ID NO: 476 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

1 11 21 31 41 51

	ATGGGGACCT	CTCCGAGCAG	CAGCACCGCC	CTCGCCTCCT	GCAGCCGCAT	CGCCCGCCGA	60
	GCCACAGCCA	CGATGATCGC	GGGCTCCCTT	CTCCTGCTTG	GATTCTCTAG	CACCACCACA	120
5	GCTCAGCCAG	AACAGAAGGC	CTCGAATCTC	ATTGGCACAT	ACCGCCATGT	TGACCGTGCC	180
	ACCGGGCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATTTG	240
	ACCAACACAA	GGCTGCGCGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
	AATGGCATAG	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGGCCAAT	GATTGAGAAA	360
	TTACCTTTTG	CTGCTTGAC	TGACCGAGAA	TGCACTTGCC	CACCTGGCAT	GTTCAGTCT	420
10	AACGCTACCT	GTGCCCCCA	TACGGTGTGT	CCTGTGGGTT	GGGGTGTGCG	GAAGAAAGGS	480
	ACAGAGACTG	AGGATGTGCG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
	TCTAGTGTGA	TGAAATGCAG	AGCATACACA	GACTGTCTGA	GTCAGAACCT	GGTGGTGATC	600
	AAGCCGGGGA	CCAAGGAGAC	AGACAACGTC	TGTGGCACAC	TCCCGTCCCT	CTCCAGCTCC	660
	ACCTCACCTT	CCCCTGGCAC	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
	GTCCCTTCCT	CCACTTATGT	TCCCAAGGCG	ATGAACTCAA	CAGAAATCAA	CTCTTCTGCC	780
15	TCTGTTAGAC	CAAGGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
	TCAGCAAGGG	GGAAGGAAGA	CGTGAACAAG	ACCCTCCCAA	ACCTTCAGGT	AGTCAACCCAC	900
	CAGCAAGGCC	CCCACCACAG	ACACATCCTG	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
	GGCGAGAAGT	CCAGCAGGCC	CATCAAGGGC	CCCAAGAGGG	GACATCCTAG	ACAGAACCTA	1020
20	CACAAGCATT	TTGACATCAA	TGAGCATTGT	CCCTGGATGA	TTGTGCTTTT	CCTGCTGCTG	1080
	GTGCTTGTGG	TGATTGTGGT	GTGCAGTATC	CGGAAAGCT	CGAGGACTCT	GAAGAAAGGG	1140
	CCCCGCGAGG	ATCCAGTGTC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAACC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCCTGAAG	1260
	CTTGTAGCAG	CCCAAGTGGG	AAGCCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
25	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	CGGGGCTTAC	1380
	GCACTCTGCG	AGCACTGAGC	CATCCGGGGC	CCCGAGGCCA	GCCTCGCCCA	GCTAATTAGC	1440
	GCCCTGCGCC	AGCACCGGAG	AAACGATGTT	GTGGAGAAGA	TTCTGTGGCT	GATGGAAGAC	1500
	ACCAACCCAGC	TGGAAACTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCG	1560
	AGCCCCATCC	CCAGCCCCAA	CGCGAAACTT	GAGAAATTCG	CTCTCCTGAC	GGTGGAGCCT	1620
30	TCCCACACAG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCTT	TCTCCGCTGT	1680
	GACTCTACAT	CCAGCGGCTC	CTCCGCGCTG	AGCAGGAACG	GTTCTTTTAT	TACCAAAGAA	1740
	AAGAAGGACA	CAGTGTTCGG	CGAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
35	GCTGAGGACA	AACTAGACCG	GCTATTTCGA	ATTATTGGAG	TCAAGAGCCA	GGAAGCCAGC	1920
	CAGACCTCC	TGGACTCTGT	TTATAGCCAT	CTTCCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence
Protein Accession #: NP_055267.1

40	1	11	21	31	41	51	
	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLLGFLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDC	PAGTVVSEHC	TNTSLRVCSS	CPVGTFTRE	NGIEKCHDCS	QPCPWPMIEK	120
	LPCAALTDRE	CTCPPFMFQS	NATCAPHTVC	PVGWGVRRKG	TETEDVRCKQ	CARGTFSDVP	180
45	SSVMKCKAYT	DCLSNLTVI	KPGTKETDNV	CGTLPSFSSS	TSPPSGTAIF	PRPEHMETHE	240
	VPSSTYVPGK	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLFNLQVNVH	300
	QQQPHRRHIL	KLLPSMEATG	GEKSSPTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
	VLVIVVVCIS	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNRKWIYY	CNGHGDILK	420
	LVAAGVGSQW	DKIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
50	ALRQHRNRDV	VEKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSPNAKL	ENSALLTVEP	540
	SPQDKNKGFF	VDESEPLLR	DSTSSGSSAL	SRNGSFITKE	KKDTVLRQVR	LDPCDLQPIF	600
	DMMLHFLNPE	ELRWIEEIPQ	AEDKLDRLFE	IIGVKSQEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

60	1	11	21	31	41	51	
	GCTCTGCCCA	AGCCGAGGCT	GCGGGGCGGG	CGCCGGCGGG	AGGACTGCGG	TGCCCCGCGG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACTTGAC	CCTGTTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCGCGGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCGCCCGTG	180
	AGTCCGGCCG	AGCCACCTGA	GCCCGAGCCG	CGGGACACCG	TGCTCTCTGC	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCTT	GAGGAGCTGG	CTCGCCGCCC	CATGGGCGCG	GCTGCGCCCT	300
65	CGGCCACCGC	TGCTGCTGCT	CCTGCTGCTG	CTGCTCCTGC	TGCAGCCGCG	GCCTCCGACC	360
	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGCC	ATTCTCTAGA	420
	TTGGAAGCTG	AACACTCTC	CACCTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTAGCTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTGCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	GCAGTGCAGC	600
70	TTCAAGGGCA	AGGACCCACA	GCGCGACTGT	CAAACTACA	TCAAGATCCT	CCTGCGGCTC	660
	AGCGGCAGTC	ACCTGTTTAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTCAACCT	GGCAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAAGATGG	780
	AAGGGCCGTT	GTCCTTTCGA	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGAGCCCAA	900
75	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCCTGA	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCTTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGG	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
80	TCTTTCCTCA	AGGCCCTAGT	GCTGTGCTCA	CGGCCCGACG	ATGCTTCCCT	CTTCAACGTG	1200
	CTGCAGGATG	TCTTCAAGCT	GAGCCCCAGC	CCCCAGGACT	GGGTGACAC	CCTTTTCTAT	1260
	GGGGTCTTCA	CTTCCCATGT	GCACAGGGGA	ACTACAGAAG	GCTCTGCCGT	CTGTGCTTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGCTTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCGGGTG	CCCAACCCCC	GGCCTGGAGC	GTGCATCACC	1440
	AACAGTGCCC	GGGAAGGAA	GATCAACTCA	TCCCTGCAGC	TCCAGACCG	CGTGTGTAAC	1500
85	TTCTCAAGG	ACCCTTCTCT	GATGGACGGG	CAGGTCCGAA	GCGCATGCT	GCTGTGTCAG	1560
	CCCCAGGCTC	GCTACACGCG	CGTGGCTGTA	CACCGCGTCC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCT	TCTGGGCGAC	TGCTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGCACA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAACTCG	1740

CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCTCAC ACTCGGGCGT AGTCCAGGTG 1800
CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGACCCCC 1860
TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTGAGCC TCTACAGGCC TCAGCTGGCC 1920
ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT 1980
TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
CAGCCCCAACA CAGTGAACAC TTTGGCTTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100
TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCTCCTT GCCACGTGCT ACCCACTGGG 2160
GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGTGGTCT ACTAGAGGAG 2220
GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280
CAAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCTGTG GAGTGCACCA 2340
GCTGTGGGCA AGGCCAGCTG GGGTGCAGAC AGGTCTCTACT GGAAGGAGTT CCTGTGTATG 2400
TGCAAGCTCT TGTGTCTGGC CGTGTCTGCT CCAGTTTAT TCTTGTCTTA CCGGCACCGG 2460
AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA CGGTGCACCC CAAGACCTGC 2520
CCTGTGGTGC TGCCCTCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG 2580
CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC 2700
CCCCGGCCCC GGGTCCGCTT TGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760
TCCAGAGGAC GCTGCCCTGG CTTACAGGGG TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
TCCCTTCCGC TCTGCTCTTC GTGGAAACAG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880
GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCAACC AGACACCCAA 2940
ACAGCCGTGG CCCAGAGGT CCGTGGCCAA TATGGGGGCC TGCTAGGTT GGTGGAAACAG 3000
TGCTCCTTAT GTAAACTGAG CCCTTTTGTT AAAAAACAAT TCCAAATGTG AAACTAGAAT 3060
GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA 3120
GGGGTGTCTG GGTGCTATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAC 3180
TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
CAGGACCCAG TTGGGCTGGG TGGTCTTCTG CTGTCCAGTC AGCCGAGGAT GTAGTTGTGT 3300
TGCGCTGCTT CCCACCACT CACGGACCCG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360
GGTCTTGGGC TCGGACCCAA CTCTGGGACC TTCCAGCCT GTATCAGGCT GTGGCCACAC 3420
GAGAGGACAG CCGGAGTCA GGAGAGATT CGTGACAATG TACGCCCTTC CCTCAGAAAT 3480
CAGGGAAGAG AGTGTGCGCT GCCTTCTCTC GTTGTGTGCT GAGAACCCTG GTGCCCTTC 3540
CCACCATATC CACCTCGCT CCATCTTGA ACTCAAACAC GAGGAACATA CTGCACCCCTG 3600
TGCTCTCTCC CAGTCCCCAG TTCACCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA 3660
TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
ATGCACTTTA TGTCTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
Protein Accession #: XP_044533.3

1 11 21 31 41 51
MLRTAMGLRS WLAAPWGALE PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFEAEHISNY TALLLSRDRG TLYVGAREAL FALSSNLSPL PGGEYQELLW GADAEEKKQC 120
SPFKGDPQRD QNYIKILLP LSGSHLFTCG TAAFSFMCTY INMENFTLAR DEKGNVLLED 180
GKGRCPDFDN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAP 240
VASAYIPESL GSLQDDDKI YFFPSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKALQLC SRPDGPFPPN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRVF SGLYKEVNR TQQWYTVTHP VPTPRGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHFLMD QQVRSRMLLL QPQARYQORVA VHRVPLGHT YDVLFLGTGD GRLHKAHSV 480
PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSGSG KHVSLYQQL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQNTVNTLA CPLLSNLAIR LWRNGAPVN ASASCHVLPT GDLLLVGTQQ LGFEQCWSLE 660
EGFQQLVASV CPEVEDGVA DQTEGGSVV VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
MCTLPVLAVL LPVLPLLRYH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 480 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

1 11 21 31 41 51
GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60
GCCCAGAAAG AGAAGCTCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCCTG 120
AGCACCTGCG CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCTC 180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
AGTGGGACAC CCGACATCTT AACCGGCAC TTCACAATG ATGACTTTGA GATTGGGCGT 300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTT 360
ATCGTGGCGC TCAAGGTCTT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
CTGCGCAGAG AGATCGAAT CCAGGCCAC CTGCACCATC CCAACATCCT CGCTCTCTAC 480
AACTATTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
CTCTACAGG AGCTGCAGAA GAGCTGCACA TTGACGAGC AGCGAACAGC CACGATCATG 600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG 720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCCTGA CTACCTGCCC 780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGTGG ATCTGTGTG CATTTGAGTG 840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCTTTGAGA GTGCATCACA CAACGAGACC 900
TATCGCGCAG TCGTCAAGGT GGACCTAAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
GACCTCATCT CCAACTGCT CAGGCATAAC CCTCGGAAC GGCTGCCCTT GGCCAGGCT 1020
TCAGCCCAAC CTTGGGTCCG GGCCTAATCT CGGAGGGTGC TGCTTCCCTC TGCCCTTCAA 1080
TCTGTGCGCT GATGTGCTCT GTCAATCACT CCGGTGCGTG TGTGTGTATG TCTGTGTATG 1140
TATAGGGGAA AGAAGGGATC CTAACCTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 481 Protein sequence
Protein Accession #: NP_004208

1 11 21 31 41 51

MAQKENSYPN	PYGRQTAPSG	LSTLPQRVLR	KEPVTPSALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTPDILTR	HFTIDDFEIG	RPLGKGKFGN	VYLAREKKSH	FIVALKVLFK	SQISEKGVSH	120
QLRRSEIQA	HLHFNILRL	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKRVVHRD	IKPENLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGLDLYL	240
PPEMIEGRMH	NEKVDLWICG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLPLAQ	VSHPWVRAN	SRRLVPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1	11	21	31	41	51	
AGAACGGCTT	CCGCGCGGAG	CTGTGCAGCT	CCTTATCATG	GGGACAATTC	ATCTCITTCG	60
AAAACCCACAA	AGATCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTTG	TAGCAGCTGA	120
CCGAAGGTC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCCTTATGTG	TGCAGTTCTA	CTAATAGTAT	AGCTTTAACT	GCCTATACTT	ACCTGACCAT	240
TTTTGATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCATTG	GGTTTGAAAG	ATTAGAAATC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTTGGGAG	CTCTCTTTAT	ATTAAAAGAA	AGTGCAGAAC	GCTTTTGGGA	420
ACAGCCCGAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTITCAA	480
CCTGTTTCAG	ATGCTTTCTA	TTGGGAATAA	ACCTTTTGCT	TATGTCCTAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCGA	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCGAAT	GAATCCATTT	GTTTGTATTG	ATCTTGCTGG	660
AGCATTGTCT	CTTTGTATTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTGGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAAC	ACCACCCCAT	GTTATTGGTC	AGTTGGACAA	840
ACTCATCAGA	GAGGTATCTA	CCTTAGATGG	AGTTTTAGAA	GTCCGAAATG	AACATTTTGG	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCAATGA	AGAATTGCGA	GAGATGCCAA	960
TGAACAAATG	GTTCTTGCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAAT	TTCAAGGATG	ACTGGATTAG	GCCTGCCTTA	TTGTCTGGGC	CTGTTGCAGC	1080
CAATGTCCCTA	AACCTTTTCAG	ATCATCAAGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTTGAAC	CCAATTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAATTTTC	1200
ATTTAACT	CCTGGGAAAA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GGTCTCAATC	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGATTTGGAG	CAACTCAAGG	ATTGAGGACT	GGTTTACAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	GAATTGGACA	ACCAAGACCA	TGATAGACTC	TAACCTATT	1440
TTATAAGGAA	TATTGACTCC	TTGGCTTCCA	ATTTATTTAG	TAATCCAAC	TTGCATTGAC	1500
TGTTAATCA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTACATT	TCATGAAACC	1560
TATGAAACTA	TATTTTGTGA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCTTTAAATA	GGCTTCCTTT	AGAAAATGTG	TTCTTTTAAA	TTTGGATTTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGTCAGT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTGA	CATTACTAAG	ATACGATATT	TCTTTTTTTT	TCCGAGACGG	AGTCTTGCTC	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAACTTAAGG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTTGTGTT	GTTTTGTGAG	ATGGAGTCTC	ACTCTGTGCG	CCAGGCTGGA	1920
ATGCACTGGC	ATGATCTCAG	CTCACTGCAA	CCTCTGCTCT	CTGAGTTCAA	ATGATCTCC	1980
TGCCTCAGCC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTAA	GTAAGACCGG	GGGATTTTAC	CATGTTGGCC	AGGCTGGTCT	TGAACCTCTG	2100
ACCTCATGAT	CCACCCACCT	TAGCCTCCCA	AAGTGTCTGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTTCTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAATGTCTG	TTCAAAAAGT	AAAGTCTCTC	TTTATAGCTT	TTCCAAACCT	2280
AATTGCTAAA	TTTTTCTTTG	AGGTTCTCTC	GAATTATGTC	TTACAACTA	AAAGCAAAAA	2340
TTTTTAGCAG	AAATTTTGGG	ATACATTTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

1	11	21	31	41	51	
MGTIHLFRKP	QSPFGKLLR	EFRLVAADRR	SWKILLFGVI	NLICTGFLLM	WCSSTNSIAL	60
TAYTYLTIFD	LFSMTCLIS	YWVTLRKPS	VYSFGFERLE	VLAFASTVL	AQLGALFILK	120
ESAERLEQ	BIHTGRLLV	TFVALCFNLP	TMLSIRNKP	AYVSEAAST	WLQEHVADLS	180
RSLCGIIPGL	SSIFPLRMP	FVLIDLAGAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMYPMVS	GKVLQTTTP	HVIGQLDKLI	REVSTLDGVL	EVRENEHFWL	GPGSLAGSVH	300
VRIRRDANEQ	MVLAHVTRNL	YTLVSTLTQ	IFKDDWIRPA	LLSGPVAANV	LNFSDDHVIP	360
MPLLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTRPYG	FGLNHGHTPY	420
SSMLNQGLGV	PGIGATQGLR	TGFTNIPSR	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCCGCGGC	GGGAGCTGAG	CGAGGCGGAG	CGGCCCGCGC	TCCGGGCCCC	GACCCCTCCC	60
CCGCGGCGGC	GTAGCGCGCC	CCAGAGCTG	GGCATCAAGT	GCGTGCTGGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCCT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCCACTG	CGCTGGACAC	CTTCTCTGGT	ACGTACGTTT	AATCGCCCGT	GCGGCGCGGT	240
GGCTGCGGGC	GGCTGTGCA	CCGGGAGCT	GGGCGGGCGC	TCTGCGGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCCC	CGAGGTGGCG	CTGGTGGCGC	CCAGGACGCT	360
CTTCTCTAAT	CAGGCTCTCC	CCGCCCGGCC	CCTGCAGTGC	AAGTCTCTGT	GGATGGAGCT	420
CCGGTGGCGA	TGAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTTGACCG	ACTTCGTTCC	480
CTTTGCTACC	CGGATACCGA	TGCTTCTCTG	GCGTGCTTCA	GCGTGGTGCA	GCCAGCTCC	540
TTTCAAACA	TCACAGAGAA	ATGGCTGCCC	GAGATCCGCA	CGCACAAACC	CCAGGCGCCT	600
GTGCTGCTGG	TGGGCAACCA	GCGCGACCTG	AGGGACGATG	TCAACGTACT	AAATTCAGCTG	660

GACCAGGGGG GCGGGGAGG CCCCCTGCC CAACCCAGG CTCAGGCTCT GGCCGAGAAG 720
 ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
 TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAGGTG TGCACACCT CTCCGCTGC CGCTGGAAGA AGTTCCTCTG CTTCGTTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACPSVVQPSS 180
 FQNI TEKWL P EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK 240
 IRACCYLECS ALTQKNLKEV FDSAILSIAE HKARLEKRLN AKGVRTL SRC RWKFPFCFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGCG GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
 GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTCTCTCTGT CAAATCTCTG TGGATGGAGC TCCGGTGGCG 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTT CTTTGTCTAC 300
 CCGGATACCG ATGTCTTCTT GCGTGCTTTC AGCGTGGTGC AGCCAGCTC CTTTCAAAAC 360
 ATCAGAGAGA AATGGCTGCC CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCACCC AGGCCGACCT GAGGGACGAT GTCACCGTAC TAATTCAGCT GGACGAGGGG 480
 GGCCGGGAGG GCGCCGTGCC CCAACCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC 540
 TGCTGCTACC TTGAGTGCTC AGCCTTGAGC CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660
 GTGCGCACCC TCTCCGCTG CCGCTGGAAG AAGTCTCTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSP VQLVDGAPVR IELWDTAGQE DFDRLRLSLCY PDTDVPLACF SVVQPSFPQN 120
 ITEKNLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPO AQGLAEKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKRLNAGK VRTL SRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 | | | | |
 GGCACCGATT CGGGGCTGCG CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGCGGCGC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACACAG TAAGCAAGCA 240
 CCTCACAAA CTTTAGCAGC AAGATTCTAT GATGGTCATA TCACCTTTCA AACAGCGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCAG ACTACAAAAA AACTGCAAC CACCAGCCCA 360
 ATTACCTACA CCCTGGTCC CACCCAGGCC ACACCAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCTTTATT CACTGCCACC CACCATCACC 480
 CCACAGCTCT ATACAGCTGG AACCACTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACACAGC CACCTTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
 ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGCG AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCCTGCTCC ACGGTCTCTG GGGCCACCCCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAG GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CGGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTACCAA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAACAACAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
 TACACAATTG TGCTTCTCTG GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
 GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCGGGGGGGA ATGAAAAATA TGGAAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAATTT CCCTCAGAGT GTGGTCTCTT CAAACAATGT AAACCCCAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTATTATTA TGAAGATAT AGTGAGCTGT TTAATTTCTA GTTTCCTTTA GAATATTTTA 1560
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
 ATTTTATTTT ACCCTGTATC TTAACAAAGC CTTTGTCTTG TTATCAAATG GACTTTTCAGT 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGGAGAC GGAGTTTCAC TCTTGTCAAC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 TGATTCTCCT GCTTCAGCTT CCGGAGTAGC TGGGATTACA GGCACACACT ACCACGCTG 1980
 GCTAATTTTT GTATTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGGC CCGGCTCTTA AATGTTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG 2160

GTTGTCTAAG TGTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 CTTGATGACT CCGTCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAG GCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATTCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACCT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460
 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTGA 2520
 CCTACAAGAA CAATGACACC ACACCTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCAG ATAACAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAACAAT TAGTCAGTTG CTCATTTTAA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTITGA TAATAGAGAA 2820
 ACTTCGCTAA CCACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880
 TTCTGCACTT CATATCCATA TTTCTTATG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAAITTTTAT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCTT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
 Protein Accession #: NP_055213.1

1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPPAKQAP 60
 HQTLLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPY TYTLVTTQAT PNNSHATFPV 120
 TEVTVPSPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNNT QPSNQTLPLA TLSIALHKST 180
 TGQKPDQPTH AVGTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCIKA 240
 EMGIQLIVQD KESVFSRRY FNIDPNATQA SGNCGRKSN LLLNFQGGFV NLTFTKDEES 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL 360
 QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRQCS SGYQRI

Seq ID NO: 490 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAAT 300
 AAAGGACAAC GATGCCATAA TCCCAAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAAGA ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGT GACTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCAGACA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTGATT ATACATTCTAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTCC 960
 CCAAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TGTTCATGTC CTATATATCT TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAATAAAAA AAA

Seq ID NO: 491 Protein sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPFMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNP

Seq ID NO: 492 DNA sequence
 Nucleic Acid Accession #: NM_000577.1
 Coding sequence: 41..520

1 11 21 31 41 51
 GGCACGAGGG GAAGACCTCC TGTCTATCA GGCCTCCCC ATGGCTTTAG AGACGATCTG 60
 CCGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
 GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAATGT 180
 CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGCAAGT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCTTT 360
 CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCTGCC CCGTGTGGTT 420
 CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
 CGTCATGGTC ACCAATTTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCTGCCTGT 540
 TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCC 600

GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTCGCA CAAAGCCCTT CCATGTGGCC 780
 TCTGCATTCA GGATCAAAAC CCGACCACTG GCCCAACTCT CTCTCTCTTT GCCACTGCCT 840
 CTCTCTCCCT CATTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
 ACCAAGTGGC TCCACACCCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGGGTT TGTGAAAAT GAAAATTAGG ATTTTCATGAT TTTTTTTTTT CAGTCCCCGT 1020
 GAAGGAGAGC CCTTCATTGT GAGATTATGT TCCTTCGGGG AGAGGCTGAG GACTTAAAT 1080
 ATTCCTGCAT TTGTGAAATG ATGGTGAAG TAAGTGGTAG CTTTTCCCTT CTTTTCTTC 1140
 TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCCATA 1200
 ATTTTTTTTT TCCTTTTAAA ACATCTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTG 1260
 CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC 1320
 TCCTATCAGA AGTTTCTCAG CTCCTCAAGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCCT 1380
 TCTTCCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTCTG GCACTTGGAG 1440
 ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
 CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAT GCCTAAAAA AAAAAAAA 1680
 AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGNPNVLE EKIDVVP IEP 60
 HALEFLGHHG KMCCLSKVSG DETRLQLEAV NITDLSENK QDKRFAPFIR DSGPTTSPES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQED

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCGCGCGCGC CCGCGCGCGC CGCGCGCGCC 60
 GGCTTTTGTG GTCTCCGCTT CCTCGGCGCG CGCGCGCTCT GGACCGCGAG CCGCGCGCGC 120
 CGGGACCTTG GCTCTGCGCT TCGCGGCGCG GAACTGCGCA GGACCGCGCC AGGATCCGAG 180
 AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CCGGCGCGCG CATGGAGCTC CCGGCGCGAG 240
 GCTGTGGTGT GCTATGTGCG CGCGCAGCGC TGGTCCGCTG CGCGCGCGGG GACCGCGCCA 300
 GCAAGAGCGG GAGCTGCGCG GAGGTCCGCG AGATCTACGG AGCCAAGGGC TTCAGCCTGA 360
 GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGTGTCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CCGCGCTCCG GGACAGCAGC CGCGTCTGCG AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540
 TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGTGCGAG GCCACCTTCC 600
 CCGGCGCCTT CCGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTGCGCG GGTGCCAACC TGCACTGGA GGAGAGCGTG GCCGAGTTCT 720
 GGGCCGCGCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCTGTATG 780
 ACTACCTGGA CTGCTCGGGC AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCCCCGA 840
 GAGAGCTGCG CCGTGGGGCC ACCCGTGCCT TCGTGGCTGC TCGTCTCTTT GTGCAGGGCC 900
 TGGGCGTGGC CAGCGACGTG GTCCGGAAGG TGGCTCAGGT CCGCTGCGG CCGGAGTGCT 960
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCTT GGGAGTCCCC GCGCCAGGC 1020
 CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCGT TGCCCAACCG GCCGACCTGG 1080
 ACCCGAGTGT GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140
 CATCGGGTGT GAGAGTGTG ATCGGAGCGG TGCAACGCTG GCTGGCGGAG GCCATCAACG 1200
 CCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAACCCCA 1260
 AGGTCAACCC CCAGGGCCTT GGGCTGAGG AGAAGCGCGG CCGGGGCAAG CTGGCCCGCG 1320
 GGGAGAGGCC ACCTTCAGCG ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 GCGACGTCCA GGAATTCTGG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTAGTACG CGTGTCTGGA ACGGGATGCG CAGAGGCCGG TACCTCCCGG 1500
 AGGTCAATGG GTACGGCTCG GCCAACAGG TCAACAACCC CGAGGTGGAG GTGACATCA 1560
 CCAAGCGGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC 1620
 TGCGCAGCGC CTACAACGGC AACACGCTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
 GCTCGGCGAG CGGTGATGCG TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCCC TTGACCCATG CCTTCCACGG CCTGTGAGG CAGGAAGGAC 1800
 AGAAGACCTC GGTGCGCAGC TGCCCCCAGC CCGCGACCTT CCTCTGCGCC CTCTCTCTCT 1860
 TCCTGGCCCT TACAGTAGCC AGGCCCGCGT GCGGTAACCT GCCCAAGGC CCCAGGGACA 1920
 GAGGCCAAGG ACTGACTTGT CCAAAAATAC AACACAGAG ATATTAAAT CACCTCAGCC 1980
 TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
 GTCCCAAGCC CAGGCTGGC CTGCGCTGCC TTTCTGCTTT TTAATTTTGT ATGAGGTCCT 2100
 CAGGTGAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160
 TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGACCGCGCG CAGAAGCAGC CCCTCGAGGC 2220
 CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGGCC AGCCCTGGCC CACCCCCAG 2340
 CCTCCAGAGA AGCCCCGACG GCGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
 TCTGAGATGA TGCATGATGC CCTCCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTCC 2460
 CTGCGCCCTT GAGGGGCCCC AGCCTGTGCA GGGTGAGGCC TGAGACAGCA CCACTGTCTG 2520
 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCAAGTAGG GGCCTCCAT GCGCAGATGA 2580
 GGGGCCACTG ACCACCTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG 2640
 GGAGGCGAGC TGGGCTCTGC CAATGTGGGC TGCCCCCTCG ACACAGGGCT CACAGGGCAG 2700
 GCCTTGTCTG GGTTCAGGGC TGTGGAGGA CCCCAGGGGC TGAGGAGCAG CCAGGACCCG 2760
 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTACCGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCTTC GGCTGTCAAC TGCTCAGAG GATGTGTTG GCTGGTGAGA 2880
 CCGCGCACTG CACACGGGAA TCCTTAGGTC CCTTCCGAC CCAGCCAGCT GCACCTGAGG 2940
 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAACATGCG ATCCATTAC TGACACTTCC 3000
 TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTGAGGGC CCGCAGGGCC 3060
 CACCTTGGAC CCGTGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120

CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180
TGTGGTGTGG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
TCCTGAACCG ACTGACCCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC 3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTGAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
CCTTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
CCTTCTCCA CAAGGTCCCC CCACCGCTCA GTGTACGGG GTGACGTTGT TTCTTTTGAG 3660
TCCTTGTATG AATAAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
Protein Accession #: NP_002072.1

1 11 21 31 41 51
MELRARGWNL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSQVP QAEISGEHLR 60
ICPQGYTCCT SEMEENLANR SHALETALR DSSRVLQAML ATQLRSFDDH FQHLNDSER 120
TLQATFPFAG GELYTONARA FRDLYSELRL YVRGANLHLE ETLAEFWARL LERLFLQLHP 180
QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFAVA RSFVQGLGVA SDVVRKVAQV 240
PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVKLGCL ANQADLDAEW RNLLDSMVL 300
TDFKWTSGV ESVIGSVITW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360
RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMLSTA SDDRWNMGMA 420
RGRYLPVVMG DGLANQINNP EVEVDITKPD MTRRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
ASDDGSGSGS

Seq ID NO: 496 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

1 11 21 31 41 51
GGGCGAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA 60
AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA 120
GGGGTCTGGA CTCAGCTTT CTGGAAGGCA GTACAGCGG AATTCTGGC CATGCTTATT 180
TTTGTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
GTGACATGG TTCTCATCTC CCTTTGCTTT GGAATCAGCA TTGCAACCAT GGTGCAGTGC 300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC 360
AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CTTGGGAGTC 480
ACCATGGTTC ATGGAATCTT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC 600
TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTGTC AATCAATTAT 660
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
GAAAACCATT GGATATATTG GGTGGGGCCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
TATGATATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
AAAGCTGCCC AGCAAAACAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGSTA 900
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960
GAGGAGAAGA AGGGGAAAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020
CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCTCTCAG ATTTCTCTCC ACCCATTAAG 1080
GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGTG GTTTCATGTC ATATTACTCA 1140
GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
TCCAAATCTA AAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260
TCTAGTTACC TTTCATTAA ACCTAATTTT AACCGTGTGT CAAGATTGAG TTAAGTCTTG 1320
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCTCT CTCTACTGGA ATATTGGTAT 1380
AGTCAATTCT TATTGAATA TTTATTCTAT TAACTGAGT TTAACAATGG C

Seq ID NO: 497 Protein sequence
Protein Accession #: NP_001641.1

1 11 21 31 41 51
MSDRPTARRW KGKGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60
GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
AQCLGAIIGA GILYLVTPPS VVGGLGVTMV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
KRTDVTGSIA LAIGFSVAIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYWVGPPIG 240
AVLAGGLYBY VFCPDVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH 300
VIDVDRGEK KGKQSGEVL SSV

Seq ID NO: 498 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

1 11 21 31 41 51
CCCCCTTGTG ATTAATACAT TAAAAAGATT CAATCTTTAC CCTGAGGTAA TTTTGGCCAG 60
TTGGTACCGG ATTTATACCA AAATAATGGA CTTGATTGGT ATTCAAACCA AGATATGTTG 120
GACGGTTACC AGAGGAGAAG GACTCAGTCC TATTGAAAGC TGTGAAGGAT TGGGAGATCC 180
TGCTTGCTTT TATGTTGCTG TAAATTTTAT TTTAAATGGA CTAATGATGG CATATTCTT 240
CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTACAG TGTGTGCTT 300
CTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
CTCATATCCA TTTCTGTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
ACTTTATAGA GGAAGCTTGA TTGCACTCTG CATTTCCAAT GTATTTTCA TGTCTCTTG 480
GCAGTTTGCT CAGTTGTGAC TTCTTACTCA GATTGCATCA TTATTGTCAG TATATGTTGT 540
CGGGTACATT GATATATGTA AATTACGGAA GATCATTAT ATACACATGA TTTCTCTTGC 600
ACTTTGTTT GTTTGTATGT TTGGGAACCT AATGTTATTA ACTTCTTATT ATGCTTCTTC 660
TTTGTAATT ATTTGGGGTA TTCTGGCAAT GAAACCACAT TTCTGAAAA TAAATGTATC 720

5 TGAACCTAGT TTATGGGTTA TTCAAGGATG TTTTGGTTA TTTGGAAC TG CATACTTAA 780
ATACCTTGACA TCTAAAATTT TTGGTATTGC AGATGACGCT CATATTGGCA ACTTACTAAC 840
ATCAAAATTC TTTAGTTATA AGGATTTTGA TACTTTATTG TATACCTGTG CAGCGGAGTT 900
TGACTTTATG GAAAAGAGAGA CTCCACTGAG ATACACAAAG ACATTATTGC TTCCAGTTGT 960
TCTTGTAGTG TTTGTTGCTA TTGTTAGAAA GATTATTAGT GATATGTGGG GTGTCTTAGC 1020
TAAACAACAG ACACATGTAA GAAAACACCA GTTTGATCAT GGAGAGCTGG TTTACCATGC 1080
ATTGCAATTG TTAGCATATA CAGCCCTTGG TATTTTAATT ATGAGACTAA AACTCTTCTT 1140
GACACCACAC ATGTGTGTTA TGGCATCACT GATCTGCTCA AGACAGCTAT TTGGATGGCT 1200
CTTTTGCAA GTACATCCTG GTGCTATTGT GTTTGCTATA TTAGCAGCAA TGTCATACA 1260
AGGTTGAGCA AATCTGCAAA CCCAGTGGAA TATTGTAGGG GAGTTCAGCA ATTTGCCCCA 1320
AGAAGAACTT ATAGAATGGA TCAAATATAG TACTAAACCA GATGCAGTGT TTGCGGGTGC 1380
CATGCCACG ATGCGCAAGT TTAAGCTCTC TGCACTTCGG CCCATTGTGA ATCATCCACA 1440
TTATGAAGAC GCAGGCTTGA GAGCCAGAAC AAAAATAGTA TACTCAATGT ATAGTCGGAA 1500
AGCAGCCGAA GAGTGAAGC GAGAACTGAT AAAGTTAAAA GTGAACATT ACATTCTAGA 1560
AGAGTCAATG TGTGTAAGAA GTCCAAAGCC TGGTTGCGT ATGCTGAAA TTTGGGATGT 1620
AGAAGATCCT GCCAATGCTG GGAAGAACTCC CTTATGTAAC CTCTTGGTGA AGGATTCCAA 1680
ACCTCACTTC ACCACTGTAT TCAGAACAGG TGTTTACAAA GTCCCTAGAAG TTGTAAGAA 1740
ATGACTGCTA CATGACCTGC TGCTACGGA GAACTACATC TGTAATGGTT TTAATGTTTT 1800
GCTAAGTCAT GTGTGTTTCA TATCCCAAAA ACTTTTATAG GTAACGTGTT TCAAAATAGAA 1860
AACGTTTTAT TTGTTCAATT TGAATGTCAT TCTAATTATA AAAATGACTT ACACCTTTAT 1920
CAATTGGTTA CTATTTCAAT GCACCTTTA AAATTGCTA TGCAAAAGAG TATATGCTTG 1980
TACTTGACTT TAATATTGTT GCTAAAGTGA GCAAAGCTAC CTGTATAAAG AAAACACAGT 2040
GGGTGTGAC AAGGATGACA TGAAATATA GGACAATTCT GACAATGTAG GGGCTGATTT 2100
TATAGTGTAA GACTATTTAA TGCCCTTGC TTCTTTTTT TCCTCTTGC TCTTGTCTTT 2160
25 TGGACATTT AGTGATTGTA AGTTCCTCGG TCATGTCAGC CCCTGTCATC AACTTGAGTT 2220
ACAGTAGATG GGGCAGACAT GAGATGTTTG CTATATAAAA CTATCTGTTT GTTTTACTTC 2280
CTTGTGCGCT TTTGTTCTC TGTTCTCTTG TTAATGAAGC TTTTCCCTGCC CATTATTAAT 2340
CCAACTCTCT GGACCTTGTG GTTAGGAAAT TCCCTAACT TCCAGCCATA TGGCATTATC 2400
GTGTCTCTTT CTCTCTCTCT CTGTCTCTCT CTCTCTCTCT CTCTCTCTCT TTTTCTGTCA 2460
30 AATAAGTACT GTTTACTCAT TTAGTTGCTT ATCAAGTACT TATCTTGGT TTTAAAAAAA 2520
ATTAATGGTA ACTGATTTTT TCTCATTTTT AGCATTATTC AAATGTTTAT ATTTTAATAC 2580
CTTTAAACCA CTTTAAAGTT TTTTCATGTT TAATTATAGT TTTAAGAAAA ACTATTTTGA 2640
ACAACCCCAA ATATAGTGCA TCTAGAAACT AATGTATATT TGATTAGACA TCATTATATAG 2700
TGGAACAGTA GACTGTAGTA CATGGTAATT TTTCTTTTAC TATTAAGATA CAATAAAAA 2760
35 TGACTAATT TGCTGTCAA AATGTAAAGA ATAATGATA ATGGAGTTTT TTATATTTTA 2820
CTTTAAGAT TGCCTGTCTT TAATAAGACA AAGCCTTAAG CCTTATGTTA TAATTTTGGT 2880
TCTAAAAACC ATCATTTTCA TATAAGGAAT AAGTATATTT CGTCTCTCTC TTTAGTTTTT 2940
TTCTTCTAT TTTATTTTAT TTTGAAAAAT TTCTACACCT TCTTTGAATT CCTTGTATGA 3000
ATTTTTGTTT CTTAGAAGTT AATTTGTGTG AAATGAGATT CTTCAAAACG ATGAAACCTC 3060
40 ATAGCTCTGA GAAAGGTTTT TAGGGTTTTA AATTCCTAAGC AAAGCGTGAC TATGGCTGAC 3120
AGACTACACA TTTAATTATA CAGCTTCTCT TTCTTAACCA CAGGCAGATT AACCTCATTG 3180
TGGATTGTCC TTCAGACCTT AGTCTCAGG CATGGTTTCT GGTGCCCACT CCTGGAAGCC 3240
GCTGTTCCCT TTCTACCTTC TTACCAGAGC CCAAGGGCAG GCCTGGTCCC GGGGAAGCAG 3300
45 CAGCTTGCTG ACATAAGTCA CAGTCAAGG CTGAGGAGTG TGCCCTCAGA GAAGCACCGC 3360
CCCCCAGTCT TGTGCCAGCG CCTAGAGCCG CAGCTCCAG GGATGCTCCT TCCCTGGAGG 3420
CAGCCCAGGA GAGGGACTCT GGCAGCGTTC TTCAGATTTG TGGCCACTGT TTCTCATTG 3480
CTGTTTACT GTTTTATTTT CTTAGGCTTT TGCTAGTTTT AGAAAAAGG GAAGCAGCCC 3540
TTGATTTGTG GATTAAGAGC AACTTTGAG CGATGATGCA CAACAGTCCA GGAATATGGG 3600
CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660
50 TGCTTATCTG TGATTGTGTC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720
ATTTTTAAAA ATTATCTTT TACATTTATT TTATATTTTT CTCACCCCA GTAATTTCTC 3780
TCCAAGAGAG TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAATAAAGC ATTAATAATA 3840
CTATTATAAC TGCTTCATTT GCTGGGAACC ATTAAGTA ATATAAATTA GCTTTTTCCA 3900
GAGGATCTCT TTTGTAGCAG TGTTATGAA TGAACCCCC AGCAAAATAT GGCTATATAT 3960
55 TAGGGGAGCC AGTTTGGAGC AGAGGCCCTGA AGGTCCCTGC TATGCAGCCG TGGCCACAGC 4020
TCGACGCCCA AGCACTGTGG AGCATCCACA CCTTTGATGG CAATGCAGAT TGGTAGCAGG 4080
TTCCATAGCG GTACAAAACA GTATTAAAGC TCAGTGTGTT GCATATTGTT AGCATTTACA 4140
AATATTTTTG CTATTAGTAT AGGAAAGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200
60 TTGCTACAAC ATTTTCGAAA ACAAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260
AAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAAT 4320
GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380
ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 499 Protein sequence
Protein Accession #: BAA74900.1

70 1 11 21 31 41 51
PLVINILKRF NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSP IESCEGLGDP 60
ACFYVAVIFI LNLGMMALFF IYGTYLSGSR LGGLVTVLCF PFNHGECTRV MWTPLRESF 120
SYFFLVQLML LVTHILRATK LYRGLIALC ISNVFFMLFW QFAQFVLLTQ IASLFAVYVV 180
GYIDICKLRK IYIYHMSLA LCFVLMFGNS MLLTSYYASS LVIIWIGILAM KPHFLKINVS 240
ELSLWVIQGC FWFPGTVILK YLTSKIPGIA DDAHIGNLLT SKFPSYKDFD TLLYTCAAEF 300
75 DPMERETPLR YTKTLLLPV LVVFVAIVRK IISDMWGVLA KQQTHVRKHQ FDHGELVYHA 360
LQLLAYTALG ILIYRLKLFPL TPHMCMASL ICSRQLFGWL FCKVHPGAIV FAILAAMSQ 420
GSANLQTNW IVGEFSNLPQ BELIEWIKYS TKPDVAFAGA MPTMASVKLS ALRPIVNHPPH 480
YEDAGLRART KIVYSMSYRK AAEVVKRELI KLKVNYYILE ESWCVRRSKP GCSMPFIWDV 540
EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 500 DNA sequence
Nucleic Acid Accession #: NM_001276.1
Coding sequence: 127..1278

85 1 11 21 31 41 51
AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGAAGAGGCC CCTGTCTAGG 60
TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA 120

5
10
15
20
25
30

```

GCCAGAAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180
TGCTCTGCAT ACAAACGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300
GCCAATATAA GCAACGATCA CATCGACACC TGGAGTGGGA ATGATGTGAC GCTCTACGGC 360
ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTGC TGTGCGAGGA 420
TGGAACTTTG GGTCTCAAGG ATTTTCCAAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480
TTCATCAAGT CAGTACCGCC ATTCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540
TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAAATGAAG 600
GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660
TCTGCGGGGA AGGTCACCAT TGACAGCAGC TATGACATG CCAAGATATC CCAACACCTG 720
GATTTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCCTGGGAC CACAGGCCAT 780
CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCTG ACAGATTGAG CAACACTGAC 840
TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900
CCCACTCTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960
TCAGGACCCG GAATTCACGG CCGGTTCCACC AAGGAGGCAG GGACCCCTGC CTACTATGAG 1020
ATCTGTGACT TCTCTCGCGG AGCCACAGTC CATAGAACCC TCGGCCAGCA GGTCCCTAT 1080
GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAAG AAAGCGTCAA AAGCAAGGTG 1140
CAGTACCTGA AGGATAGGCA CTGGGCAGGC GCCATGGTAT GGGCCCTGGA CTGGATGAC 1200
TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
GCACTCGCTG CAACGTAGCC CTCTGTCTG CACACAGCAC GGGGGCCAAAG GATGCCCCGT 1320
CCCCCTCTGG CTCAGCTGG CCGGAGCCT GATCACCTGC CCTGCTGAGT CCCAGGCTGA 1380
GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTAGCTCA 1440
GCCTCGTGG GCAGAGAGGT AGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500
GACTCGGGAT TAGTACACTT TGTGTGATGA TTAATGGAAG TGTTTACAGA TCCCCAAGCC 1560
TGGCAAGGGA ATTTCTTCAA CTCCTGCCCC CTTAGCCCTC CTTATCAAAG GACACCATTT 1620
TGGCAAGCTC TATCACCAGG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680
TACCCCTGCG AAAGACCTTC TGAACCTTC ACTTAGGAAC GTAATCGTGT CCCTATCCT 1740
ACTTCCCTTT CTAATTCACA CAGCTGCTCA ATAAAGTACA AGAGTTTAA AGTGTGTTGG 1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCATC 1860
TCTTCTGGGT TCCTTCTCT GAGCCTTGGG ACCCTTGAGC TTGCAGAGAT GAAGGCCGCC 1920
ATGTT

```

Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

35
40
45

```

1 11 21 31 41 51
| | | | |
MGVKASQTGF VVLVLLQCCS AYKLVCIYTS WSQYREGDGS CFPDADRFL CTHIISFAN 60
ISNDHIDTWE WNDVTLYGLM NTLKNRNPNL KTLISVGGWN FGSQRFKIA SNTQSRRTFI 120
KSVPPFLRTH GFDGLDLAWL YPGRDRKHQF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
GKVTIDSSVD IAKISOHLDF ISMTYDFHG AWRGTTHHS PLFRQEDAS PDRFSNTDYA 240
VGYMLRLGAP ASKLVMIPT FGRSFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYIC 300
DFLRGATVHR TLGQVVPYAT KGNQWVGYDD QESVSKVQY LKDRQLAGAM VWALDLDDFQ 360
GSFCGQDLRF PLTNAIKDAL AAT

```

Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

50
55
60
65

```

1 11 21 31 41 51
| | | | |
GCTGCCTAGG GTCTGGAAGG CTCGGGCACC TCCCCTCTCC GGGGCTCCTG CTCCCACCCC 60
TCCGGCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCTG TGGCCGCGGT GCTTTTAATT 120
TTCCCCCAGC TCAGAACTCT GCTGCTCGGC CCCCAGGAGA GCAACAACTC AACCGGAAAG 180
ATGTGGAAGG TGTCACTCT GCTCTTCGTT TTGGGAAGCG CGTGGCTCTG GGTCTTGCCA 240
GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGCGGCG 300
GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACACGCGA AGACCGCTAT 360
AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAAACAG CATTCGCATC 420
GAGGATCTGC CAACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480
GCCTCAAACG TGGCCACACG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540
GTTGAGAAAG ATGTTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGTAC 660
TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720
TTCTGACTCT GTGGCCCTGT CCTGAGCTC GTGGGGAGAA GATGACCTCG GGAACATTG 780
CGGGCCCATT CAGATTCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840
TCACCAAGAT TGGTTCTTAA ACTTT

```

Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

70
75

```

1 11 21 31 41 51
| | | | |
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSSEDRY 60
KSLGTLTVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVGDGTQTT 120
VEKDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP

```

Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

80
85

```

1 11 21 31 41 51
| | | | |
CACTGCTCTG AGAATTTGTG AGCAGCCCCC AACAGGCTGT TACTTCACTA CAACTGACGA 60
TATGATCATC TTAATTTACT TAATTTCTCT GCTATGGGAA GACACTCAAG GATGGGGATT 120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
AGAAGCACGG TCTGGCAAA ACAGGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
TGAAGGCGGC CATCTGCAA CTTACAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300

```


TGTCGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATG TGAAGCCAGG 360
 GCCCAACTGT GGATTTGGAA AAATGCGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
 TGAAGATGAG GATGCTATT GCTACACCC ACACGCAAGG GAGTGTGGTG GCGTCTTTAC 480
 AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCTCAAT GAGTACGAAG ATAACCAAAT 540
 CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATTT 600
 TGACCTTGAA GATGACCCAG GTTGCTTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
 TGATGTCCAT GGCCTTGTGG GAAGATACTG TGGAGATGAG CTTCAGATG ACATCATCAG 720
 TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
 CCAATCAAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG 840
 TACTACTTCT ACTGGAATA AAAACTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
 AAAAAAAGGA TGATCAAAAC ACACAGTGTT TATGTTGGAA TCTTTTGGAA CTCCTTTGAT 960
 CTCCTGTGTA TTATTAACAT TTATTTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
 TAGGGAAAT TAGGAAATAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
 ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTT TCTTTTCAGT CATTTTCTA 1140
 TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCAT TTGAAATTTT GGAATCCTGC 1200
 TCTATGTACA GTTTGTATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
 TCATTGATTA TCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTTCT ATGATATGAA 1320
 TGTTTTATGC ATTATTTAAG CCGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCAATAAT 1380
 ATTTGTGCAA TAAATATCCT TGAACACACA AAAAAAATAA AA

Seq ID NO: 505 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MIILYLFLLL LWEDTQGWGF KDGIHFNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEARKIGFHF VCAAGWMAKG RVGYPIVKPG PNCQFPGKTI IDYGIRLNRS 120
 ERWDAYCYNP HAKECGGVFT DPKIIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDIIS TGNVMTLKLFL SDASVTAGGF 240
 QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 506 DNA sequence
 Nucleic Acid Accession #: NM_007115.1
 Coding sequence: 69..902

1 11 21 31 41 51
 | | | | |
 GAATTGCGAC TGCTCTGAGA ATTTGTGAGC AGCCCTAAC AGGCTGTAC TTCACTACAA 60
 CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
 GGGGATTCAA GGATGGAATT TTTTCATACT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180
 ACCACAGAGA AGCACGGTCT GGCATAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240
 GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCGACC AGAAAAATTG 300
 GATTTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
 AGCCAGGGCC CAACGTGATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGCTCTCA 420
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG 480
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA CGGTATTTCAT CTGAGTTTCT 600
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
 GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
 GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
 ATACAAGTAC TACTTCTACT GGAATAAAAA ACITTTTAGC TGGAAAGATT AGCCACTTAT 900
 AAAAAAATAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAACTCTT TGGAACTCCT 960
 TTGATCTCAC TGTATTATT AACATTATT TATTATTTT CTAAATGTGA AAGAAATACA 1020
 TAAATTTAGG AAAATTGGA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080
 ATCCCACTGC ATAGAATAAA CAATCGTTAA CATTTTCATA TTTTTCCTT TCAGTCATTT 1140
 TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCATTGAA ATTTTGAAT 1200
 CCTGCTCTAT GTACAGTTT GTATTACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
 TGAAATCATT GATTATTCTA CAAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
 ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTCAG GTCATTTTCA 1380
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 507 Protein sequence
 Protein Accession #: NP_009046.1

1 11 21 31 41 51
 | | | | |
 MIILYLFLLL LWEDTQGWGF KDGIHFNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEARKIGFHF VCAAGWMAKG RVGYPIVKPG PNXFGKTI IDYGIRLNRS 120
 ERWDAYCYNP HAKECGGVFT DPKIIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDIIS TGNVMTLKLFL SDASVTAGGF 240
 QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 508 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

1 11 21 31 41 51
 | | | | |
 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGGTGTC 60
 AAAGCCCAGG CCCGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120
 GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCCG 180
 CTAAGGAGCC CAATGCCGTG GCGCCGAAGG AGGTGGAGCT CATCCTTGTC AAGGAGCAGA 240
 ACGGAGTGCA GCTCACCAGC TCCACCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCC 300
 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCCT GTCCGTGATT GGCCTTGTCT 360
 TGGACCTGGC CAACGTCTGG CCGTCCCTT ACCTGTGCTA CAAAAATGGT GCGGTGCTCT 420

	TCCTGGTCCC	CTACCTGCTC	TTCATGGTCA	TTCGTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAAC	AGGGAAGGGG	CCGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAAGGTGT	GGGCTTCAAG	GTCACTCTCA	TCTCACTGTA	TGTCGGCTTC	TTCTACAACG	600
5	TCATCATCGC	CTGGGCGCTG	CACATCTCTT	TCTCCTCCTT	CACCACGGAG	CTCCCCTGGA	660
	TCCACTGCAA	CAACTCCTGG	AACAGCCCCA	ACTGCTCGGA	TGCCCATCCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGGCTCT	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGCACCTC	CACCAGAGCC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCTGT	GTGCTGGTCA	TGCTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCCTCA	960
10	CTGCCCTGCT	GTGCGTGGG	GTCAACCTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTCCGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	TGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
	TCTCCTCCGG	CTTGTCTGTC	TTCTCCTTCC	TGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
15	CCATCGGGGA	CGTGCCCAAG	GACGGGCCAG	GGTGTATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TCGCCACGCT	CCCTCTGTTC	TCAGCCTGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCACCC	1380
	TGGGTATGCA	CAGCGCCATC	GGTGGTATGG	AGTCAGTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCCAGCTGCT	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATGTCCTTG	GCGACCTTCC	1500
20	TCCTGTCCCT	GTTCGTGCTC	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCAAT	1560
	TTGACGCGGG	CACGTCCATC	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCTTGGT	1620
	TCTATGGTGT	TGGGCGATTG	AGCGACGACA	TCCAGCAGAT	GACCGGGCAG	CGGCCAGCC	1680
	TGTACTGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCTGCTTT	TCTCCTGTTT	GTGGTGGTGG	1740
	TCAGCATTGT	GACCTTCAGA	CCCCCCCCACT	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
	ACGCGCTGGG	CTGGGTCTATC	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCTT	1860
25	ACAAGTTCTG	CAGCCTGCCT	GGGTCTTTTC	GAGAGAAACT	GGCCTACGCC	ATTGCACCCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTTACGCTC	CGCCACTGGC	1980
	TCAAGGTGTA	GAGGAGCAG	AGACGAAAGC	CCCAGGAAGT	CATCCTGCAA	TGGGAGAGAC	2040
	ACGAACAAAC	CAAGGAAATC	TAACTTTTCA	GAGAAAGGAG	GGCAACTTCT	ACTCTTCAAC	2100
	CTCTACTGAA	AACACAAACA	ACAAAGCAGA	AGACTCCTCT	CTTCTGACTG	TTTACACCTT	2160
30	TCGCTGCCGG	GAGCGCACCT	CGCCGTGTCT	TGTGTGCTG	TAATAACGAC	GTAGATCTGT	2220
	GCAGCGAGGT	CCACCCGTTT	GTGTCTCCCT	CAGGGCAGAA	AAACGTCTAA	CTTCATGCTG	2280
	TCTGTGTGAG	GCTCCCTCCC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GGCCAGGGGG	2340
	CACGTGTGTT	TGAGGCGGGG	ATCACGATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCGGTG	2400
	CTCACAGTAG	CTTCTAGAC	CATTACTTTT	GCCCATATTA	AAAAGCCAA	TGTCCTGCTT	2460
35	GGTTTAGCTG	TGCAGAAGGT	GAAATGGAGG	AAACACAAAC	TTATGCAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCAGCAGA	GGCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGCTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	ACGAGAGAGA	AATAAACTC	CTTGAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCCTGT	GGGTCTTGT	GGTGTAGGGA	ACGGCCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	GACGCATGCA	GGGCCCCCAC	2820
	AGGAGCATGT	CCTATCCCTG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCAG	2880
	AACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCAG	GACGCATGCA	GGGCCCCCAC	2940
	TGGAGCGTGT	ACTACCCAG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	CCTCAGGAGC	CCACAGGAG	CGTGTACTAC	CCACAGGAGC	ATGCAGGGCC	3060
	CCCACAGGAG	CGTGTACTAC	CCCAGGATGC	ATGCAGGGCC	CCCACAGGAG	CGTGTACTAC	3120
	CCCAGGAGC	ATGCAGGGCC	CCCATGCAGG	CAGCCTGCAG	ACCAACACTC	TGCTGGGCTT	3180
	TGAGCCGTGA	CCTCAGGAA	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTGCAG	ATGGCTTTT	AAAATCATAT	TTACCTGTGA	3300
50	ATCAAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTCAAGAA	TAAATAGCAA	TACTGAGTGA	AGGATGTTGG	CCAAAAGCTG	CTTTCATGG	3420
	CACACTGCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCCCTAAG	3480
	TCGGTGGGCC	TGCTACCTGT	CTGCCGAGG	GCAGGGGCCG	TGCAGGGCCA	GTCATGGCTG	3540
	TCCCTTGCAA	GTGGACGTGG	GCTCCAGGGA	CTGGAGTGTG	ATGCTCGGTG	GGAGCGGTCA	3600
	GCCTGTGAAC	TGCCAGGAGC	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TTGCCCTCTG	3660
55	GGGAGGACCA	CAGGAGCGG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GCGGCTTCCC	CATTGCCTTC	TGGGAGGGA	CACAGAGGAC	AGTTTCCCCA	TGCCTTCTG	3780
	GTGTTTGAAG	ACAGACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCCGTGT	3840
	AGCAACCCAG	GTGTTGTTCC	TGCTGTGTTG	CCAATCTCTA	TTACGATCG	TGTGGGTCCC	3900
60	TAAGCACAA	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

65	1	11	21	31	41	51	
	MSKSKCSVGL	MSSVVAPEKE	FNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVEAQDR	60
	ETWKKIDFL	LSVIGFAVDL	ANVWRFPYLC	YKNGGGAFLV	PYLLEFMVIAG	MPLFYMELAL	120
	GQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFYFNVII	AWALHYLFSS	FTTELPWIHC	180
70	NNSWNSPNC	DAHFGDSSGD	SSGLNDFTGT	TPAAEYFERG	VLHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSGLKVWITA	TMPIYVLTAL	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAAATQVCF	SLGVGFGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVPSFLGY	MAQKHSVPIG	DVAKDGPGLI	FIIYPEAIAT	LPLSSANAVV	FPIMLLTLGI	420
	DSAMGMESV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHPAA	480
	GTSILFGLVI	EAIGVAFYFG	VGQFSDDIQ	MTGQRPSLYW	RLCNKLVSPC	FLLFVVVSI	540
75	VTRFPHYGA	YIFPDWANA	GWVIATSSMA	MVPIYAAKYP	CSLPGSPREK	LAYAIAPERD	600
	RELVDGRGEVR	QFTLRHNLKV					

Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

80	1	11	21	31	41	51	
	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
85	AGCCCCCTGG	TCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCC	240

AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
 TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCTCTA AGAAGCCAG 420
 AATAATGCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
 CCGCCCTGGC CCGGGGTGTC CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
 CGCCCCAGC TCGCCCGCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600
 CTCCGCGCGC TCCAGAACT GCGCCTGCGC AACAAATGGCC ACAGTGTGCA ACTGACCCCTG 660
 CCTCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGAAGG CCACCGTTTC 780
 CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCCCTT 840
 GGGCGCCCGG GAGGCTTGGC CGTGTGGGCC GCCTTCTTGG AGGAGGGCCC GGAAGAAAAC 900
 AGTGCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
 CAGGTCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
 TATGAGGGGT CTCTGACTAC ACCGCTCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080
 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCTT GTGGGGACCT 1140
 GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAAG CTTTGAATGG GCGAGTGATT 1200
 GAGGCTCTCT TCCCTGTCTG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
 AATTCTGCC TGGCTGTCTG TGACATCCTA GCCCTGGTTT TTGGCTCTCT TTTTGTCTG 1320
 ACCAGCGTCG CGTTCTTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
 TGTGAGAGC CAGCAAGAG CATCTGAGG GAGGCCGTA ACTGTCTGT CTGCTCAT 1500
 ATGCCACTTC CTTTAACTG CCAAGAAAT TTTTAAATA AATATTATA AT

Seq ID NO: 511 Protein sequence
 Protein Accession #: NP_001207.1

1 11 21 31 41 51
 MAPLCPSWL PLLIPAPAPG LTVQLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
 GEEDLPSEED SPREDPPGE EDLPGEEDLP GEEDLPVVKP KSEEGSLKL EDLPTEAPG 120
 DPQEPQNAH RDKEGDDQSH WRVGGDPPWP RVSPACAGRF QSPVDIRPOL AAFCPALRPL 180
 ELGLFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRY RALQLHLHWG AAGRPGSEHT 240
 VEGHFRPAEI HVVHLSTAPA RVDEALGRPG GLAVLAFL EGPENSAEY QLSRLLEEIA 300
 EESGSETQVPG LDISALLPSD FSRFYQYEGS LTPPCAQGV IWTVFNQTVM LSAKQLHTLS 360
 DTLWFGDSR LQLNFRATQP LNRVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
 GLLFVATVSA FLVQMRRQHR RGTGGVSYR PAEVAETGA

Seq ID NO: 512 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3978

1 11 21 31 41 51
 ATGGTGGGTG AAGGACCCTA CCTTATCTCA GATCTGGACC AGCGAGGCCG GCGGAGATCC 60
 TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGCAGCC CTGTGCAAGG 120
 TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC 180
 ACCGCGGTGA TGGTGAAGG CTACCGGCAA AGGCTGACCG TAGACACCTT GCCCCATTG 240
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCCCTTG GATGAAGAG 300
 GTAGCAAGGG TGGGTCTCTG GAAGGCCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360
 ACACGCGTGT TGATGGACAT CGTGCCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420
 CCGACAGTTC TCATTCACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480
 GTTGGCATTG GACTGTGCAT AGCCCTTTTT GCCACCGAGT TTACCAAAGT CTTCTTTTGG 540
 GGCCTTGCCT GGGCCATCAA CTACCGCACG GCCATCCGGT TGAAGGTGGC GCTCTCCACC 600
 TTGGTTTTTG AAAACCTAGT GTCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG 660
 CTCAATATAC TGTCAAGTGA TAGCTATTCT TTGTTTGAAG CTGCCTTGT TTGCTCTTGG 720
 CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGCGGCGT ACGCCTTTTT CATCTGCGG 780
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCOA GATGTTTATG 840
 CCCAAGCTCA ATTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900
 ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT 960
 TTTACCAACA CTATCCAAGA TATAAGAAGG AGGGAAAGAA AATTACTGGA AAAAGCTGGA 1020
 TTTGTCCAAA GTGGAAACTC TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTGCTG 1080
 ACATTATCCT GCCACATCCT CCGTGAAGCG AAACCTACCG CACCCGTGGC ATTTAGTGTG 1140
 ATTGCCATGT TTAATGTAAT GAGGTTTTCC ATTGCAATCT TGCCCTTCTC CATCAAAGCA 1200
 ATGGCTGAAG GAAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAAGCCCC 1260
 CCATCTTACA TCACCAACCC AGAAGACCCA GATACTGTCT TGCTTTAGC AAATGCCACC 1320
 TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATGGA GAACCAAGAA 1380
 AGGCATTTAT GCAAGAAACA GAGGTGAGG GCATACAGTG AGAGGAGTCC ACCAGCCAAG 1440
 GGAGCCACTG GCCCAGAGGA GCAAAGTGAC AGCCTCAAAT CGGTCTGCA CAGCATAAAG 1500
 TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCCGAG TCCTGGCTTG GAGGTGGCCA 1560
 GCAAGTGGT TGGGAGAAAT CATCAGAGGA TACAGGCCTC ATGGATTTC TGCTAAAGAC 1620
 AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCAAGAAG TGGATAGGAC TCAAAGGGCA 1680
 GCCAAATACC TGGGGAAGAT CTGCGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740
 CTCTTGCAG CTCTCTAGG ACAGATGACG CTGCAGAAAG GGGTGGTGGC AGTCAATGGA 1800
 ACTTTGGCCT ACGTTTCACA GCAGGCATGG ATCTTTCATG GAAATGTGAG AGAAAAATA 1860
 CTCTTTGGAG AAAAGTATGA TCACCAAGG TATCAGCACA CAGTCCGCGT CTGTGGCCTC 1920
 CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCTC 1980
 AACCTCTCTG GGGGCGAGAG GCAGAGGATT AGCCTGGCCC GCGCTGTCTA CTCGACCGT 2040
 CAGCTCTACC TGCTGGACGA CCCCTGTGCG GCGGTGGAGC CCCAGTGGG GAAGCAGTC 2100
 TTTGAGGAGT GCATTAAGAA GACGCTCAGG GGAAGACAG TCGTCTGGT GACCCACCAG 2160
 CTACAGTTCT TAGAGTCTTG TGATGAAGTT ATTTTATTAG AAGATGGAGA GATTGTGAA 2220
 AAGGAACCC ACAAGAGATT AATGAGGAG AGAGGGCGCT ATGCAAAACT GATTCAAC 2280
 CTGOGAGGAT TGCAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC 2340
 TTCAAGGAGA GCCCTGTCTG GAGAGAGGAA GATGCTGGTA TAATCGGGTA CCTCTTTCT 2400
 CTCTTCACTG TGTCTCTCTT CCTCCTGATG ATTGGCAGCG CTGCTTCAG CAATCTGTG 2460
 CTGGGTCTCT GGTGGACAA GGGCTCAGG ATGACCTGTG GGGCCAGGG CAACAGGACC 2520
 ATGTGTGAGG TCGGCGCGT GCTGGCAGC ATCGGTGAGC ATGTGTACCA GTGGGTGTAC 2580
 ACTGCAAGCA TGGTGTTCAT GCTGGTGTGTT GCGCTACCA AAGGCTTCGT CTCACCAAG 2640

ACCACACTGA TGGCATGCTC CTCTCTGCAT GACACGGTGT TTGATAAGAT CTTAAAGAGC 2700
 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760
 ATGGACGAGC TGGATGTGAG GCTGCCGTTT CACGACAGAGA ACTTTCTGCA GCAGTTTTTT 2820
 ATGGTGGTGT TTATTCTCGT GATCTTGGCT GCTGTGTTTC CTGCTGTCTT TTAGTCGTG 2880
 GCCAGCCTTG CTGTAGGCTT CTTCACTCTG TTACGCATTT TCCACAGAGG AGTCCAGGAG 2940
 CTCAGAAGGG TGGAGAAATG CAGCCGGTCA CCCTGGTTCA CCCACATCAC CTCCTCCATG 3000
 CAGGCGCTGG GCATCAATCA CGCCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA 3060
 TCCAAAGGCC TGTCATTGTC ATACATCATC CAGCTGAGCG GACTGTCTCA AGTGTGTGTG 3120
 CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGTCTAG GGAATACATT 3180
 TCGACCTGTG TTCTCTGAATG CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG 3240
 CCCAGCTGTG GGGAGATCAC CTTACAGAGC TATCAGATGA GATACAGAGA CAACACCCCC 3300
 CTTGTTCTCG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTTGGA 3360
 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGGT GGAGCCAGCC 3420
 AGTGGCACA TCTTTATTTA TGAGGTGGAT ATCTGCATTC TCAGCTTGGG AGACCTCAGA 3480
 ACCAAGCTGA CTGTGATCCC ACAGGATCCT GTCTCTTTTG TAGGTACAGT AAGGTACAAC 3540
 TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAACATT 3600
 ATGAGAGACA CAATAATGAA ACTCCAGAA AAATTACAGG CAGAAGTCAC AGAAATGGA 3660
 GAAACTTCT CAGTAGGGGA ACCTCAGCTG CTTGTGTGG CCGAGCTCT TCTCCGTAAT 3720
 TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCCTG 3780
 GTTCAGAAAC CCATCAAAGA TGCCCTCAAG GGCTGCATCT TGCTGACCAT CGCCCAACCGC 3840
 CTCACACAG TTCTCAACTG CGATCACGTC CTGGTTATGG AAAATGGGAA GGTGATTGAG 3900
 TTTGACAAGC CTGAAGTCTT TGCAGAGAAG CCAGATTCTG CATTTCGGAT GTTACTAGCA 3960
 GCAGAAGTCA GATTGTAG

Seq ID NO: 513 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MVGEGPYLIS DLDQRGRRRS FAERYDPSLK TMIPVRPCAR LAPNFVDDAG LLSFATFSWL 60
 TPVMVKGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVMKFOR 120
 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEPTKVFFW 180
 ALAWAINYRT AIRLKVALLST LVFENLVSKF TLTHISVGEV LNILSSDSYS LFEAALFCPL 240
 PATIPILMVF CAAAYAFILG PTALIGISVY VIFIPVQMFN AKLNSAFRRS AILVTDKRVQ 300
 TWNEFLTICR LIKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 TLSCHILRR KLTAAPVAFSV IAMFNVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNKQ RHLCKQORSE AYSESPPAK 480
 GATGPBEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD 540
 KDESRLRLTW PQEVDRTQRA AKYLKILGI CGNVGSGKSS LLAALLGQM LQKGVVAVNG 600
 TLAYVSQQAQ IFHGNVRENI LFGEKYDHQR YQHTVRVCGL QKDLNLPYG DLTEIGERGL 660
 NLSGGQRQRI SLARAVYSDR QLVLLDDPLS AVDAHVGKHF FEBCIKKTLR GKTIVLVTHQ 720
 LQFLESCDEV ILLEDGEICE KQTHKELMEE RGRYAKLIHN LRGLQFKDPE HLYNAMVEA 780
 FKESPAEREE DAGIIGYLLS LPTVFLFLM IGSAAFSNWM LGLWLDKGSR MTCGPQGNRT 840
 MCEVGAVLAD IGQHVYQWVY TASMVFLMVF GVTKGVFPTK TTLMASSSLH DTVFDKILKS 900
 PMSFFDTTPT GRMLNRFESKD MDEL DVRLPF HAENFLQOFF MVVFILVILA AVFPAVLLVV 960
 ASLAVGFPII LRIPIHRGVQE LKKVENVSRS PWFTHITSSM QGLGIIHAYG KKESCITYTS 1020
 SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW 1080
 PSCGEITFRD YQMYRDNTP LVLDLSLNLN QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTIRYN LDPFESHTDE MLWQVLERTF 1200
 MRDITMKLPE KLGAEVTEAG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMSKTDITL 1260
 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKVIE FDKFEVLAEK PDSAFAMLLA 1320
 AEVRL

Seq ID NO: 514 DNA sequence
 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

1 11 21 31 41 51
 CACACGCGCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCGCGG CCCGACAGAA 60
 ACTTCGCGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CAGAAAAAAC 120
 AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGCGACGGG 180
 CGCAAGATGG CCCAGGAGAA CCCCAAGATG CACAACCTGG AGATCAGCAA GCGCCTGGGC 240
 GCGAGATGGA AACTTTTGTG GGAGACGGAG AAGCGGCCGT TCATCGACGA GGCTAAGCGG 300
 CTGCGAGCGC TGCACATGAA GGAGCACCGG GATTATAAAT ACCGCGCCCG GCGGAAAAAC 360
 AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCCGGC GGTGTCTGGC CCCCCGCGG 420
 AATAGCATGG CGAGCGGGGT CCGGGTGGGC GCGGCGCTGG GCGGCGCGGT GAACACAGCG 480
 ATGGACAGTT ACGCGCACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC 540
 CAGCTGGGCT ACCCGCAGCA CCGGGGCTCT AATGCGCACG GCGCAGCGCA GATGCAGCCC 600
 ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACCTCA TGACCAAGTC GCAGACCTAC 660
 ATGAACGGCT CGCCCACTTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTCCGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCC TGTGTTTACC 780
 TCTTCTCTCC ACTCCAGGGC GCCTTGCAG GCCGGGGACC TCCGGGACAT GATCAGCATG 840
 TATCTCCCGG GCGCGGAGGT GCCGGAACCC GCCGCCCCCA GCAGACTTCA CATGTCCAG 900
 CACTACCAGA GCGGCGCGGT GCCCGCACG GCCATTAAAG GCACACTGCC CCTCTCACAC 960
 ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGAAAA 1020
 TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCCG TACGCTCAAA 1080
 AAAAA

Seq ID NO: 515 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
 HSARMYNNME TELKPPGPQQ TSGGGGNSST AAAAGGNQKN SPDRVKRFMN AFMVWSRGQR 60
 RKMAQENPKM HNSEISKRLG AEWKLSET E KRPFIDEAKR LRALHMKHP DYKYRPRRKT 120
 KTLMKDKYKT LFGGLLAPGG NSMASGVGVG AGLGAGVNRQ MDSYAHMNGW SNGSYSMMQD 180

QLGYPOHPGL NAHGAAQMQP MHRYDVSAIQ YNSMTSSQTY MNGSPTYSMS YSQOQTGMA 240
 LGSMSVVKV EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPPEP AAPSRLLHMSQ 300
 HYQSGPVPQT AINGTLPLSH M

5 Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

10 1 11 21 31 41 51
 | | | | |
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAAGAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCTCTTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 15 AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGT TCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGAAAA 420
 TGACAAAAAT GGAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACGGCA 480
 20 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAAATAA TCAATTTATT ACATGTGATT GTGATTATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTGG TGTGAAAAATG TGACAAACAC ACTTATCTGT CTCTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AATGGGGCC GCAATT

25 Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

30 1 11 21 31 41 51
 | | | | |
 MMAGMKIQLV CMLLLAFSSW SLCSDEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNLMNS PAETGEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFPQHE 120
 LIQEDILDG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYVV

35 Seq ID NO: 518 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109..2940

40 1 11 21 31 41 51
 | | | | |
 ACCTAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCTTATTG CAACCTGAAG TTGTGACTC TCCTGGTTC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAGACA ATGGGTATAA TGGATTGCTC 240
 45 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCCTCA TCTCAACAT TAAGGAAATG 300
 ATAAGTGAAG CTTTATTGTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT 360
 ATAAAGATT TAATACCTGC CACATGGAAG GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAAAATG CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAT ACATTCAATT CACACCTAAT 540
 50 TTCTCTACTA ATGATACTT AACAGCTGGC TACGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGCCC ACCTCCGTGT GGGTGTGTTT GATGAGTATA ACAATGACAA ACCCTTCTAC 660
 ATAAATGGGC AAAATCAAA TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TAATACCAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 55 AGTTTATCTT CTGTGGTTGA ATTTTGTAA GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTTACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCTCCACAT ATTCTGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTTGAA 1140
 60 ATTCTACCT TGTGGGGCAT TGCCAGTTTC GACAGCAAG GAGAGATCAG AGCCCAGCTA 1200
 CACCAAAATA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAA AAGCATCAG CATTTGTTCA GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320
 AAAGTGAATG GAAAGAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTCTCTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440
 65 CTGGGTTCAT CTGAGCCCCC AATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
 TTCTTTGTTT CAGATATATC AAATCCCAAT AGCATGATTG ATGCTTTTCA TAGAATTTCC 1560
 TCTGGAAGTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC 1620
 AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
 70 GGACGAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
 TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAAACA TACCATCAT 1860
 TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGGCT CCAACTCAGC TGTGCCCCA 1920
 GCCACTGTGG AAGCCTTTGT GGAAGAGAGC AGCCTCCATT TTCTCTATCC TGTGATGATT 1980
 TATGCCAATG TGAACAGGG ATTTTATCCC ATCTTAATG CCCTGTGAC TGCCACAGTT 2040
 75 GAGCCAGAGA CTGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
 GTTATAAAAA ATGATGGAAT TTAATCGAGG TATTTTCTT CCTTTGCTGC AAATGGTAGA 2160
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCAGC CCCTCTATT 2220
 CCAGGGAGTC ATGCTATGTA TGTACAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
 GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
 80 AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCCACC TGATGTGTTT 2400
 CCACCATGCA AAATTTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAAT GACCCATCT 2460
 TGGACAGCAC CTTGAGTACG CTTTGTATCAG GGCCAGGCTA CAAGCTATGA AATAAGAAATG 2520
 AGTAAAGATC TACAGAATAT CCAAGATGAC TTAAACAATG CTATTTTAGT AAATACATCA 2580
 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640
 85 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCAGGCG 2760
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
 GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCAATTGCC TTATTATAGT TGTGACACAT 2880

CATACCTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
 CATACTAACA AAGTCAAATT AACATCAAAA CTGTATTAAA ATGCAITGAG TTTTGTGACA 3060
 ATACAGATAA GATTTTACA TGGTAGATCA ACAATTCITT TTGGGGGTAG ATTAGAAAAAC 3120
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG 3180
 GCAAAGGGAA GGGTAAAGTC GGACCACTGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240
 AATAGCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACCTGTCTG TGTGAAGCAA 3300
 TCATTAGATT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360
 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTACCT 3420
 CTTGCTATTT TGTATATAT ATTTTCTGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
 TTTACTGTA AGAGGTAACC TTTAAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
 TTTATGACAA AGGTCTATTG AATTTATTG TNTGTAAGTT TCTACTCCA TCAAAGCAGC 3600
 TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
 TACCTAGGAA A

Seq ID NO: 519 Protein sequence
 Protein Accession #: NP_006527.1

1 11 21 31 41 51
 MTQRSIAGPI CNLKFVTLV ALSSLEPFLG AGVQLQDNGY NGLLIAINPO VPENQNLIEN 60
 IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAA 120
 GDDPYTLQYR GCGEGKYIH FTPNFLLNDN LTAGYGSRRR VFVHEWAHLR WGVFDEYNND 180
 KPFFYINGNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LPKEGCTFIY NSTQATASI 240
 MFMQSLSSVV EFCNASTHQN EAPNLQNMOC SLRSANDVIT DSADFHHSFP MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQAAEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSLKKGK EVVEKLNKGA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSSGSTI HSIALGSSAA PNLEELSRLT GGLKFPVPDI SNSNSMIDAF 480
 SRISSTGDI PQHQIQLST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
 FDPDGRKYIT NNFITNLTPR TASLWIPGTA KPGHWYITLN NTHHSLQALK VTVTSRASNS 600
 AVPPATVEAF VERDSLHFFH PVMIIYANVQ GFYPIILNATV TATVEPETGD PVTLLRLDDG 660
 AGADVIKNDG IYSRYFFSFA ANGRYSKLVH VNHSPISTP AHSIPGSHAM YVPGYTANGN 720
 IQMNAPRKSV GRNEEERKNG FSRVSSGGSP SVLVGPAGPH PDVFPCKII DLEAVKVBEI 780
 LTLSTWAPGE DFDGQATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPPQ AGIREIFTFS 840
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
 LILKGVLTAM GLIGIICLI VVTHHTLSRK KRADKKENG KLL

Seq ID NO: 520 DNA sequence
 Nucleic Acid Accession #: NM_000228.1
 Coding sequence: 82..3600

1 11 21 31 41 51
 GCTTTTCAGGC GATCTGGAGA AAGAACGGCA GAACACACAG CAAGGAAAGG TCCTTTCTGG 60
 GGATCACCCC ATTGGCTGAA GATGAGACCA TTCTTCTCTT TGTGTTTTCG CTGCTCTGGC 120
 CTCTGCTCATG CCCAACAAAGC CTGCTCCCGT GGGGCTGCT ATCCACCTGT TGGGACCTG 180
 CTTGTTGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAG CAAGCCTGAG 240
 ACCTACTGCA CCCAGTAGG CGAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCCAGGCAG 300
 CCTCACAAC ACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCGG CCCCATGGC 360
 TGGTGGCAGT CCGAGAATGA TGTGAACCT GTCTCTCTG AGCTGGACCT GGACAGGAGA 420
 TTCCAGCTTC AAGAAGTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCCGG CATGCTGATT 480
 GAGCGCTCCT CAGACTTCGG TAAGACCTGG CGAGTGTACC AGTACCTGGC TGCCGACTGC 540
 ACCTCCACCT TCCCTCGGGT CGGCCAGGGT CGGCCTCAGA GCTGGCAGGA TGTTCGGTGC 600
 CAGTCCCTGC CTCAGAGGCC TAATGCAAGC CTAAATGGGG GGAAGGTCCA ACTTAACCTT 660
 ATGGAATTAG TGTCTGGGAT TCCAGCAACT CAAAGTCAA AAATTCAGA GTGGGGGAG 720
 ATCACAACCT TGAGAGTCAA TTTCACCAGG CTGGCCCTG TGCCCCAAG GGGCTACCAC 780
 CCTCCAGCG CTTACTATGC TGTGTCCAG CTCCGCTGCG AGGGGAGCTG CTTCTGTGAC 840
 GGCCATGCTG ACTGCTGCGC ACCCAAGCCT GGGGCTCTG CAGGCCCTC CACCGCTGTG 900
 CAGGTCCAGC ATGTCTGTGT CTGCCAGCAC AACACTGCCG GCCCAAATTG TGAGCGCTGT 960
 GCACCCCTCT ACAACAACCG GCCTCGGAGA CCGGCGGAGG GCCAGGACGC CCATGAATGC 1020
 CAAAGGTGCG ACTGCAATGG GCACTCAGAG ACATGTCACT TTGACCCCGC TGTGTTTGGC 1080
 GCCAGCCAGG GGGCATATGG AGGTGTGTGT GACAATTGCC GGGACACAC CGAAGGCAAG 1140
 AACTGTGAGC GGTGTCACT GCACTATTTC CGGAACCGGC GCCCGGAGC TTCCATTGAG 1200
 GAGACCTGCA TCTCTGCGA GTGTGATCCG GATGGGGCAG TGCCAGGGGC TCCCTGTGAC 1260
 CCAATGACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320
 AAGCCGGGCT TCACTGGACT CACCTACGCC AACCCGACGG GCTGCCACCG CTGTGACTGC 1380
 AACATCCTGG GGTCCCGGAG GGACATGCCG TGTGACGAGG AGAGTGGGCG CTGCCTTTGT 1440
 CTGCCCAACG TGTGGGTGCC CAAATGTGAC CAGTGTGCTC CCTACCACTG GAAGCTGGCC 1500
 AGTGGCCAGG GCTGTGAACC GTGTGCTGC GACCCGCACA ACTCCCTCA GCCACAGT 1560
 CAACCACTTC ACAGGGCAGT GCCCTGTGGG GAAGGCTTTG GTGGCTGAT GTGCAGCGCT 1620
 GCAGCCATCC GCCAGTGTCC AGACCGGACC TATGGAGACG TGGCCACAGG ATGCCGAGCC 1680
 TGTGACTGTG ATTTCCGGGG AACAGAGGGC CCGGCTGCG ACAAAGCATC AGGCCGCTGC 1740
 CTTGCGCGCC CTGGCTTGAC CGGGCCCGC TGTGACCACT GCCAGCGAGG CTAAGTCAAT 1800
 CGCTACCGCG TGTGCTGGC CTGCCACCT TGTCTCCAGA CCTATGATGC GGACCTCCGG 1860
 GAGCAGGCCG TGCCTTTTGG TAGACTCCG AATGCCACCG CCAGCTGTG GTCAGGGCCT 1920
 GGGCTGGAGG ACCGTGGCCT GGCCTCCCG ATCCTAGATG CAAAGAGTAA GATTGAGCAG 1980
 ATCCGAGCAG TTCTCAGCAG CCCCGCAGTC ACAGAGCAGG AGGTGGCTCA GGTGGCCAGT 2040
 GCCATCCTCT CCTCAGGCG AACTCTCCAG GCCTTGCAGC TGGATCTGCG CCTGAGGAG 2100
 GAGACGTTGT CCTTCCGAG AGACCTGGAG AGTCTTGACA GAAGCTTCAA TGGTCTCCTT 2160
 ACTATGATAT AGAGGAAGAG GGAGCAGTTT GAAAAATAA GCAGTGTCTG TCCTTCAGGA 2220
 GCCTTCCGGA TGCTGAGCAG AGCCTACGAG CAGTCAGCCC AGGCTGCTCA GCAGGTCTCC 2280
 GACAGCTCGC GCTTTTGGGA CCAGCTCAGG GACAGCCGGA GAGAGGCAGA GAGGCTGGTG 2340
 CGGCAGGCGG GAGGAGGAGG AGGCACCGGC AGCCCAAGC TTGTGGCCCT GAGGCTGGAG 2400
 ATGTCTCTGT TGCCTGACCT GACACCCACC TTCAACAAGC TCTGTGGCAA CTCACGGCAG 2460
 ATGGCTTGCA CCCCAATATC ATGCCCTGGT GAGCTATGTC CCCAAGACAA TGGCACAGCC 2520
 TGTGGCTCCC GCTGCAGGGG TGTCTTCCC AGGGCCGGTG GGGCCTTCTT GATGGCGGGG 2580
 CAGGTGGCTG AGCAGCTGCG GGGCTTCAAT GCCCAGCTCC AGCGGACAG GCAGATGATT 2640

AGGGCAGCGG AGGAATCTGC CTCACAGATT CAATCCAGTG CCCAGCGCTT GGAGACCCAG 2700
 GTGAGCGCCA GCCGCTCCCA GATGGAGGAA GATGTCAGAC GCACACGGCT CTAATCCAG 2760
 CAGGTCCGGG ACTTCTTAAC AGACCCCGAC ACTGATGACG CCACTATCCA GGAGGTCAGC 2820
 GAGGCGGTGC TGGCCCTGTG GCTGCCCA CA GACTCAGCTA CTGTTCTGCA GAAGATGAAT 2880
 GAGATCCAGG CCATTGCAGC CAGGCTCCCC AACGTGGACT TGGTGCTGTC CCAGACCAAG 2940
 CAGGACATTG CGCGTGGCCG CCGGTTGCAG GCTGAGGCTG AGGAAGCCAG GAGCCGAGCC 3000
 CATGCAGTGG AGGGCCAGGT GGAAGATGTG GTTGGGAACC TGCGGCAGGG GACAGTGCCA 3060
 CTGCAGGAAG CTCAGGACAC CATGCAAGGC ACCAGCGGCT CCCTTCGGCT TATCCAGGAC 3120
 AGGGTTGCTG AGGTTTCAGCA GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180
 AAGCAGCTGG GTGACTTCTG GACACGGATG GAGGAGCTCC GCCACCAAGC CCGGCAGCAG 3240
 GGGGCAGAGG CAGTCCAGGC CCAGCAGCTT GCGGAAGGTG CCAGCGAGCA GGCAATTGAGT 3300
 GCCCAAGAGG GATTTGAGAG AATAAAACAA AAGTATGCTG AGTTGAAGGA CCGTTGGGT 3360
 CAGAGTTCCA TGCTGGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG 3420
 GAGCTGTTTG GGGAGACCAT GGAGATGATG GACAGGATGA AAGACATGGA GTTGGAGCTG 3480
 CTGCGGGGCA GCCAGGCCAT CATGCTGCGC TCGGCGGACC TGACAGGACT GGAGAAGCGT 3540
 GTGGAGCAGA TCCGTGACCA CATCAATGGG CGCGTGCTCT ACTATGCCAC CTGCAAGTGA 3600
 TGCTACAGCT TCCAGCCGCT TGCCCCACTC ATCTGCGGCC TTTGCTTTTG GTTGGGGGCA 3660
 GATTGGGTG GAATGCTTTC CATCTCCAGG AGACTTTCAT GCAGCCTAAA GTACAGCCTG 3720
 GACCACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT 3780
 GGGACAGTTA CACTTGACAG ACAAAGATGG TGGAGATTGG CATGCCATTG AAATAAGAG 3840
 CTCTCAAGTC AAGGAAGCTG GGCCTGGCAG TATCCCGCGC CTTTAGTTCT CCACTGGGGA 3900
 GGAATCTGAG ACCAAGCACA AAAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960
 AAAATCTTTG G

Seq ID NO: 521 Protein sequence
 Protein Accession #: NP_000219.1

1 11 21 31 41 51
 MRPFLLCFA LPGLLHAQQA CSRGACYPPV GDLLVGRTRF LRASSTCGLT KPETYCTQYG 60
 EQQMKCKCD SRQPHNYSH RVENVASSSG PMRWQSQND VNPVSLQLDL DRRFQLQEVN 120
 MEFGQMPAG MLIERSSDFG KTRVYQYLA ADCTSTFPRV RQGRPQSQWD VRCQSLPQRP 180
 NARLNGKKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQLRLQGGC FCHGHADRC A PKGASAGPS TAVQVHDCV CQHNTAGPNC ERCAFFYNRR 300
 PWRPAGQDA HECQRDCNG HSETCHFDPA VFAASQGA YG GVCNCRDHT EGNKNCERQCL 360
 HYFRNRRPGA SIQETICISCE CDPDGA VPGA PCDFVTGQCV CKEHVQGERC DLCKPGFTGL 420
 TYANPQCHRR CDCNLSRRR DMPCEESGR CLCLPNVVG P KCDQCAPYHW KLASGQGCER 480
 CACDPHNSQ PTVQPVHRAV PCREGFGGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG 540
 TEGPGCDKAS GRCLCRPGLT GPRCDQCRG YCNRYPVCA CHPCFQTYDA DLREQALRFG 600
 RLNRNATSLW SGPGLEDRGL ASRILDAKSK IEQIRAVLSS PAVTEQEVAV VASAILSLRR 660
 TLQGLQLDLP LEEETLSLPR DLESLLDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720
 AYEQSAQAQ QVSDSSRLLD QLDRSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSLPLDL 780
 TPTFNKLCGN SRQMACTPIS CPGLCPQDN GTACGSRGRG VLPRAAGAFI MAGQVAEQLR 840
 GFNAQLQRT R MIRAAEESA SQISSAQLR ETQVSASRSQ MEEDVRTRL LIQQRVDFLT 900
 DPDTDAATIQ EVSEAVLALW LPTDSATVLQ KMNEIQAI A RLPNVDLVLS QTKQDIARAR 960
 RLQAEAEER SRAHAVEGQV EDVVGNLRRQ TVALQEAQDT MQGTSRSLRL IQDRVAEVQ 1020
 VLRPAELVLT SMTQQLGDFW TRMEELRHQA RQQGAEAQQA QQLAEGASEQ ALSAQEGFER 1080
 IKQKYAELKD RLQSSMLGE QGARIQSVKT EAEELFGETM EMMDRMKDME LELLRGSQAI 1140
 MLRSADLTGL EKRVEQIRDH INGRVLYYAT CK

Seq ID NO: 522 DNA sequence
 Nucleic Acid Accession #: NM_001944.1
 Coding sequence: 84..3083

1 11 21 31 41 51
 TTTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGACTT 60
 TTTACCCAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120
 CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAAATGCG AATAGAGACT AAAGGTCAAT 180
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAA GCAAAAACGT GAATGGGTGA 240
 AATTGTGCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAAA AAGAAACCCA ATTGCCAAGA 300
 TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCCGCC TTTTGGAAAT TTTGTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTGCGGCT CTAATGCCC 480
 AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCCTCCAGT ATTTTCACAA CAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCCTCA 600
 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCA TTGAATTCTA 660
 AAATGCTCTT CAAATTTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCTTAAGCA 720
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT 780
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
 GTAAATATTA AGTGAAGAAAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900
 CAGCAGTAT TGAAGAAAAT ATTTAAGTT CTGAATTACT TCGAATTCAA GTAACAGATT 960
 TGGATGAAGA GTACACAGAT AATTTGGCTT CAGTATATTT CTTTACCTCT GGGAAATGAAG 1020
 GAAATTTGGT TGAATATCAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080
 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAACCTTAG TATTGCTGTC AAAAAACAAG 1140
 CTGAATTTCA CCAATCAGTT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200
 AGGTAATAAA TGTAAGAGAA GGAATTCAT TCCGTCTGCG TTCCAAGACA TTTACTGTGC 1260
 AAAAAGGCAT AAGTAGCAAA AATTGCTGG ATTATATCTT GGGAAACATAT CAAGCCATCG 1320
 ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAATATGT CATGGGAGT AACGATGGTG 1380
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAATT TGTCAAAAAT ATGAACCGAG 1440
 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500
 CCGGTAAAAA TTCTACAGGC ACGTATATG TTAGAGTACC CGATTTCAT GACAATTGTC 1560
 CAACAGCTGT CCTCGAAAAA GATGCAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCCG 1620
 CTGAACACT GAAATAAGTA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680
 TAAAGTTGCC TGCGGTATGG AGTATCACAA CCTCAATGC TACCTCGGCC CTCTCAGAG 1740
 CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCACTGT GACAACAGG 1860

	GCATCTGTGG	AACCTCTTAC	CCAACCAAA	GCCCTGGGAC	CAGGTATGGC	AGGCCGCACT	1920
	CAGGGAGGCT	GGGGCCTGCC	GCCATCGGCC	TGCTGCTCCT	TGGTCTCCTG	CTGCTGCTGT	1980
	TGGCCCCCTT	TCTGCTGTGT	ACCTGTGACT	GTGGGGCAGG	TTCTACTGGG	GGAGTGACAG	2040
5	GTGGTTTAT	CCCAGTTCTT	GATGGCTCAG	AAGGAACAAT	TCATCAGTGG	GGAAATTGAAG	2100
	GAGCCCATCC	TGAAGACAAG	GAAATCACAA	ATATTGTGTG	GCCTCCTGTA	ACAGCCAATG	2160
	GAGCCGATTT	CATGGAAGT	TCTGAAGTTT	GTACAAATAC	GTATGCCAGA	GGCAGACGG	2220
	TGGAAGGCAC	TTACAGGAATG	GAAATGACCA	CTAAGCTTGG	AGCAGCCACT	GAATCTGGAG	2280
	GTGCTGCAGG	CTTTGCAACA	GGGACAGTGT	CAGGAGCTGC	TTCAAGGATC	GGAGCAGCCA	2340
10	CTGGAGTTGG	CATCTGTTC	TCAGGGCAGT	CTGGAACCAT	GAGAACAAGG	CATTCCACTG	2400
	GAGGAACCAA	TAAGGACTAC	GCTGATGGGG	CGATAAGCAT	GAATTTTCTG	GACTCCTACT	2460
	TTTCTCAGAA	AGCATTTGCC	TGTGCGGAGG	AAGACGATGG	CCAGGAAGCA	AATGACTGCT	2520
	TGTTGATCTA	TGATAATGAA	GGCGCAGATG	CCACTGGTTC	TCCTGTGGGC	TCCGTGGGTT	2580
	GTGCACTTT	TATTGCTGAT	GACCTGGATG	ACAGCTTCTT	GGACTCACTT	GGACCCAAAT	2640
15	TTAAAAAAT	TGCAGAGATA	AGCCTTGGTG	TTGATGGTGA	AGGCAAAGAA	GTTCAGCCAC	2700
	CCTCTAAAGA	CAGCGGTAT	GGGATTGAAT	CCTGTGGCCA	TCCCATAGAA	GTCACGAGA	2760
	CAGGATTTGT	TAAAGTGCCAG	ACTTTGTGAG	GAAGTCAAGG	AGCTTCTGCT	TTGTCCGCCT	2820
	CTGGGTCTGT	CCAGCCAGCT	GTTTCCATCC	CTGACCCCTT	GCAGCATGGT	AACTATTTAG	2880
	TAACGGAGAC	TTACTCGGCT	TCTGGTTCCC	TCGTGCAACC	TTCCACTGCA	GGCTTTGATC	2940
20	CACCTTCTAC	ACAAAATGTG	ATAGTGACAG	AAAGGGTGAT	CTGTCCCATT	TCCAGTGTTT	3000
	CTGGCAACCT	AGCTGGCCCA	ACGCAGCTAC	GAGGGTCACA	TACTATGCTC	TGTACAGAGG	3060
	ATCCTTGCTC	CGCTCTAATA	TGACCAGAA	GAGCTGGAAT	ACCACACTGA	CCAAATCTGG	3120
	ATCTTTGGAC	TAAAGTATTC	AAAAATAGCAT	AGCAAAGCTC	ACTGTATTGG	GCTAATAATT	3180
	TGGCACTTAT	TAGCTTCTCT	CATAAATCGA	TCACGATTAT	AAATTAATG	TTTGGGTTCA	3240
25	TACCCCAAAA	GCAATATGTT	GTCACTCCTA	ATTCTCAAGT	ACTATTCAAA	TTGTAGTAAA	3300
	TCTTAAAGTT	TTTCAAAACC	CTAAATCAT	ATTCCG			

Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

30	1	11	21	31	41	51	
	MMGLFPRTTG	ALAIFVVVIL	VHGLRIETK	GQYDEEMTM	QQAQRQKRE	WVKFAKPCRE	60
	GEDNSKRNP	AKITSDYQAT	QKITYRISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIENS	ASNSLVMILN	180
35	ATDADEPNHL	NSKIAPKIVS	QEPAGTPMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSQA	240
	DKDGEGLSTQ	CECNKVKQDV	NDNPFMFRDS	QYSARIEENI	LSSSELLRFQV	TDLDEEYTDN	300
	WLAVYFSTSG	NEGNWFBIQT	DPRTNIEGILK	VVKALDYEQ	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTYO	AIDEDTNKAA	420
40	SNVKYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPYTFALD	QPVKLPVAVS	540
	ITTLNATSAL	LRAQEQIIPG	VYHISLVLT	SQNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTPSGTRYGR	PHSGRLGPAA	IGLLLLLGLL	LLAPLLLLT	CDCGAGSTGG	VTGGFIPVPD	660
	GSBGTIHQWG	IEGAHPDEKE	ITNICVPPVT	ANGADFMES	EVCTNTYARG	TAVEGTSME	720
45	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDGQEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSPFLDSL	PKFKKLAEIS	LGVDBEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQGASAL	SASGSVQPAV	SIPDPLQHGN	YLVETETYS	ASLVQPSSTAG	FDPLLTQNV	960
	VTERVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRLI			

Seq ID NO: 524 DNA sequence
Nucleic Acid Accession #: XM_058069.2
Coding sequence: 1..1413

55	1	11	21	31	41	51	
	ATGAAGTTTC	TTCTAATACT	GCTCCTGCAG	GCCACTGCTT	CTGGAGCTCT	TCCCTGAAC	60
	AGCTCTACAA	GCCCTGGAAAA	AAATAATGTG	CTATTGGGTG	AAAGATACTT	AGAAAAATTT	120
	TATGGCCTTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAATG	180
60	AAGGAAAAAA	TCCAAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
	ACATCTACCC	TGGAGATGAT	GCACGCACCT	CGATGTGGAG	TCCCCGATGT	CCATCATTTT	300
	AGGGAATGCT	CGCGGGGCC	CGTATGGAGG	AAACATTATA	TCACCTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTACGCAA	TCCGGAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCTTT	GAAATTCAGC	AAGATTAAAC	CAGGCATGGC	TGACATTTTG	480
	GTGGTTTITG	CCCGTGGAGC	TCATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
65	CTAGCCCATG	CTTTTGGACC	TGGATCTGGC	ATTGGAGGGG	ATGCACATTT	CGATGAGGAC	600
	GAATTCCTGA	CTACACATTC	AGGAGGCACA	AACTTGTTC	TCACTGCTGT	TCACGAGATT	660
	GGCCATTCCT	TAGGTCTTGG	CCATTCTAGT	GATCCAAAGG	CCGTAATGTT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCCTTC	TCTGCTGATG	ACATACGTGG	CATTCACTCC	780
70	CTGTATGGAG	ACCCAAAAGA	GAACCAACGC	TTGCCAAATC	CTGACAATTC	AGAACCAGCT	840
	CTCTGTGACC	CCAATTGAG	TTTGTATGCT	GTCACTACCG	TGGGAAATAA	GATCTTTTTC	900
	TTCAAGACA	GGTCTTCTG	GCTGAAGGTT	TCTGAGAGAC	CAAAGACCAG	TGTTAATTTA	960
	ATTTCTTCCT	TATGGCCAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACTGGT	TAATTAGCAA	TTTAAGACCA	1080
75	GAGCCAAAT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTC	CTAATTCTGT	GAAAAAAT	1140
	GATGCAGCTG	TTTTTAACCC	ACGTTTATAT	AGGACCTACT	TCTTTGTAGA	TAACCGATAT	1200
	TGGAGGTATG	ATGAAAGGAG	ACAGATGATG	GACCTCGGTT	ATCCCAACT	GATTACCAAG	1260
	AACCTCCAAG	GAATCGGGCC	TAAATATGAT	GCAGTCTTCT	ACTCTAAAAA	CAAATACTAC	1320
80	TATTTCTTCC	AAGGATCTAA	CCAAATTGAA	TATGACTTCC	TACTCCAACG	TATCACCAAA	1380
	ACACTGAAAA	GCAATAGCTG	GTTTGGTTGT	TGA			

Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

85	1	11	21	31	41	51	
	MKFLILLIQ	ATASGALPLN	SSTSLEKNV	LPGERYLEKF	YGLEINKLFV	TKMKYSQNLN	60
	KEKIQEMQHF	LGLKVTGQLD	TSTLEMMHAP	RCGVFDVHHF	REMPGGPVWR	KHYITYRINN	120

YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVPARGAHGD FHAPDGKGGI 180
 LAHAFGPGSG IGGDAHFDEED EFWTTHSGGT NLFLTAVHEI GHSGLGLHSS DPKAVMPPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIPF 300
 FKDRPFWLKV SERPKTSVNL ISSLWPTLPS GIEAAEYIEA RNQVFLPKDD KYWLISNLRP 360
 EPNYPKSIHS GFPPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRTK TLKSNSWFGC

Seq ID NO: 526 DNA sequence
 Nucleic Acid Accession #: NM_024423.1
 Coding sequence: 64..2590

1 11 21 31 41 51
 | | | | |
 15 GGCAGGTCTC GCTCTCGGCA CCCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC 60
 COGATGGCGG COGCTGGGCC COGGCGCTCC GTGCGGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCTCG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCGAGA CAAAATAAAT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGCTC AAGTGATCCT GATTTCAAG TCTTAAATGA TGGGTCAGTG 300
 20 TACACAGCCA GGGCTGTGTC GCTGTCTGAT AAGAAAAGAT CATTACCAT ATGGCTTTCT 360
 GACAAAGGA AACAAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCTTGTCT CTATGCAAGA GAATTCCTTG GCCCTTTTCC CATTGTTTCT TCAACAAGTT 540
 GAATCTGATG CAGCACAGAA CTATACCTGC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600
 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 25 CCGTGTGGATC GTGAAGAATA TGATGTTTTT GATTTGATG CTTATGCGTC AACTGCAGAT 720
 GGATATTTCAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCCCTGTTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGGCG 900
 CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACCTG GGCCTTTTTT TGTGCATCCC 960
 30 AGCAGACGGG CAATCACCCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCATTGATAA TGAAGATACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080
 ACTTGATACA TAACAGTAAC AGATTCAAAT GATAATGCAC CCCTTTTTCAG ACAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AATGTCATTC AATGTGGAAA TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAAATTAACAC TGCCAAATGG AGAGTCAATT TTACCAATTT AAAGGGAAT 1260
 35 GAAAATGGAC ATTTCAAAAT CAGCACAGAC AAAGAACTA ATGAAGGTGT TCTTTCTGTT 1320
 GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATGG AGTAAACAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTTCCAGA GTGACAGCCT TGAACAGAGC CTGGTTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCCT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 40 ATTAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560
 AATAGAAATG GCAATGTTTT AAGGTACAAA AAATGTCATG ATCTTAAAGG TTGGATCACC 1620
 ATTGATGAAA TCTTTCTGTT AATCATAACT TCCAAAATCC TGGATAGGGA GGTGAAACT 1680
 CCCAAAAATG AGTTGTATTA TATTACAGTC CTGGCAATAG ACAAGATGA TAGATCATGT 1740
 ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800
 GAATATGTAG TCATTGTCAA ACCAAAATG GGGTATACCG ACATTTTAGC TGTGTATCCT 1860
 45 GATGAACCTG TCCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC 1920
 AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGTCTTTC ATATCAGAAA 1980
 AATGCTGGAT TTCAGGAATA TACCATTCTT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040
 GCAACAAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACCTCA GTGTGCTGCG 2100
 ACTTCAAGGA GTACAGGAGT AATACTTGA AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160
 50 ATAGCACTGC TCTTTCTGTT ATTGCTAACT TTAGTATGTG GAGTTTGTGG TGCAACTAAA 2220
 GGGAAACGTT TTCTGTGAAGA TTTAGCACAG CAAAACCTAA TTATATCAAA CACAGAAGCA 2280
 CCTGAGAGC ATAGAGTGTG CTCTGCCAAT GGATTTATGA CCCAACTAC CAACAACCTC 2340
 AGCCAAAGTT TTTGTGTGAT TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAACCATT 2400
 55 GAAATGATGA AAGGAGGAAA CCAGACCTTG GAATCCTGCC GGGGGGCTGG GCATCATCAT 2460
 ACCCTGGACT CTTCAGGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG 2520
 GAGTGGCACA GTTTTACTCA ACCCCGCTCTC GGTGAAGAAT CCATTAGAGG ACACACTGGT 2580
 TAAAAATTAA ACATAAAGA AATGTGATCG ATGTAATCAG AATGAAGACC GCATGCCATC 2640
 CCAAGATTAT GTCTCTCACT ATAACTATGA GGAAGAGGA TCTCCAGCTG GTTCTGTGGG 2700
 60 CTGCTGCAGT GAAAAGCAGG AAGAAGATGG CCTTGACTTT TTAATAATT TGGAAACCAA 2760
 ATTTATTACA TAGCAGAAAG CATGCAACAA GAGATAATGT CACAGTGCTA CAATTAGGTC 2820
 TTTGTGAGAC ATTTCTGAGG TTTCCAAAA TAATATTGTA AAGTTCAAT TCAACATGTA 2880
 TGTATATGAT GATTTTTTTC TCAATTTTGA ATTATGCTAC TCACCAATTT ATATTTTAA 2940
 AGCCAGTTGT TGCTTATCTT TTCCAAAAG TGAATAATGT TAAACAGAC AACTGGTAAA 3000
 65 TCTCAAACTC CAGCAGTGA ATTAAGGTCT CTAAAGCATC TGCTCTTTT TTTTTCACG 3060
 GATATTTTAG TAATAAATAT GCTGGATAAA TATTAGTCCA ACAATAGCTA AGTTATGCTA 3120
 ATATCACATT ATTATGATT CACTTTAAGT GATAGTTTAA AAAATAACA AGAAATATTG 3180
 AGTATCACTA TGTGAAGAAA GTTTTGGAAA AGAAACAATG AAGACTGAAT TAAATTAATA 3240
 ATGTTGCAGC TCATAAGAA TTTGGACTCA CCCCTACTGC ACTACCAAT TCATTGACT 3300
 70 TTGGAGGCAA AATGTGTTGA AGTGCCCTAT GAAGTAGCAA TTTTCTATAG GAATATAGTT 3360
 GGAAATAAAT GTGTGTGTGT ATATTATTAT TAATCAATGC AATATTAAAA ATGAAATGAG 3420
 AACAAAGAGG AAAATGTTAA AAACCTGAAA TGAGGCTGGG GTATAGTTTG TCCTACAATA 3480
 GAAAAAAGAG AGAGCTCTCT AGGCCTGGGC TCTTAAATGC TGCATTATA CTGAGTCTAT 3540
 75 GAGGAAATAG TTCTGTGCTA ATTTGTGTAA TTTGTTTAAA ATTGTAAATA AATTAACCTT 3600
 TTCTGTTTTT TGTGGGAAGG AAATAGGGAA TCCAATGGAA CAGTAGCTTT GCTTTGCACT 3660
 CTGTTTCAAG ATTTCTGCTAT CCACAAGTTA GTAGCAAACT GGGGAATACT CGCTGCAGCT 3720
 GGGGTTCCCT GCTTTTGTGT AGCAAGGGTC CAGAGATGAG GTGTTTTTTT CGGGGAGCTA 3780
 ATACAAAAAA CATTTTAAAA CTTACCTTTA CTGAAGTTAA ATCTCTTATT GCTGTTTCTA 3840
 80 TTCTCTCTTA TAGTGACCAA CACTTTTTTA ATTTAGATCC AAATAACCAT GTCTCTCTAG 3900
 AGTTTAGAGG CTAGAGGGAG CTGAGGGGAG GATCTTACTG AAAGCACCTT GGGGAGATTG 3960
 ATTTGCTTTA AACCTAAGCC CCACAAACTT GACACCTGAT CAGGTCTGGG AGCTACAAAA 4020
 TTTCAATTTT CTCTCACTG CCCTTCTTCT GAGTGGCATT GGCCTGAATC AAGGAAAGCC 4080
 AGGCCTTGTG GGGCCCTTCT TTTGGGCTTT CTGCTAAAGC AACACCTCCA GCAGAGATTG 4140
 CCTTAAGTGA CTCCAGGTTT TCCACCATCC TTCAGCGTGA ATTAATTTTT AATCAGTTTG 4200
 85 CTTTCTCCAG AGAAATTTTA AGAAATAGAA ATTTTGAATG TATAAAGGAA 4260
 AAAGATCAAG TTGTCATTTT AGAAGAGAGG GAACCTTGGG AGAAGAGCAG CCAAGTAGGT 4320
 TATTTGTACA GTCAGAGGGC AACAGGAAGA TGCAGGCCTT CAAGGGCAAG GAGAGGCCAC 4380
 AAGGAATATG GGTGGGAGTA AAGCAACAT CGTCTGCTTC ATACTTTTTT CTAGGCTTGG 4440

Seq ID NO: 527 Protein sequence
Protein Accession #: NP_077741.1

Seq ID NO: 528 DNA sequence
Nucleic Acid Accession #: NM_001941.2
Coding sequence: 64..2754

387

	AGCACAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTGT	AGACAAGTAC	1020
	TCATTGATAA	TGAAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
	ACTTGTATCA	TAACAGTAAC	AGATTCAAAT	GATAATGCAC	CCACTTTTCA	ACAAAATGCT	1140
5	TATGAAGCAT	TTGTAGAGGA	AAATGCATT	AATGTGGAAA	TCCTACGAAT	ACCTATAGAA	1200
	GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAAT	1260
	GAAAATGGAC	ATTTCAAAT	CAGCACAGAC	AAAGAACTA	ATGAAGTGT	TCTTTCTGTT	1320
	GTAAGCCAC	TGAATTATGA	AGAAAACCGT	CAAGTGAACC	TGGAAATGG	AGTAACAAAT	1380
	GAAGGCCAT	TTGCTAGAGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1440
10	GTTCATGTGA	GGGATCTGGA	TGAGGGGCT	GAATGCACTC	CTGCAGCCCA	ATATGTGCGG	1500
	ATTAAAGAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
	AATAGAAATG	GCAATTGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GTTTGAACCT	1680
	CCCAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
15	GAATATGTAG	TCATTGGCAA	ACCAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGATAA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
20	GCAACAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACCTA	GTGTCGTGCG	2100
	ACTTCAGAGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCCTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTITGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTGTAAGA	TTTAGCACAG	CAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAACTTAC	CAACAACTCT	2340
25	AGCCAAAGTT	TTCTGTGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCAT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGGACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAAAAT	TGCTATCGATG	TAATCAGAAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
30	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTAA	2700
	AATAATTTGG	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TTAGGCTCTT	GTGAGACATT	CTGGAGGTTT	CCAAAATAAA	TATTGTAAAG	2820
	TTCAATTTCA	ACATGTATGT	ATATGATGAT	TTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAAATTTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
35	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACCTGGAAT	AAGGTCTCTA	AAGCATCTGC	3000
	TCCTTTTCTT	TTTTACGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAAAC	3060
	ATAGCTAAGT	TATGCTAATA	TCACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAGAA	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAAGA	AACAATGAAG	3180
	ACTGAAATTA	ATTAATAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCACT	3240
40	ACCAAATTC	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
	TCTATAGGAA	TATAGTTGGA	AATAAATGTG	TGTGTGTATA	TTATTATTAA	TCAATGCAAT	3360
	ATTTAAATG	AAATGAGAAC	AAAGAGGAAA	ATGGTAAAAA	CTTGAATGA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAATAGAA	AAAAGAGAGA	GCTTCTTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAATAGTTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
45	GTAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAAACG	3600
	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTCGC	TGCAGCTGGG	GTTCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTCGG	GGAGCTAATA	ACAAAACAT	TTTAAACTTT	ACCTTTTACT	AAGTTAAATC	3780
	CTCTATTGCT	GTTCCTATT	TCTCTTAG	TGACCAACAT	CTTTTAAAT	TAGATCCAAA	3840
50	TAAACATGTC	CTCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
	GCACCTGGG	GAGATTGATT	GTCCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTACTCAG	3960
	GTCTGGGAGC	TACAAAATTT	CATTTTCTC	CTCACTGCC	TTCTTCTGAG	TGGCATTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGG	CCCCTTCTTT	CGGCTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTTCC	ACCATCTTTC	AGCGTGAATT	4140
55	AATTTTAAAT	CAGTTGCTT	CTCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAAT	4200
	TTGAATGTAT	AAAAGAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCTTA	GGCTTGGCAC	TGCCCTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTTGA	4440
60	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTGTGTCAGA	ACAAACAAGG	CATTATGGG	AATTGTTGTA	TTCTTCTGCG	AGCCCTCCTT	4620
	CTGGGCACTA	AGAAGGTCTA	TGAATTAAT	GCCTATCTAA	AATCTGATT	TATCTCTACA	4680
	TTTTCTGTTT	TCTAATTTGA	CCCTAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
65	CCCCCCCCC	TTTTTTTTT	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
	GCTCCGATCT	CTGCTACTG	AAAGCTCCGC	CTCCCGGGT	CATGCCATTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCTGCG	CTCGGCTCC	CAAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
70	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
	TGATCATACG	AATTGGAATCA	ATCTTGAAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAAT	GGAATTCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAGC	CAGTTTATC	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
	CTAGTGCCGA	TAAACTTTCT	CAAGAGGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
75	TAAACATCTC	TTGTGCTCTT	GAACATGCTG	AAAACCACT	GGTCTGCATG	TATGCCCCGA	5460
	TTTGTAATTC	TTTTCTCTCA	AATGAAAAT	TAAATTTAGG	GATTCAITTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTAATT	CCTTATATGT	GTAAGGTGAA	ATTATGTTGA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAG	GCTTTCAATT	TTCCCCAGT	GAATGATTTA	GAATTTTTTA	5640
80	TGTAATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAATGCAGT	5700
	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAT	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTGTTT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTTCAA	GATGATCACT	TTGCAAAAT	ATGCTTATGG	CTGGCATGGA	5940
85	AATAGAAATA	CTCAATATG	TCTTTGTGTT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
	ATTATCAAT	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAGATA	TTAGAAGGTG	GTTATAATG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180

AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
 GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
 CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
 AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACCT CTATTGTAAC 6480
 CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAT 6540
 ACCGGATACA TTTCACTGTG CTTTCAGTAT TGATTGGTTT GAATATTGGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGCTACTTAC 6660
 TTTCTGTGTA CTTTGAAG GCTACTTAT TCCTCTCTTA GCTTCTCAT TAAATCAAT 6720
 GAACAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTT AGGGAATAA AGTTTGTGCA 6900
 TATATATAAT CCCGAAACAT G

Seq ID NO: 529 Protein sequence
 Protein Accession #: NP_001932.1

1 11 21 31 41 51
 | | | | |
 20 MAAAGRRSV RGAVCLHLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDP FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS 120
 KTRHTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVOK 180
 EPLNLFYIER DTGLNFCSTRP VDREYDVDF LIAYASTADG YSADLPPLP IRVEDENDNH 240
 25 PVFTEAIYNF EVLESSRPGT TVGVVCAADR DEPDTMHTRL KYSILQQTTPR SPGLPSVHPS 300
 TGVITTVSHY LDREVVDKYS LIMKVQMDMG QFFGLIGTST CIITVTDSDN NAPTFRQNAV 360
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKONE NGHFKISTDK ETNEGVLVSV 420
 KPLNYEENRQ VNLEIGVNNE APPARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI 480
 KENLAVGSKI NGYKAYDPEN RENGNGLYKK LHDPKGWITI DEISGSIITS KILDREVETP 540
 30 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPAILQE YVVICKPKMG YTDILAVDPD 600
 EPVHGAPFFY SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGX WAILAILLGI ALLPSVLLTL VCGVFGATKG 720
 KRFPEDLAQQ NLIISNTEAP GDDRVCSSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGGNQTL ESCRAGHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE 840
 35 DRMPQDYVL TYNVEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 530 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

1 11 21 31 41 51
 | | | | |
 40 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCAGAG 120
 45 CCATGGCCCA GTTTGGAGGC CTGCCCTGTC CCCTGGACCA GACCTGCCC TTAGATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CACACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
 ATGCCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGSAAAA CCTTCCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGG AAAGTGACGT 360
 CAGTGATTCC TGGCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 50 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGGTGACTG CACCATTCCT CTTGGAAGCC TGCAAAATTC TCTGCTTGAT GGAAGTGGCC 660
 55 CCCTCCCCAT TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCCTGCCTG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
 CCCTGTGTGA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTG ATCAAGGTCT 840
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGTCTA CAGATGGCTG 900
 GCCCATGTGC TGGAAAGTGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT 960
 60 TCCACCCAGG CGTGTGTAAAC ATCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 531 Protein sequence
 Protein Accession #: NP_057667.1

1 11 21 31 41 51
 | | | | |
 65 MFQTGGLIVF YGLLAQTMAG FGGLPVPLDQ TLPLNVNPAI PLSPTGLAGS LTNALSNGLL 60
 SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSTVP GLNNIIDIKV TDPQLLELGL 120
 70 VQSPDGHRLY VTIPLGILKQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGPLPI QGLLDSLTI LNKVLPVLVQ GNVCPVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIK

Seq ID NO: 532 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

1 11 21 31 41 51
 | | | | |
 80 CTCAGGCGAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAAAGT 60
 TCCTGGAAGT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCCTCCCA CAGATGTGTC ATCCCTTGGC AGAGGCTCCT GCTCAGAGCC 180
 TCACTTCTAA CTTCTTGAA CCGCCCAACC ACTGCCAAGC TCACTATTGA ATCCAGCCCG 240
 85 TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAAATCTGCC CCAGCATCTT 300
 TTTGGCTACA GCTGTGACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
 GTAATAGGAA CTCAACAAGC TACCCAGGG CCGCATACA GTGGTCGAGA GATAATATAT 420
 CCCAATGCAT CCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTTA 480

5
10
15
20
25
30
35
40
45

CAGCTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
CAGAGCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAAT 780
GCCAGGCGCA GTGATTCACT CATCTGAAT GTCTCTATG GCCCGGATGC CCCCACTATT 840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCTG CCACGCAGCC 900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTCTCCAGCA ATCCACCCAA 960
GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
CCCAAAACCT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
CTCCCGGTCA GTCCCGGCT GCAGCTGTCC AATGACAACA GGACCTCTAC TCTACTCAGT 1260
GTCAACAGGA ATGATGTAGG AACCTATGAG TGTGGAATCC AGAACGAAT AAGTGTGAC 1320
CACAGCGACC CAGTCATCTT GAATGTCTCT TATGGCCAG ACGACCCAC CATTTCCTCC 1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
CCACCTGACG AGTATTCTTG GTGATTGAT GGGAACTCC AGCAACACAC ACAAGAGCTC 1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGAATCTATA CCTGCCAGGC CAATAACTCA 1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGG TCTCTGCGGA GCTGCCCAAG 1620
CCCTCCATCT CCAGCAACAA CTCCAAAACC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
GTCAGTCCA GGTGTCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTACA 1800
AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
GACCCAGTCA CCTGGATGT CCTCTATGGS CCGGACACCC CCATCATTTT CCCCCAGAC 1920
TCGTCTTACC TTTGGGAGC GAACCTCAAC CTCTCTGCC ACTCGGCTC TAACCCATCC 1980
CCGAGTATT CTGGGCTGAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
GCCAAAATCA CGCCAAATAA TAAACGGGACC TATGCTGTG TTGTCTCTAA CTGGCTACT 2100
GGCCGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
TAGCAGCCTT GGTGTAGTTT CTTCATTTC GGAAGACTGA CAGTTGTGTT GCTTCTTCT 2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTCTTTT ACCAAGGATA TTTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGG CTGTGGTGGC CGCACCTGTA GTCCAGTTA CTCGGGAGGC 2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATG CAGTGAGCCC AGATCGCACC 2520
ACTGCATCCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAA AAAAGAAAGC 2580
TCGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640
AACTTTAATG AACTAATGTA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATGTC TGATTCTTTA AATGTCTTGT 2760
TTCCAGATT TCAGGAAACT TTTTCTTTT TAAGCTATCC ACTCTTACAG CAATTTGATA 2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
AGACTTGGGA AACTATTCTA GAATATTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 533 Protein sequence
Protein Accession #: NP_004354.1

50
55
60

1 11 21 31 41 51
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLQ 60
HLFGYSWKYK ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTEBPE TQDATYLLWV 180
NNQSLPVSFR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQS TQELFIPNIT VNNSGSYTCQ 300
AHNSDTGLNR TTVTTIIVYA EPKPPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVWNI 360
QSLFVSPRLQ LSNDRNRLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGDDPTI 420
SPSYTYRRPG VNLSLSCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSAGHSRRT VKTTIVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
LPVSPRLQLS NGNRTLFLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPIISP 600
PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQHTQVL FIAKITPNNN GTYACFVSNL 660
ATGRNNSIVK SITVSAGSTS PGLSAGATVG IMIGVLVGA LI

Seq ID NO: 534 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

65
70
75
80

1 11 21 31 41 51
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT 60
TGGAATATGT ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCTCTG ATCGGCATAT TGTGGGCGAT CTGCCCTCTC TGCCTGTCTG TTTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTGTGAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCCAACCTC TTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
TGATGACGAG TGAAGAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GGGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCGGGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCCTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATCA ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
ATTGTCATT CTCTGCTGGA CTTTTGGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

Seq ID NO: 535 Protein sequence
Protein Accession #: NP_008883.1

85

1 11 21 31 41 51

MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAN 60
 IGIFVGLICLF CLSVLGIYGI MKSSRKILLA YFILMPIVYA FEVASCITAA TQRDPFTPNL 120
 FLKQMLERYQ NNSPNNDDQ WKXNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180
 DADYPWPRQC CVMNKLKPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 | | | | |
 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CTTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTCTTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
 TCCGGTGGCG CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCCAGGA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
 CGGTCTCTTG TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGCT CTAAGTCCC 540
 TGTGCGCCTT CCCCTTCCA CACTGTCCAT TCTTCTCTCC ATTACAGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTTCATAATA A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 | | | | |
 MRASSFLIVV VFLLIAGTLVL EAAVTGVPVK GQDTVKGRVP FNGQDPVKQG VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEGSCG MACFPVPQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 | | | | |
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTGCG GGCAGCTGCT TCACCCCTCT 60
 CTCTGCGAGC ATGGGGCTCC CTGCTGGACC TCTCGCTCTC CTCTCTCTTC TCCAGGTTTG 120
 CTGGCTGCAG TCGCGCGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CCGCCAGGCG CTGGGGAAAG TATTTCATGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAATAATGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTCTTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
 CTTGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACGGGAGGA 600
 GATTGCGAAG TATGAGCTCT TTGCCACGCG TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCAGG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAAGCAAGAG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAAT GCACTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACTCACA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCACC ACCCACCTG AGAGCAACCA GGGCATCCTG ACAACAGGA AGGGTTTGA 1260
 TTTTGAAGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAAGAGG CCCCTTTTGT 1320
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCCACTCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGTACCG 1500
 CATCTGAGA GTCTGACAGC GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGTGT 2100
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CTTACTCCCA GAAGATGACA CCGTGACAA 2160
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCAAGCCGGA GGTGGTTCTC CGCAATGACG TGGACCAAC 2280
 CATCATCCCG ACACCAATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGCCCT ACACACCTC 2400
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCGCG TCCCTGAGCT CCCTCACCTC 2460
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCTC TGCAGGGCTG 2580
 GGGACCAAAC GTGAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
 GACTTCCGAG CTTGTGAGGA AGTGCCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCTAG AGGCCAAGTT TCCAGAAGCC 2820
 TCTTACCTGC CGTAAATATG TCACCTCTGT GTCTGGGCG TGGGCTGCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940

TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCCT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCGCTCC TGCAATTCTG GTTCCAGAC CCCAATGCCT CCCATTCGGA 3060
TGGATCTCTG CGTTTTTATA CTAGATGTGC CTAGGTGCC CTTTATTTT TATTTTCCCT 3120
5 GTTGGGTGCG TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
Protein Accession #: NP_001784.2

10 1 11 21 31 41 51
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
15 KGPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLEN KPLDREBIAK 180
YELFGHAYSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDMGDGGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEM AVGHEVQRLT VTDLDAPNSP 360
AWRATYLIMG GDDGDHETIT THESNQIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
20 DPAGWLAMPD DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
VNDHGFPEP RQITICNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFILPVL 660
GAVLALLFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIP TMYRPRPAN PDEIGNPIIE NLKAANTDPT APPYDTLLVF 780
25 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLW EMGSRFKKLA DMYGGEDED

Seq ID NO: 540 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

30 1 11 21 31 41 51
ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GCGCGCGGCC CGGGGGCGGG 60
CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
35 AAGGCGCGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
GCGAGACAAC GAGATCCAGA GGAATCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATAGG 360
40 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTT CACGTTTTTT CATGTTGCG 420
AAGCAGTGTCT CCGCTGTTTG TGCGAGCATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
CTCCTGGAAG AGCCCATGCC CTCTCTTTAC CTCAAGTGTG GTAAATTCG CTACTGCAAT 540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
45 AGCTGTGTGG GGTGTGGCT GGCATCCTC CTGCTGTGG CCTCCATTGC AGCCGGCCTC 660
AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
Protein Accession #: Eos sequence

50 1 11 21 31 41 51
MRLQRPRQAP AGGRRAPRGG RGSFYRPDPG RGARRLRRFO KGGEGAPRAD PFWAPLGTMA 60
LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRRVW CHVCERENTF ECQNPRRCKW 120
TEPYCVIAAV KIPRPFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFFY LKCKKIRYCN 180
55 LGGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASTAAGL SLS

Seq ID NO: 542 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

60 1 11 21 31 41 51
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
TGCGGCGCCG AAGCGGCGCG CGCTAGCGGC GCCCGCGGCC GAGGAGAAGG AAGAGGCGCG 120
65 GGAGAAGATG CTGGCCGCGA AGAGCGCGGA CGGCTCGCGC CCGGCAGGCG AGGGCGAGGG 180
CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAAOCCGCTG GCCATCATCG TGGGGACCAT 240
TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGACG GCTCGCCGGG 300
GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
CGCGGAGCTC GGCACCAACA TCTCCAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT 420
70 CTACGGCTCG CTGCCCCGCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGCGCTTC 480
ATCGCAGTAC ATCGTGGCCC TGGTCTTGG CACCTACCTG CTCAAGCCG TCTTCCCCAC 540
CTGCCCGGTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
GGCGGTGAAC TGCTACAGCG TGAAGGCCGC CACCGGGTTC GTCAGATCG GAAAGGGTGA 720
CAGCTCTCTG GCCCTGGCCC TGATCATCTT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 780
75 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAAGTGGATG TGGGGAACAT 840
TGTGCTGGCA TTATACAGCG CCTCTTTTGC CTATGGAGGA TGGAAATTA TGAATTTGCT 900
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCG GCCATCATCA TCTCCCTGCC 960
CATCGTGAGC CTGCTGTACG TGCTGACCAA CCTGGCCTAC TTCACCAACC TGTCACCGCA 1020
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGCGCTCAT 1080
80 GTCCTGGATC ATCCCCGCTT TCGTGGGCTT GTCTTGCTTC GGCTCCGTC ATGGGTCCCT 1140
GTTCAATATC TCCAGGCTCT TCTTCTGTGG GTCCCGGAAA GGCCACCTGC CCTCCATCCT 1200
CTCCATGATC CACCAACAGC TCTCAACCCC CGTGGCGTCC CTGCTGTTCA CGTGTGTGAT 1260
GACGCTGCTC TACGCTCTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1320
CAACTGGCTC TGGCTGGCCC TGGCCATCAT CGGCATGATC TGGCTGGGCC ACAGAAAGCC 1380
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCTC GTGTTCTTCA TCTGGCCTG 1440
85 CCTCTTCTG ATCGCGCTCT CCTTCTGAAA GACACCCGTG GAGTGTGGCA TCGGCTTCTC 1500
CATCATCTCT AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1560
GTGGCTCTCT CAGGCACTCT TCTCCACGAC CGTCCCTGTG CAGAGGCTCA TGCAGGTGGT

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

1	11	21	31	41	51	
MAGAGPKRRA	LAAPAAEEKE	EAREKMLAAK	SADGSAPAGE	GEVTLQRNI	TLNGVAIIV	60
GTIIGSGIFV	TPTGVLKEAG	SPGLALVWVA	ACGVFSIVGA	LCYAEIGTTI	SKSGGDYAYM	120
LEVYGSPLPAP	LKLWIELLII	RPSSQYIVAL	VFATYLLKPL	FPTCPVPPEEA	AKLVACLCLVL	180
LLTAVNCYSV	KAATRVQDAF	AAAKLLALAL	IILLGFVQIG	KGDVSNLDPN	FSFEGTKLDV	240
GNIVLALYSG	LFAYGGWNYL	NFVTEEMINP	YRNLPLAIII	SLPIVTLVYV	LTNLAYFTTL	300
STEQMLSSSEA	VAVDFGNVHL	GVMSWIIPVF	VGLSCFGSVN	GSFLTSSRLP	FVGSREGLHP	360
SILSMIHPQL	LTPVPSLVFT	CVMTLLYAFS	KDIFSVINFP	SFFNWLCAVAL	AIIGMIWLRH	420
RKPELERPIK	VNLALPVFFI	LACLFLIAVS	FWKTPVECGI	GFTIILSGLP	VYFVGWVWNK	480
KPKWLLQGI	STTVLCQKLM	QVVPQET				

Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

1	11	21	31	41	51	
TAAAAAGCAA	AAGAATTCGC	GGCGCGCTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCGCT	60
TCTGGATATG	AAATTCAGC	TGCTTGCTGA	GTCCTATTGC	CGGCTGCTGG	GAGCCAGGAG	120
AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACTGGAGTA	180
TCITTTGAGG	ACTCTGAGT	GGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
TGTCTCTGGT	CTTCATCTTC	CGCGTCTGG	TGTACCTGGT	GACGCGCCAG	CGTGTGTGGA	300
GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGCTCC	AACGTCTGCT	360
TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
CATGCCCTTC	ACTGCTCGTG	GTCATGCACG	TGGCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
GTGGGCTCTG	GTGACATAT	GTCTGCAGCC	TAGTGTTCAC	GGCGAGCGTG	GACATCGCCT	600
TTCTCTATGT	GTTCCATCA	TTCTACCCCA	AATATATCCT	CCCTCCTGTG	GTCAAGTGCC	660
ACGCAGATCC	ATGTCCCAAT	ATAGTGGACT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAACA	720
TTTTACCCCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
TCATCTACCT	GGTGAGCAAG	AGATGCCAAG	AGTGCCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
TGTGCACAGG	TCATACCCCT	CACGGTACCA	CCTCTTCTCG	CAACAAAGAC	GACCTCCTTT	900
CGGGTGACCT	CATCTTCTG	GGCTCAGACA	GTCATCCTCC	TCTCTTACCA	GACCGCCCCC	960
GAGACCATGT	GAAGAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGGTCTG	GCAAGTTGGG	1020
CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
CATGAGGTAG	GGGAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCCTAGTCC	1140
TCAACTCCAG	CCACTGCCC	CAGCTCGACG	GCACTGGGCC	AGTCCCCCT	CTGCTCTGCA	1200
GCTCGGTTTC	CTTTCTAGA	ATGGAATAG	TGAGGCGCAA	TGC		

Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

1	11	21	31	41	51	
MNWSIFEGLL	SGVKNYSTAF	GRIWLSLVFI	FRVLVYLVT	ERVWSDHDKD	FDNTRQPGC	60
SNVCFDEFFP	VSHVRLWALQ	LILVTCPSLL	VVMHVAYREV	QEKRHREAHG	ENSGRLYLNP	120
GKKRGGSLWNT	YVCSLVFKAS	VDIAFLYVPH	SPYPKYILPP	VVKCHADPCP	NIVDCFISKP	180
SEKNITFLFM	VATAAICLL	NLVELIYLV	KRCHECLAAR	KAQAMCTGHH	PHGTTSSCKQ	240
DDLSSGDLIF	LGSDSHPLLL	PDRPRDHVKK	TIL			

Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

1	11	21	31	41	51	
CGGGCGAAGC	AGCGCGGGCA	GCGAGATGCA	GCACCGAGGC	TTCCTCCTCC	TCACCTCCT	60
CGCCCTGCTG	GCGCTCACCT	CGCGGTCCG	CAAAAAGAAA	GATAAGGTGA	AGAAGGGCGG	120
CCCGGGGAGC	GAGTGCCTG	AGTGGGCTG	GGGGCCCTGC	ACCCCGAGCA	GCAAGGATTG	180
CGGCGTGGGT	TTCCGCGAGG	GCACCTGCGG	GGCCAGAGCC	CAGCGCATCC	GGTGCAGGGT	240
GCCCTGCAAC	TGGAAGAAGG	AGTTTGAGG	CGACTGCAAG	TACAAGTTTG	AGAACTGGGG	300
TGCGTGTGAT	GGGGGCACAG	GCACCAAGT	CCGCCAAGGC	ACCGTGAAGA	AGGCGCGCTA	360
CAATGCTCAG	TGCCAGGAGA	CCATCCGCGT	CACCAAGCCC	TGCACCCCA	AGACCAAGC	420
AAAGGCCAAA	GCCAGAGAAAG	GGAAGGGAAA	GGACTAGACG	CCAAGCCTGG	ATGCCAAGGA	480
GCCCTGTGTG	TCATATGGGG	CCTGGCCACG	CCCTCCCTCT	CCCAGGCCCG	AGATGTGACC	540
CACCAAGTGC	TCTGTCTGCG	TCGTTAGCTT	TAATCAATCA	TGCCTGCCT	TGTCTCTCTC	600
ACTCCCCAGC	CCACCCCTTA	AGTGCCCAAA	GTGGGGAGGG	ACAAGGGATT	CTGGGAAGCT	660
TGAGCCTCCC	CCAAGCAAT	GTGAGTCCCA	GAGCCCGCTT	TTGTTCTTCC	CCACAATTCC	720
ATTACTAAGA	AACACATCAA	ATAAACTGAC	TTTTTCCCCC	CAATAAAAGC	TCTTCTTTT	780
TAATAT						

Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

1	11	21	31	41	51	
MQHRGFLLLT	LLALLALTSA	VAKKKDRVKK	GGPGSECAEW	AWGPCTPSSK	DCGVGFREGT	60
CGAQTQIRIC	RVPQNWKEF	GADCKYKFEN	WGACDGGTGT	KVRQGTLLKA	RYNAQCQETI	120
RVTKPTPKT	KAKAKAKKGK	GKD				

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1

Coding sequence: 1..786

5 1 11 21 31 41 51
| | | | | |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
10 AAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACA TCCGGCTGTG GGCCTCCAG 240
CTGATCTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAATAAGC ACAAGGTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
TACCACCTGC CCGTGGTGT GAAATGTGGG ATGACCCCT GCCCAACCT TGTGACTGC 540
15 TTTATTCTA GGCACACAGA GAAGACCGTG TTTACCATTT TTATGATTTT TCGCTCTGTG 600
ATTGTCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAGA GAGCACAGAC GCATAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

Seq ID NO: 549 Protein sequence
Protein Accession #: NP_006774.1

25 1 11 21 31 41 51
| | | | | |
MDWGLHTFI GGVNKHSTSI GKVMITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
KNVCYDHPFP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRGE KRNDFKDIED 120
IKKHVKRIEG SLWWTYTSI FFRILFEAAF MYVFYFLYNG YHLPWLKCG IDPCPNLVD 180
30 FISRPTEKT VFTIFMISASV ICMLLNVAEL CYLLLLKVCFR RSKRAQTQKN HPNHALKESK 240
QNMENELISD SQQNAITGFP S

Seq ID NO: 550 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

35 1 11 21 31 41 51
| | | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60
TCACCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGCCAT GGACATCCCC CAGACCAAGC 120
40 AGGACCTGGA GCTCCCAAG TTGGCAGGGA CCTGGCCTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCCGA GGACACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
45 TGGCGAACGA GGCCACGCTG CTGATACTG ACTACGACAA TTTCTGTTT CTCTGCTTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCCTGGTG 480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCGCCCT 600
CCAGGAAGAC CAGACTCCCA CCCTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCC 660
50 TTTCAAGAA TAACACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCT 720
TCTCTGTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAAC CTGAGGAGCAT G

Seq ID NO: 551 Protein sequence
Protein Accession #: NP_002562.1

55 1 11 21 31 41 51
| | | | | |
MDIPQTKQDL ELPLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR 60
60 WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLDIDYD NFLFLCLQDT TTPIQSMMQ 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPF RP

Seq ID NO: 552 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

65 1 11 21 31 41 51
| | | | | |
ACTTGGCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
70 TCGCCGCTG CTGCTGTGCT CCTCGCTGCG CGGTGTGCCC CGGAGAGGCT GAGCAGCCTG 120
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCTGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGGCCAG GGCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCAACCCC CAAGACGAGC 360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCAGGA GTACCGCATC CAGCTCCGCG 420
75 TCTCAAAGC TCGGAGGAG CCAACATCC AGGTCAACCC CCGGGCATC CCGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCAAG 540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGT CACATTGAGT 600
CGTCCAGAC TGTGGAGTGG AGTGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
80 TGGTTAAGA AGACAAAGAT GCCCAGTTT ACTGTGAGCT CAACTACCGG CTGCCAGTG 720
GGAACCATAT GAAGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCG ACAGAAAAG 780
TGTGGCTGGA AGTGGAGGCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGT 840
GTTTGGCTGA TGGCAACCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCAGCACCA 900
GGGAGGAGA GGAAGAGACA ACCAACGACA ACGGGTCTCT GGTGCTGGAG CCTGCCCGGA 960
85 AGGAACACAG TGGGCGCTAT GAATGTGAG CCGTGAACCT GGACACCATG ATATCGCTCG 1020
TGAGTGAACC ACAGGAACCTA CTGGTGAAC ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAG 1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGAG GGCCTGTG 1200

WO 02/086443

TTCACTGTGCA	TGACCTGAAAC	CGGGAGGACG	GAGGCGGCTA	TCGCTGCGTG	GGCTCTGTGC	1260
CCGACATGCA	CGGCGTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCCCTTT	1320
GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
GTAAGAGCTC	AGGGCACC	CGGCCACCA	CTCCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
AACAAGCAAC	AGATCCACAG	CGAGTCTGTA	TGCTCCTGAA	TGTCCTCGTG	ACCCCGGAGC	1500
TGTTGGAGAC	AGGTGTGAA	TGCAOGGCT	CCAAGACCT	GGGCAAAAC	ACCGACATCC	1560
TCTTCTGGA	CTGGTCAAT	TTAACCAACC	TACACACCA	CTCCAACACA	ACCATGGCC	1620
TCAGCATCTC	CTACGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
TGGCGAGGAC	GGAGAGCCGG	GGCGTGTGTA	TCTGGGTGT	GATTGTGTGC	ATCCCTGGTC	1740
TGGCGGTGCT	GGCGCTGTG	CTTATTTTC	TCGTATGAA	GGGACAGTC	CGGTGCAGGC	1800
GCTCAGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTGTAA	GACCGAACT	GTAGTTGAAG	1860
TTAAGTCA	TAAAGTCCCA	GAGAGATGG	CGCTCTGCA	GGGCAGCAGC	GGTGACAAGA	1920
GGGCTCCGG	AGACACAGGA	GAGAAATACA	TGCTCTGAG	TGATCTGCC	CGAATCACTT	1980
CAGCTCCCTT	CCCTGCCTGG	ACCATCCCA	GCTCCGTCTG	CACCTCTCTC	TCAGGCCAAG	2040
CCCTCAAAG	GACTAGAGAG	AGACCTCCTG	CTCCCCTCAC	CTGCACACC	CCTTTCAAG	2100
GGCCATGGG	TAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
TGTCACCAC	ATCTCCTCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
CCGAGCGGGT	AGGAGAGTTT	CTTCCAGAA	GTGTTTTTC	TTTACACACA	TTATGGCTGT	2280
AAATACCTGG	CTCCTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCCC	2340
CAAAGGCTGG	CTTGCACCAT	CGAGGTGCAC	CATGAAGTGT	AGGACACAGC	GGAGCCGAGC	2400
GCGTGCTCAT	GTGGAAGTGC	CCTGTTTACA	CCCGTCCGG	AGAGCACCCC	AGCGGCATCC	2460
AGAAGCAGCT	GCAGTGTGCA	AGCCACCAC	CTCCTGTCCG	CCCTCTCAA	GTCTCTGTG	2520
ACATTTTTTC	TTTGGTCTAG	AGCCAGGAAC	TGGTGTCAAT	TTCTAAAAG	TACGTCCCGG	2580
GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CACGACATCT	GGGAGGCGGA	GGCGGGCGGA	2640
TCACAAAGCT	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCTCTGCT	CTACTAAAAA	2700
TACAAAAAAA	AATTAGCTAG	CGGTAGTGGT	TGCGACCAT	AGTCCGACGT	ACTCGGAAGG	2760
CTGAAGCAGG	AGGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
CAGTGCACTC	CAGCCTGGGC	AACACAGCA	GACTCCGCTG	CGAGGAAAAA	AAAAAGAAAG	2880
ACCGTGACCT	CGGTTGAGCA	AGCTGGGCGC	GTGTTTCGAG	TTACGTTGAA	TTAGCCTCAA	2940
TCCCGTGTTT	CACCTGTCTC	CATAGCCCTC	TTGATGATC	ACGTAAAACT	GAAAGGCAGC	3000
GGGGAGCAGA	CAAAAGTAGAG	GTCTACAGTC	TGCTTCATGG	GGATTAAAGC	TATGGTTTAT	3060
TTAGACACCA	ACTTCTACAA	ACCAAGCTCA	GGGCCCAAC	CCTAGAAGGG	CCCAATAGAG	3120
AGAAATGGTAC	TAGGGATGGG	AAAAACGGGC	CTGGCTAGAG	CTTGGGTGCT	GTGTGTCTGT	3180
CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	TATGTCCAAA	3240
TGTTTTCTTT	TATATATGTA	TGTTATATATA	TATATGAAAA	TAGATATATA	TATGAAAAAT	3300
AAAGCTTAAT	TGTCCGAGAA	AATCATACAT	TGCTTTTTTA	TTCTCATATG	GTATCCACAGG	3360
AACCTGGGGG	CCTGTGGAAC	TACAAACAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTTACCCA	GAGCAGACAG	3480
CTACCTCTAT	TTTCAGCAGC	AAAAACGTCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
TGTTATGAGG	AGCTATGTCC	CTTCTCATCG	TTTCCGTCCA	CTT		

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

	1	11	21	31	41	51	
45	GLPLRLVCAFL	LAACCCCPRV	AGVPGEAEQP	APELVEVEVG	STALLKCGLS	QSQGNLSHVD	60
	WFSVHKKEKT	LIFRVRQGGG	QSEPEYEQR	LSLQDRGATL	ALTQVTQPDE	RIFLQCGKRP	120
	RSQEYRIQLR	VYKAAPEEPNI	QVNPGLGIPVN	SKEPEEVATC	VGRNGYPIQP	VIWYKNGRPL	180
50	KEEKNRVIHQ	SSQTVESSGL	YTLQSLIKAQ	LVKEDKDAQF	YCELNRYRLPS	GNHMKSGREV	240
	TPVPFYFTEK	WVLEVEPVGM	LKEGDRVEIR	CLADGNPPPH	FIS1KQNPST	RAEAESTTND	300
	NGVLVLEPAR	KEHSGRYEQQ	AWNLDTMISL	LSEPEQLLVN	YVSDVRVSPA	APERQEGSSL	360
	TLTCEAESSQ	DLEFPQLREE	TQVQLERGPV	LQLHLDLKREA	GGGYRCVASV	PSIPGLNRTQ	420
	LVKLAIFGPP	WMAFKERKVN	VKEMVLNLNS	CEASGHPRPT	ISWNVNTASV	EQDQDPQRVL	480
55	STLNLVLTPE	LLETGVECTA	SNDLGKNTSI	LFLELVNLTT	LYPDNSTTTG	LSTSTASPTP	540
	RANSTSTERK	LEPESRGGV	IVAVIVCILV	LAVLGAVLVF	LTYSKKGKLP	RSQKQEITLP	600
	PSRKTLVVVE	VKSDKLPEEM	GLQVSSGDK	RAPVQGEKY	IDLRE		

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

	1	11	21	31	41	51	
65	TCGAGCCTGG	CGGTAGAATC	TTCCAGTAG	GCGGCGCGGG	AGGGA AAAA	GGATTAGGG	60
	GCTAGGCCGG	GCGGATCCCG	TCCTCCCCCG	ATGTGAGCAG	TTTTTCGAAA	CCCGCTCAGG	120
	CGRAGGCTCG	CAGAGAGAGT	GGAGTCGGTA	CGCGGGCCGG	GAACATGAGG	CAGCTCTCTC	180
	TATTTCTGAC	CAGCGTGGTT	CCTTTCGTGC	TGGCGCCGCG	ACCTCGGATG	GACCCGGGGT	240
	TCGGCCCCCA	CAGAGAGACT	CAGAGAGCTTG	ATTCTTTGCT	CTCAGACTAC	GATATTCTCT	300
70	CTTTTATCTAA	TATCCAGCAG	CATTCCGGTAA	GAAAAGAGAG	TCTACAGACT	TCAACACATG	360
	TAGAACCAT	ACTAATCTTT	TCAGCTTTAG	AAAGGCATTT	TAAATTATAC	CTGCATCAAA	420
	GTAGCTAAGC	TTTTTACAAA	AATTTCAAGG	TCGTTGGTGT	GGATGGTAAA	AACGAAAGCG	480
	AGTACATCGC	AAAATGGCAG	GACTTCTTCA	CTGGACAAGT	GGTTGGTTEAG	CCTGACTCTA	540
	GGGTTCTAGC	CCACATAAGA	GATGATGATG	TTATAATCAG	AATCAACACA	GATGGGGCCG	600
75	AATATAACAT	AGAGCCACTT	TGGAGATTGT	TTAATGATAC	CAAGAGACAA	AGAATGTTAG	660
	TTTATAAAT	TGAAGATATC	AAGAATGTTT	CACGTTTGCA	GTCTCCAAAA	GTGTGTGGTT	720
	ATTTAAAAAT	GGATAATGAA	GAGTTGCTCC	CAAAGGGGTT	AGTAGACAGA	GAACCAACTG	780
	AAGAGCTTGT	TCAATCAGTG	AAATTAACAG	CTGACCCAGA	TCCCATGAAG	AACAGTGTA	840
	AATTATTGGT	GGTAGCAGAT	CATCGTTCT	ACAGATACAT	GGGCAGAGGG	GAAGAGAGTA	900
80	CAACTACAAA	TTACTTAATA	GAGCTAATTG	ACAGAGTTGA	TGACATCTAT	CGGAACACTT	960
	CATGGGTAAA	TCCAGGCTTT	TCCAGGCTATG	GAATACAGAT	AGAGCAGATT	CGCATTCTCA	1020
	AGTCTCCACA	AGAGGTAAAA	CCTGGTGAAA	AGCATACAAA	CATGGCAAAA	AGTTACCCAA	1080
	ATGAAGAAA	GGATGCTTGG	GATGTGAAGA	TGTTGCTAGA	GCAATTATAG	TTTGATATAG	1140
	CTGAGGAAGC	ATCTAAAGTT	TGCTTGGCAG	ACCTTTTCAC	ATACCCAGAT	TTTGATATGG	1200
85	GAACTCTTGG	ATTAGCTTAT	GTTGGCTCTC	CCAGAGCAAA	CAGGCAATGGA	GGTGTTTGTC	1260
	CAAAAGGCTTA	TTATAGCCCA	GTTGGGAAGA	AAAATATCTA	TTTGAATAGT	GGTTTGAACA	1320
	GCACAAAGTA	TTATGGTAAA	ACCATCTTAA	CAAGAAGAGC	TGACCTGGTT	ACAACTCATG	1380

	AATTGGGACA	TAATTTTGGG	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCGGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCAGCAGA	1500
	ACAATAAGAT	GTTTTCAAAAC	TGCAGTAAAC	AATCAATCTA	TAAGACCATT	GAAAGTAAGG	1560
5	CCAGGAGTGT	TTTTCAAGAA	CGCAGCAATA	AAGTTTGTGG	GAACCTCGAG	GTGGATGAAG	1620
	GAGAAGAGTG	TGATCCTGGC	ATCATGTATC	TGAACAAACG	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAAGGTGC	CAGTGCAGTG	ACAGGAACAG	TCCTTGCTGT	AAAACTGTCT	1740
	AGTTTGAGAG	TGCCAGAGAAG	AAGTGCCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
10	TTTGCTTGGG	TCTTGGCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTTCTGC	GAGAGGGAAC	1920
	AGCAGCTGGA	GTCCGTGTGA	TGTAATGAAA	CTGCAAACTC	CTGCAAGGTG	TGCTGCAGGG	1980
	ACCTTTCTGG	CGCTGTGTGT	CCCTATGTGC	ATGCTGAACA	AAAGAACTTA	TTTTTGAGGA	2040
	AAGGAAAGCC	CTGTACAGTA	GGATTTTGTG	ACATGAATGG	CAATGTGAG	AAACGAGTAC	2100
	AGGATGTAAT	TGAACGATTT	TGGGATTTCA	TTGACCAGCT	GAGCATCAAT	ACTTTTGGAA	2160
	AGTTTTTAGC	AGACAACATC	TTGGGTCTGT	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTG	2220
15	CTTTCAGCAT	TCTTGTCCAT	TGTGTGGATA	AGAAATTGGA	TAAACAGTAT	GAATCTCTGT	2280
	CTCTGTTTCA	CCCCAGTAAC	GTGCAAAATG	TGAGCAGCAT	GGATTCTGCA	TGGTTCGCA	2340
	TTATCAAAAC	CTTTCCTGCG	CCCCAGACTC	CAGGCCGCTC	GCAGCCTGCC	CCTGTGATCC	2400
	CTTCGGCGCC	AGCAGCTCCA	AAACTGGACC	ACCAGAGAAT	GGACACCATC	CAGGAAGACC	2460
20	CCAGCACAGA	CTCCCATATG	GACGAGGATG	GGTTTGAGAA	GGACCCCTTC	CCAAATAGCA	2520
	GCACAGCTGC	CAAGTCATTT	GAGGATCTCA	CGGACCATCC	GGTCGCCAGA	AGTGAAAAGG	2580
	TGCGCTCTCT	TAAACTGCAG	CGTCAGAAAT	GTGTTAACAG	CAAGAAACAG	GAGTGCTAAT	2640
	TTAGTTCTCA	GCTCTTCTGA	CTTAAGTGTG	CAAAATATTT	TTATAGATTT	GACCTACAAA	2700
	TCAATCACAG	CTTGATTTTT	GTGAAGACTG	GGAAATGACT	TAGCAGATGC	TGGTCATGTG	2760
	TTTGAACCTC	CTGCAGGTAA	ACAGTTCTTG	TGTGGTTTGG	CCCTTCTCCT	TTTGAAAAGG	2820
25	TAAGTGAAA	GTGAATCTAC	TTATTTTGTG	GCTTTCAGGT	TTTAGTTTTT	AAAATATCTT	2880
	TTGACCTGTG	GTGCAAAAGC	AGAAAATACA	GCTGGATTGG	GTTATGAATA	TTTACGTTTT	2940
	TGTAAATTA	TCTTTTATAT	TGATAACAGC	ACTGACTAGG	GAATGATCA	GTTTTTTTTT	3000
	ATACACTGTA	ATGAACCGCT	GAATATGAAG	CATTTGGCAT	TTATTTGTGA	GAAAAGTGGA	3060
30	ATAGTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTCAACTAA	AAACAAAGGA	GATAAATTTA	3120
	GTATACATGT	TATCTAAATT	GTGGGTCTAT	TTCTAGTTAT	TACCCAGAGT	TTTTATGTAG	3180
	CAGGGAATA	ATATATCTAA	ATTAGAAAT	CATTTGGGTT	AATATGGCTC	TTTCAATATC	3240
	TAAGACTAAT	GCTCAGAACC	TAACCACTAC	CTTACAGTGA	GGGCTATACA	TGGTAGCCAG	3300
	TTGAATTTAT	GGAACTCTAC	AACTGTTTAG	GGCCCTGATT	TGCTGGGCAG	TTTTTCTGTA	3360
	TTTTATAAGT	ATCTTCAATG	ATCCCTGTTA	CTGATAGGGA	TACATGTCTT	AGAAAATTC	3420
35	CTATTGGCTG	GGAGTGGTGG	CTCATGCTCG	TAATCCAGC	ACTTGGAGAG	GCTGAGGTTG	3480
	CGCCACTACA	CTCAGCCTG	GGTGACAGAG	TGAGATCTGC	CTC		

Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

40	1	11	21	31	41	51	
	MRQSLFLFSL	VVPFVLAPRP	PDDPGFGPHQ	RLEKLDLSLS	DYDILSLSNI	QQHSVRKRD	60
	QTSHTVETLL	TFSALKRHF	LYLTSSTERF	SQNFVIVVVD	GKNESEYTA	WQDFPTGHV	120
45	GEPSRVLAH	IRDDVVIIR	NTDGAENIE	PLWRPVNDTK	DKRMLVVKSE	DIKNVSRQLS	180
	PKVCGYLKVD	NEELLPKGLV	DREPPPEELVH	RVKRRADPDP	MKNCKLLLV	ADHRFYRYMG	240
	RGEESTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGIQIE	QIRILKSPQE	VKPGKHYNM	300
	AKSYNNEED	AWDKMLLEQ	FSPDIAEAS	KVCLAHLEFY	QDFDMGLTGL	AYVGSFRANS	360
	HGGVCPKAY	SPVKGKNIYL	NSGLTSTKNY	GKTIILTKEAD	LVTTHLHGN	FGAHDPDGL	420
50	AECAPNEDG	GKYVMYPIAV	SGDHENKMF	SNCSSQSIYK	TIESKAQECF	QERSNKCNG	480
	SRVDEGEED	PGIMYLNNDT	CMSDCTLKE	GVQCSDRNSP	CKNKCQFETA	QKKCQEAINA	540
	TCKGVSYCTG	NSSECPPPGN	AENDTVCLDL	GKCKDKGKIP	FCEREQQLS	CACNETDNC	600
	KVCCRDLGR	CVPVYDAEQK	NLFLRKGP	TVGFCDMNGK	CEKRVQDVIE	RFWDFIDQLS	660
	INTFGKFLAD	NIVGSLVFS	LIFWIPFSIL	VHCVDKLLDK	QYESLSLPH	SNVEMLSMD	720
55	SASVRIKPF	PAPQTPGRLQ	PAPVIPSAPA	APKLDHQRM	TIQEDPSTD	HMDEDGFEK	780
	PPNSSTAARK	SFEDLTDHPV	ARSEKAASFK	LQRQNRVNSK	ETEC		

Seq ID NO: 556 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

60	1	11	21	31	41	51	
	TCGAGCCTGG	CGGTAGAATC	TTCCAGTAG	GCGGCGCGGG	AGGAAAAGAG	GATTGAGGGG	60
65	CTAGGCCGGG	CGGATCCCGT	CCTCCCCCGA	TGTGAGCAGT	TTTCCGAAAC	CCCGTCAGGC	120
	GAAGGCTGCC	CAGAGAGGTG	GAGTCGGTAG	CGGGGCCGGG	AACATGAGGC	AGTCTCTCCT	180
	ATTCTGAGCC	AGCGTGGTTC	CTTTCGTGCT	GGCGCCGCGA	CCTCCGATG	ACCCGGGCTT	240
	CGGCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
70	TTTATCTAAT	ATCCAGCAGC	ATTCCGTAAG	AAAAAGAGAT	CTACAGACTT	CAACACATGT	360
	AGAAACACTA	CTAACTTTT	CAGCTTTGAA	AAGGCATTTT	AAATTATACC	TGACATCAAG	420
	TACTGAACGT	TTTTCAACAA	ATTTCAAGGT	CGTGGTGGTG	GATGGTAAAA	ACGAAAGCGA	480
	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
	ATATAACATA	GAGCCACTTT	GGAGATTGTT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
75	TTATAAATCT	GAGATATCA	AGAAATGTTT	ACGTTTGCG	TCTCCAAAAG	TGTGTGGTTA	720
	TTTAAAAGTG	GATAATGAAG	AGTTGCTCCC	AAAAGGGTTA	GTAGACAGAG	AACCACCTGA	780
	AGAGCTTGTT	CATCGAGTGA	AAAGAAAGAG	TGACCCAGAT	CCCATGAAGA	ACACGTGTAA	840
	ATTATTGGTG	TAGCAGATC	ATCGCTTCTA	CAGATACATG	GGCAGAGGGG	AAGAGAGTAC	900
80	AACTACAAAT	TACTTAATAG	AGCTAATGTA	CAGAGTTGAT	GACATCTATC	GGAACACTTC	960
	ATGGGATAAT	GCAGGTTTTA	AAGGCTATGG	AATACAGATA	GAGCAGATTC	GCATTCTCAA	1020
	GTCTCCACAA	GAGCTAAAC	CTGGTGAAAA	GCACTACAAC	ATGGCAAAAA	GTTACCCAAA	1080
	TGAAGAAAAG	GATGCTTGGG	ATGTGAAGAT	GTGCTAGAG	CAATTTAGCT	TTGATATAGC	1140
	TGAGGAAGCA	TCTAAGATT	GCTTGGCACA	CCTTTTCA	TACCAAGATT	TTGATATGGG	1200
	AACTCTTGGA	TGATCTATG	TTGGCTCTCC	CAGAGCAAA	AGCCATGGAG	GTGTTTGTCC	1260
85	AAAGGCTTAT	TATAGCCCAG	TTGGGAAGAA	AAATATCTAT	TTGAATAGTG	GTTTGACGAG	1320
	CACAAAGAA	TATGGTAAAA	CCATCCTTAC	AAAGGAAGCT	GACCTGGTTA	CAACTCATGA	1380
	ATTGGGACAT	AATTTTGGAG	CAGAACATGA	TCCGGATGGT	CTAGCAGAAT	GTGCCCCGAA	1440

5 TGAGGACCAG GGAGGGAAAT ATGTCATGTA TCCCATAGCT GTGAGTGGCG ATCACCAGAA 1500
 CAATAAGATG TTTTCAAACT GCAGTAAACA ATCAATCTAT AAGACCATTG AAAGTAAGGC 1560
 CCAGGAGTGT TTTCAAGAAC GCAGCAATAA AGTTTGTGGG AACTCGAGGG TGGATGAAGG 1620
 AGAAGAGTGT GATCCTGGCA TCATGTATCT GAACAACGAC ACCTGCTGCA ACAGCGACTG 1680
 10 CACGTTGAAG GAAGGTGTCC AGTGCAGTGA CAGGAACAGT CCTTGTCTGTA AAAACTGTCTA 1740
 GTTTGAGACT GCCCAGAAGA AGTGCCAGGA GCGGATTAAT GCTACTTGCA AAGGCGTGTCT 1800
 CTACTGCACA GGTAAATAGCA GTGAGTGGCC GCCTCCAGGA AATGCTGAAG ATGACACTGT 1860
 TTGCTTGGAT CTTGGCAAGT GTAAGGATGG GAAATGCATC CCTTCTGCGC AGAGGGGAACA 1920
 GCAGCTGGAG TCCTGTGCAT GTAATGAAAC TGACAACCTC TGCAAGGTGT GCTGCAGGGA 1980
 15 CGCTTCCGCG CGCTGTGTGC CCTATGTCGA TGTCTGAACAA AAGAACTTAT TTTTGAGGAA 2040
 AGGAAAGCCC TGTACAGTAG GATTTGTGTA CATGAATGGC AAATGTGAGA AACGAGTACA 2100
 GGATGTAATT GAACGATTTT GGGATTTCAT TGACCAGCTG AGCATCAATA CTTTGGAAA 2160
 GTTTTGTAGCA GACAACATCG TTGGGTCTGT CCTGGTTTTC TCCTTGATAT TTTGGATTCC 2220
 TTTTCAGCAT CTTGTCCATT GTGTGTAAAG TCGAAATGCT GAGCAGCATG GATTCTGCAT 2280
 20 CGGTTCCGAT TATCAAAACC TTTCTGCGC CCCAGACTCC AGGCCGCTG CAGCCTGCC 2340
 CTGTGATCCC TCGGCGCCA GCAGCTCCAA AACTGGACCA CCAGAGAATG GACACCATCC 2400
 AGGAAGACCC CAGCAGACAG TCACATATGG ACGAGGATGG GTTTGAGAAG GACCCCTTCC 2460
 CAAATAGCAG CACAGTGGC AAGTCATTG AGGATCTCAC GGACCATCCG GTCAACAGAA 2520
 GTGAAAAGGC TGCCTCCTTT AAATGTCAGC GTCAGAATCG TGTGACAGC AAAGAAACAG 2580
 25 AGTGCTAAAT TAGTCTCAG CTCTTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTG 2640
 ACCTACAATC AATACAGCT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG 2700
 GTCATGTGTT TGAACCTCCT GCAGGTAAAC AGTCTTGTG TGGTTTGGCC CTTCTCCTTT 2760
 TGAAAAGGTA AGGTGAAGGT GAATCTAGCT TATTTTGAGG CTTTCAGGTT TTAGTTTITA 2820
 AAATATCTTT TGACCTGTGG TGCAAAAGCA GAAAATACAG CTGGATTGGG TTATGAGTAT 2880
 30 TTACGTTTTT GTAAATTAAT CTTTATATAT GATAACAGGC ACTGACTAGG GAAATGATCA 2940
 GTTTTTTTTT ATACACTGTA ATGAACCGCT GAATATGAAG CATTGGCAT TTAATTGTGA 3000
 GAAAAGTGA ATAGTTTTTT TTTTTTTTTT TTTTTTTTTC CTTCAACTAA AAACAAAGGA 3060
 GATAAATTTA GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT 3120
 TTTTATGTAG CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTGGGTT AATATGGCTC 3180
 35 TTCTAATATC TAAGACTAAT GCTCAGAAC TAACCACTAC CTTACAGTGA GGGCTATACA 3240
 TGGTAGCCAG TTGAATTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG 3300
 TTTTCTGTA TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT 3360
 AGAAAATTCA CTATTGGCTG GAGTGGTGG CTCATGCGCTG TAATCCCAGC ACTTGGAGAG 3420
 3421 GCTGAGGTTG CGCCACTACA CTCAGCCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 557 Protein sequence
Protein Accession #: NP_068604.1

40 1 11 21 31 41 51
 MRQSLFLFSL VVPFVLAPRP PDDPGFGPHQ RLEKLDLSLS DYDILSLSNL QHSHVRKRDL 60
 QTSTHVELLL TFSALKRHFH LYLTSSSTERF SQNFVWVVD GKNESEYTVK WQDFFTGHVV 120
 GEPDSRVLAH IRDDDVIIIRI NTGAEYNIIE PLWRVFNVDK DKRMLVYKSE DIKNVSRLLQ 180
 45 PKVCGYLVKVD NEELLPKGLV DREPPPEELVH RVKRRADPDP MKNTCKLLV ADHRFYRYMG 240
 RGEESTTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIGIE QIRILKSPQE VKPGEKHYNM 300
 AKSYNPEERD AWDVKMLLEQ FSPDIAEAS KVCLAHLFY QDFDMGTLGL AYVGSFRANS 360
 HGGVCFKAYI SPVKKNIYL NSGLTSTKNY KXTILTKEAD LVTTHELHGN FGAHDPDGL 420
 AECAPNEDQG GKYVMYPIAV SGDHENKMF SNCSKQSIYK TIESKAQECF QERSNKKVCGN 480
 50 SRVDEBEECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA 540
 TCKGVSYCTG NSSCEPPGN AEDDTVCLDL GKCKDKGKIP FCEREQQLES CACNETDNCS 600
 KVCRRDLGR CVPYVDAEQK NLFRLKQKPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS 660
 INTFGKFLAD NIVGSVLVFS LIFWIPPSIL VHCV

Seq ID NO: 558 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20...2143

60 1 11 21 31 41 51
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTCG GTCCTGGTGC TCCTGGTGTCT 60
 GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCTGGGAGA 120
 CCTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
 CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240
 65 CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACCG TGAAGGCCAT 300
 GCGAACCCCA CGGTGCGGGG TCCAGACCT GGCAGATTG CAAACCTTGT AGGCGGACCT 360
 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAC TACTCGGAAG ACTTGCCGCG 420
 GGCAGTGATT GACGACGCTT TTGCCCGCGC CTTGCACTG TGGAGCGCGG TGACGCGCT 480
 CACCTTCACT CGCTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
 70 GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CTTTCTCTCC 600
 TGGCCCGCGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCTGGGCAA 660
 GGGCGTCGTG GTTCAACTC GGTTTGGAAA CGCAGATGGC GCGGCTGCC ACTTCCCTT 720
 CATCTTCGAG GGCGCTCCT ACTCTGCCTG CACCACCGAC GGTGCTCCG ACGGCTTGCC 780
 CTGGTGCACT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA 840
 75 GAGACTCTAC ACCCGGAGC GCAATGTCTG TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
 CCAAGGCCAA CTCTACTCCG CTTGCACAC GACGAGTCCG TCCGACGCT ACCGCTGGTG 960
 CGCCACCAAC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA 1020
 CTGAGCGGTG ATGGGGGGCA ACTCGGGGGG GAGCTGTGCT GTCTTCCCTT TCACCTTCTT 1080
 80 GGGTAAGGAG TACTCGACCT GTACAGCGA GGGCCGCGGA GATGGGCGCT TCTGGTGGCG 1140
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
 TTTGTTCTCT GTGGCGGGCG ATGAGTTCGG CCACGCGCTG GGCCTAGATC ATTCTCAGT 1260
 GCGGAGGGCG CTCTGTACCG CTTGTACCG CTTCACTGAG GGGCCCCCTT TGCATAAGGA 1320
 CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC 1380
 AACCACCAAC ACACGCGAGC CCACGGCTCC CCGACGGTTC TGCCCAACCG GACCCCCAC 1440
 85 TGTCCACCCC TCCAGCGGCC CCACAGCTGG CCCCACAGGT CCCCCTCAG CTGGCCCCAC 1500
 AGGTCCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CTTTGTAGTC CGGTGGACGA 1560
 TGCTTCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAAACAGC TGTATTTGTT 1620
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGG AGCCGCGCGC AGGGCCCCCT 1680

CCTTATCGCC GACAACTGGC CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740
 GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGGTGC 1800
 GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGGCTGGGA GCGGAGCTGG CCCAGGTGAC 1860
 CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920
 GTTTCGAGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGATGTGT 1980
 CCCCGGGGTG CCTTTGGACA CGCAGCAGCT CTTCAGTAC CGAGAGAAAG CCTATTCTCTG 2040
 CCAGGACCGC TTTCTACTGC GCGTGAAGTC CCGGAGTGAG TTGAACCAAG TGGACCAAGT 2100
 GGGGTAGCTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCTCTGCTTT 2160
 GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220
 CAAACTGGTA TTTCTGTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280
 TCACCTTGT TTTTGTGG AGTGTCTTA ATAACTTGG ATTCTCTAAC CTTT

Seq ID NO: 559 Protein sequence
 Protein Accession #: NP_004985.1

1 11 21 31 41 51
 MSLWQPLVLV LVLVGLCCFAA PRQRQSTLVL FPGDLRLNLT DRQLABEVLV RYGYTRVAEM 60
 RGEKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLRGFQTF EGDLLKWHHN 120
 ITYWIQNYSE DLPRVIDDA FARAPALWSA VTPLTFTRYV SRDADIVIQF GVAEHGDGYP 180
 FDGKDGLLAH AFPPGFIQGG DAHFDDDELW SLGKGVVVPV RFGNADGAAC HFFFIPEGRS 240
 YSACTTDGRS DGLPWCSTTA NYDTRDRFGF CPSELYTRD GNADGKPCQF PFIFQGSYS 300
 ACTTDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDGR LWCATTSNFD SDDKKGFCPD QGYSFLVLA HEGFHALGLD HSSVPEALMY 420
 PMYRFTGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480
 PTAGTGPPTS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFDKQKYW 540
 RFSEGRGSRP QGPFLIADKW PALPRKLDV FEEPLSKLFF FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSG RGKMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFVPLD 660
 THDVFYREK AYFCQDRFYW RVSSRSELNQ VDQVGVVYTD ILQCPED

Seq ID NO: 560 DNA sequence
 Nucleic Acid Accession #: NM_000213.1
 Coding sequence: 127..5385

1 11 21 31 41 51
 CGCCCGCGCG CTGCAGCCCC ATCTCCTAGC GGCAGCCAG GCGCGGAGGG AGCGAGTCCG 60
 CCCCAGAGTA GGTCCAGGAC GGGCGCACAG CAGCAGCCGA GGCTGGCCGG GAGAGGGAGG 120
 AAGAGGATGG CAGGCCCACG CCCAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC 180
 AGCGTCAGCC TCTCTGGGAC CTTGGCAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC 240
 ACGGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC 300
 CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCGCGGGCT GCCAGCGGGA GAGCATCTGT 360
 GTCATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CCTGCGGGCG 420
 AGCCAGATGT CCCCAGAGG CCTGCGGGTC CGTCTGCGGC CCGGTGAGGA GCGGCATTTT 480
 GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCGTGGAGC TGTACATCCT CATGGACTTC 540
 TCCAATCCA TGTCCGATGA TCTGGACAAC CTCAAGAAGA TGGGGCAGAA CTGGCTCGG 600
 GTCTGAGCC AGCTACACG CGACTACACT ATTGGATTG GCAAGTTGT GGACAAAGTC 660
 AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC 720
 CCCCCCTTCT CCTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT 780
 AACTGACAG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTGATGTC 840
 ATCTGACAGA CAGCTGTGTG CAGAGGGGAC ATTGGCTGGC GCCCGGACAG CACCCACCTG 900
 CTGGTCTTCT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTGTGGCT 960
 GGCATCATGA GCCGCAACGA TGAACGCTGC CACCTGGACA CCACGGGCAC CTACACCCAG 1020
 TACAGGACAC AGGATACCC GTCCGTGCCC ACCCTGGTGC GCCTGCTCGC CAAGCACAAC 1080
 ATCATCCCA TCTTGTCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTACACAC 1140
 TATTTCCCTG TCTCCTCACT GGGGGTGTCT CAGGAGGACT CGTCCAACAT CGTGGAGCTG 1200
 CTGGAGGAGG CCTTCAATCG GATCCGCTCC AACCTGGACA TCCGGGCCCT AGACAGCCCC 1260
 CGAGGCTTTC GGACAGAGGT CACCTCCAAG ATGTTCCAGA AGACGAGGAG TGGGTCTTTT 1320
 CACATCCGCG GGGGGGAAGT GGTATATAC CAGGTGCAGC TGCGGGCCCT TGAGCACGTG 1380
 GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT 1440
 TCCTTCTCGG ACGCGCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACCTGCGAG 1500
 CTGCAAAAAG AGGTGCGGTC AGCTCGCTGC AGCTTCAACG GAGACTTCGT GTGCGGACAG 1560
 TGTGTGTGCA GCGAGGGCTG GAGTGGCCAG ACCTGCAACT GCTCCACCGG CTCTCTGAGT 1620
 GACATTACGC CCTGCCTGCG GAGGGGCGAG GACAAGCCGT GCTCCGGCCG TGGGGAGTGC 1680
 CAGTGGGGGC ACTGTGTGTG CTACGGGAA GGCGCTACG AGGGTCAGTT CTGCGAGTAT 1740
 GACAATTCCT AGTGTCCCGC CACTTCCGGG TTCTCTGCA ATGACCGAGG ACGCTGCTCC 1800
 ATGGGCCAGT GTGTGTGTGA GCCTGGTTGG ACAGGCCCAA GCTGTGACTG TCCCTCAGC 1860
 AATGCCACCT GCATCGACAG CAATGGGGGC ATCTGTAATG GACGTGGCCA CTGTGAGTGT 1920
 GGCGCTGCC ACTGCCACCA GCAGTGCCTC TACACGACA CCATCTGCGA GATCAACTAC 1980
 TCGGCGATCC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGTGG 2040
 GGCACGCGCG AGAAGAAGGG GCGCAGTGT GAGGAATGCA ACTTCAAGGT CAAGATGGTG 2100
 GACGAGCTTA AGAGAGCCGA GAGGTGTGTG GTGCGCTGCT CTTCCGGGA CGAGGATGAC 2160
 GACTGCACCT ACAGCTACAC CATGGAAGGT GACGGCGCCC CTGGGCCCAA CAGCACTGTC 2220
 CTGGTGACA AGAAGAAGGA CTGCCCTCCG GGCTCCTTCT GGTGGCTCAT CCCCCTGCTC 2280
 CTCCTCTCCG TGCGCTCTCT GGCCTGCTA CTGCTGCTAT GCTGGAAGTA CTGTGCTGTC 2340
 TGCAAGGCTT GCTTGGCACT TCTCCCGTGC TGCAACCGAG GTCAATGGT GGGCTTTAAG 2400
 GAAGACCACT ACATGCTGCG GGAGAACCTG ATGGCCTCTG ACCACTTGA CACGCCCATG 2460
 CTGCGGACGCG GGAACCTCAA GGGCCGTGAC GTGGTCCGCT GGAAGGTAC CAACAACATG 2520
 CAGCGGCTCG GCTTTGCCAC TCATGCCGCC AGCATCAACC CCACAGAGCT GGTGCCCTAC 2580
 GGGCTGTCTT TGCGCCTGGC CCGCCTTTGC ACCGAGAACC TGCTGAAGCC TGACACTCGG 2640
 GAGTGCGCCC AGCTGCGCCA GAGGTGTGAG GAGAACCCTG ACAGAGTCTA CAGGCAGATC 2700
 TCGGTGTATC ACAAGCTTCA GCAGACCAAG TTCCGGCAGC AGCCCAATGC CGGGAAGAA 2760
 CAAGACCACA CCATTGTGGA CACAGTGTCT ATGGGCGCCC GCTCGGCCAA GCGGCGCCTG 2820
 CTGAAGCTTA CAGTAAGACA GGTGGAACAG AGGGCCTTCC AGGACCTCAA GGTGGCCCCC 2880
 GGCTACTACA CCCTCACTGC AGACCAAGAC GCCCGGGGCA TGGTGGAGTT CCAGGAGGGC 2940
 GTGGAGCTGG TGGACGTACG GGTGCCCTCT TTTATCCGGC CTGAGGATGA CAGCAGAAAG 3000
 CAGCTGCTGG TGGAGGCCAT CAGAGTGCCT GCAGGCATCG CCACCTCGG CCGCGCCTG 3060

5 GTAAACATCA CCATCATCAA GGAGCAAGCC AGAGACGTGG TGCTCTTTGA GCAGCCTGAG 3120
TTCTCGGTCA GCGCGGGGA CCAGGTGGCC CGCATCCCTG TCATCCGGCG TGTCTGGGAC 3180
GGCGGGAAGT CCCAGGTCTC CTACCGCACA CAGGATGGCA CCGCGCAGGG CAACCGGGAC 3240
TACATCCCGG TGGAGGGTGA GCTGCTGTTC CAGCCTGGGG AGGCGTGGAA AGAGCTGCAG 3300
GTGAAGCTCC TGGAGCTGCA AGAAGTTGAC TCCCTCCTGC GGGGCCGCCA GGTCCGCCGT 3360
TTCCACGTCC AGCTCAGCAA CCCTAAGTTT GGGGCCACC TGGGCCAGCC CCACTCCACC 3420
ACCATCATCA TCAGGGAGCC AGATGAACTG GACCGAGCT TCACGAGTCA GATGTTGTCA 3480
TCACAGCCAC CCCCTCACGG GACCTGGGC GCCCGCAGA ACCCAATGC TAAGGCCGCT 3540
GGGTCCAGGA AGATCCATTT CAACTGGCTG CCCCTTCTG GCAAGCCAAT GGGGTACAGG 3600
10 GTAAAGTACT GGATTACGGG TGAATCCGAA TCCGAAGCCC ACCTGCTCGA CAGCAAGGTG 3660
CCCTCAGTGG AGCTCAGCAA CCTGTACCGG TATTGCGACT ATGAGATGAA GGTGTGCGCC 3720
TACGGGGCTC AGGGGAGGG ACCCTACAGC TCCCTGGTGT CCGCGCCAC CCACCAAGAA 3780
GTGCGCCAGC AGCCAGGGCG TCTGGCCTTC AATGTGCTCT CCTCCACGGT GACCCAGCTG 3840
AGCTGGGCTG AGCGGGCTGA GACCAACGGT GAGATCAGAG CCTACGAGGT CTGCTATGGC 3900
15 CTGGTCAACG ATGACAACCG ACCTATTGGG CCCATGAAGA AAGTGTGTTG TGACAACCTC 3960
AAGAACCGGA TGCTGCTTAT TGAGAACCTT CGGGAGTCCC AGCCCTACCG CTACACGGTG 4020
AAGGCGCGCA ACGGGGCGCG CTGGGGGCGT GAGCGGGAGG CCATCATCAA CTGGGCCACC 4080
CAGCCCAAGA GGGCCATGTC CATCCCATC ATCCCTGACA TCCCTATCGT GGACGCCAG 4140
AGCGGGGAGG ACTACGACAG CTTCTTTATG TACAGCGATG ACGTTCTACG CTCTCCATCG 4200
20 GGCAGCCAGA GGGCCAGCGT CTCCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC 4260
TTTGCTTCCG CGGCGACGAC CAACTCCCTG CACAGGATGA CCACGACCAG TGCTGCTGCC 4320
TATGGCACCC ACCTGAGCCC ACACGTGCCC CACCGCGTGC TAAGCACATC CTCCACCCTC 4380
ACACGGGACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCGGAGG 4440
GACTACTCCA CCTCACCTC CGTCTCTCC CACGACTCTC GCCTGACTGC TGGTGTGCC 4500
25 GACACGCCCA CCCGCTTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG 4560
CAGGAGCGCG GGTGCGAGCG GCCGCTGCAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620
GGCGGTGAGC TGCATCGGCT CAACATCCCC AACCTGCGG AGACCTCGGT GGTGTGGTGA 4680
GACCTCTGTC CCAACCACTC CTACGTGTTT CGCGTGCGGG CCCAGAGCCA GGAAGGCTGG 4740
GGCGGAGAGC GTGAGGGTGT CATCACCATT GAATCCCAGG TGCAACCCGA GAGCCCACTG 4800
30 TGTCCCTGTC CAGCTCCGCG CTTCACTTTG AGCACTCCCA GTGCCCCAGG CCGCTGGTG 4860
TTCACTGCCC TGAGCCGAGA CTGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT 4920
GGGATATCG TCGGCTACCT GGTGACCTGT GAGATGGCCC AAGGAGGAGG GCCAGCCACC 4980
GCATTCGGGG TGGATGGAGA CAGCCCGGAG AGCCGGCTGA CGGTGCGCGG CCTCAGCGAG 5040
AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACTT AGGGCTTCGG GCCAGAGCGC 5100
35 GAGGGCATCA TCACCATAGA GTCCCAAGAT GGAGGACCTT TCCCGCAGCT GGGCAGCGT 5160
GCCGGGCTCT TCCAGCACCC CTTGCAAAAG CAGTACAGCA GCATCACCAC CACCCACACC 5220
AGCGCCACCG AGCCCTTCTT AGTGGATGGG CCGACCTCGG GGGCCAGCA CCTGGAGCA 5280
GGCGGCTCCC TCACCCGSCA GTGACCCAG GAGTTTGTGA GCGGACACT GACCAACAGC 5340
40 GGAAACCTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTTGACCGCA CCCTGCCCA 5400
CCCCGCCAT GTCCCATAG GGTCTCTCCC GACTCTCTC CCGGAGCCTC CTCAGTACT 5460
CCATCTTGC ACCCTGGGG GCCCAGCCCA CCCGATGCA CAGAGCAGG GCTAGGTGTC 5520
TCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC 5580
AAAGAGCTGG GAGCAGACA AGGACCACG CTTTGTCTG CACTTAATAA ATGGTTTTC 5640
TACTG

Seq ID NO: 561 Protein sequence
Protein Accession #: NP_000204.1

50 1 11 21 31 41 51
MAGPRPSPWA RLLAALISV SLSTLANRC KAPVKSCTE CVRVDKDCAY CTDEMFRDRR 60
CNTQAELLAA GQCRESVVM ESSFQITEET QIDTLRRSQ MSPQGLRVRL RPEERHFEL 120
EVFEPLSPV DLYILMDFSN SMSDDLNLK KMQNLARVL SOLTSDYITG PGKFDVKVSV 180
55 PQDMRPEKL KEPWPNDDPP FSKNVISLT EDVDEFNRKL QGERISGNLD APEGGFDAIL 240
QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTYTQYR 300
TQDYPSPVPTL VRLAKHNII PIFAVTNYSY SYEKLHTYF PVSSLGVLQE DSSNIVELLE 360
EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIYQV QLRALHEVDG 420
THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQC 480
60 CSEGWSSQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540
FQCPRTSGLF CNDRRGCSMG QVCPEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
CHCHQSLYT DTICEINYSI IHPGLCEDLR SCVQCQAWGT GEKKGRTECE CNFKVKMVD 660
LKRAEEVVVR CSFRDEDDDC TYSYTMEDGD APGPNSTVLV HKKDCPPGS FWWLIPLLLL 720
LLPLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKEG HYMLRENLM A SDHLDTPMLR 780
65 SGNLKGKRDV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840
AQLRQEVEEN LNEVYRQISG VHLQQTQKPR QPNAGKQD HTIVDTVIMA PRSAKPALLK 900
LTEKQVEQRA FHDLKVAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960
LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
70 KSQVSVRTQD GTAQGNRDYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSOMLSSQ PPPHGLDGLAP QNFNAKAAGS 1140
RKIHFNWLP SGKPMGYRVK YWIQGDSSE AHLLDSKVPS VELTNLYPC DYEMKVCAYG 1200
AQGEGPYSSL VSCRTHQEV SEPGRAPFN VSSTVQLSW AEPATNGEI TAYEVCYGLV 1260
75 NDDNRPIGPM KKVLDVDPKN RMLLIENLRE SOPYRYTVKA RAGAGWGP ER EAIINLATQP 1320
KRFMSIPIIP DIPVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDDE HLVNGRMDFA 1380
FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSSLTTR DYNLSLTRSEH SHSTTLPRDY 1440
80 ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPOSPLCP 1500
LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM AQGGGPATAP 1560
RVDGSPESR LTVGLSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1620
LQHPQLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEP VSRTLTTS 1680
LSTHMDQPF QT 1740

Seq ID NO: 562 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

85 1 11 21 31 41 51
| | | | | |

GCACGAGGGC GCTTTTGTCT CCGGTGAGTT TTGTGGGGG AAGCTTCTGC GCTGGTGCTT 60
 AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC 120
 CGGCTGTTC CCGGAGGGT CCAGAGGCCCT TTCAGAAGGA GAAGGCAGCT CTGTTTCTCT 180
 GCAGAGGAGT AGGGTCTTT CAGCCATGAA GCATGTGTG AACCTCTACC TGTTAGGTGT 240
 GGTACTGACC TACTCTCCA TCTTCGTTAG AGTGTGGAG TCCTAGAAG GCTTACTAGA 300
 GAGCCCATCG CCTGGGACCT CTGGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCAC 360
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
 ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAGC 480
 TGAGCACCGT TGTAAACAGA GAACTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540
 CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTTCGGGTG GCTCATGCTT GTAATCCTAG 600
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC 660
 CAACATGGCG AAACCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720
 GGCCTGTAAT CCCAGTTCTT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCGCGGGACG 780
 GAGGTTGACG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
 CATCTCAAAA AAAAAGAGAA AAGAAAAAGC CTGTTTAAATG CACAGGTGTG AGTGGATTGC 900
 TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTA TGCTGTGCTT 960
 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020
 TGATATTTTC AACCTTACTT CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT 1080
 TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGCCCAT 1200
 TTCTCATTTT ACATTTTAAA GTCGTTCCCT CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260
 GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
 TTTTCTCTAA CTAATAAAGT GGAATATATA TTTCAAAAA AAAAAAAAAA AA

Seq ID NO: 563 Protein sequence
 Protein Accession #: NP_037464.1

1 11 21 31 41 51
 MKHVLNLYLL GVVLTLISIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
 RSM

Seq ID NO: 564 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

1 11 21 31 41 51
 GGCACGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCCTGCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240
 AACTGAAGAA TGGGGTTCAA CTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGTC ACAATTGAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTTCAC 360
 AATGAATTTG ACACAAATGT CTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCCATG ATGCAGGATT TGACCTTGG TACTTCAAGT TTATTTCTTG CAGATACACT 600
 TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
 GATCGCTATC TGAAGGTGGT CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTTCGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
 ATCTTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT 840
 CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAGAAA 1140
 ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTCATG 1200
 TGTAGGTGAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACTGAT 1320
 GTTAGGCCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATA AATGTTTCTT 1380
 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 565 Protein sequence
 Protein Accession #: NP_076404

1 11 21 31 41 51
 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTLHNEF DTIVLPVLYL IIFVASILN 60
 GLAVWIFPHI RNKTSFIFYL KNIVVADLIM TLTFFPRIVH DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKPFQDS RMYSTFTKV LSVCVWVIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLKSLPG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRKH NQSIKRVVAV FFTCFLPYHL CRIPPTFSLH DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIIYFFMCRS FSRRLFKKSN ITRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 566 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

1 11 21 31 41 51
 ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
 GAGGACTTGG GCCTGATGGG TGCAACAGGA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
 TCCTCTGACA GCAAGGAGGA GAGGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAAGAGT 180
 CCTCAGGGAG GCGCTTCTCT CTCCATTTC GTCTACTACA CTTTATGGAG CCAATTTCAT 240
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTCGACCC AGCTCAGCTG 300
 GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTCTCTGCTC 360

CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGCTACTGCT 540
CTTGGCCTCT CGTCCGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
5 CTGATCATTT TCCTGGGTGT GATCCTAACC AAAGACAAC TGGCCCTGTA AGAGGTTATC 660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
CCGAGGAAGC TGCTCAACCCA AGATTGGGTG CAGGAAAAC TACCTGGAGTA CCGGCAGGTG 780
CCCGCAGTGT ATCTCGGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
10 AGCTATGAGA AGGTCATAAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 567 Protein sequence
Protein Accession #: NP_005356.1

15 1 11 21 31 41 51
| | | | | |
MSLEQRSPHC KPDELEAQQ EDLGLMGAQE PTGEEEEETS SSDSKEEEVS AAGSSSPPPQS 60
POGGASSIS VYVTLWSQPD EGSSSQEEEEE PSSSVDP AOL EFMFQEA LKLVAEVLVHLL 120
20 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMKPAAL LIIVLGVILT KDNCAPEEVI WEALSMGVY VGKEHMFYGE 240
PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL MLNAREPICY 300
PSLYBEVLGE EQBGV

Seq ID NO: 568 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

30 1 11 21 31 41 51
| | | | | |
GGTTACTCAT CCTGGGCTCA GGTAAGAGGG CCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
GAGCGCAAGG GAGCAGGACG GAGCCATGGA CCCCAGGAGG AAGCAGGTTG CCCAGGCCAT 120
GATCTGGAAT GCAGGCTGGC TGCTGCTGCT GCTGCTTGGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAGA TGAAGACAGT 240
35 GAAGTGCAGC CCGGCGCTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTC TCCTGGCAG TGCSGGGTG CGGTTCCGGA CTCCCGGCA AGAATGACCG 360
CGGCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAC CCGGAGGTA ATGAGAGTGC 480
40 ATACCGGCC AACCGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CCGCGGCTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTCGACGGC AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCTTGGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTTT GCACTCGGGA TGGAGTAACA GGCCCGGGT TCACGCTCAG 720
TGGCTCTGT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCTCCAGAG CCCACGACTG TGGCCTCAAC 840
45 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCAT 900
GCCAGCGCCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CAGGAGGCT CCGGGATGA 960
GGAGCCAGG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAAT CAGGGCAGTA 1020
TCTCGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
ATTGCGAGCC CTTCTGTGG CCGTGGCTGC TGGTGTCTA CTGTGAGCTT CTCCACCTGG 1140
50 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTGT 1200
CCCACCACTG GACTGGGCTG GCCAGCCCC TGTTTTCCA ACATTCGCCA GTATCCCCAG 1260
CTTCTGCTGC GCTGGTTTGC GGCCTTGGGA AATAAATAC CGTTGTATAT ATTCTGGCAG 1320
GGGTGTTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGT TCTCCGCTTG 1380
TCTCTTGTG ATGTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGA GGTGAGAGAG 1440
AGGATGTAA GCTTCTACT CACTTCTCC TAGCCAGCCT GGACTTTGGA CGGTGGGGTG 1500
55 GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCT ACTCCCCGA TCTTTGGGA 1560
ATCGGTTCCC CATATGTCTT CTTACTAGA CTGTGAGCTC CTCGAGGGA GGGACCGTGC 1620
CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAGA TTAATTACT 1680
TTGTATAGTG AAAAAAA

Seq ID NO: 569 Protein sequence
Protein Accession #: NP_055215

65 1 11 21 31 41 51
| | | | | |
MDPARKAGAQ AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGV DV 60
CTEAVGAVET IHGQFSLAVX GCGSLPFGKN DRGLDLHGLL AFILQQAQ DRCNAKINLT 120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180
AANVTVSLPV RGCVDDEFCT RDGVTGPGFT LSGSCCGSR CNSDLRNKTY FSPRIPLVR 240
70 LPPPEPTTVA STTSVTSTTS APVRPTSTTK PMPAPTSQTP RQVEHEASR DEEPRLTGGA 300
AGHQDRSNSG QYPAKGGPQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 570 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

75 1 11 21 31 41 51
| | | | | |
ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CAGGAAAAG 120
80 CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGACCTGCT CATTAGAGC 180
CTTTTGGCT TCCGTGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCC 240
TCCCGCGGC GGGGCTCGGT GGCACCTGTC ATTGCGCGT ACCAGGAGGA CCTGACTAC 300
TTGCGCAAGT GCCTGCGCTC GGCCAGCGC ATCTCCTCC CTGACCTCAA GGTGTCATG 360
GTGGTGAATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
85 GCGGCGACCG AGCAGGCGCG CTCTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
GGTGAGACGG AGGCAGCCT GCAGGAGGGC ATGGACCGTG TGGCGGATGT GGTGCGGGCC 540
AGCACCTTCT CGTGCAKATC GCAGAAATGG GGAGGCAAGC GCGAGGTCAT GTACAGGCC 600

TTCAAGGCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTGA GTCTTGAGAG AGGATCCCCA AGTAGGGGGA 720
 GTGCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTCT CCTGAGCAGC 780
 GTGCGGTACT GGATGGCCTT CAAOGTGGAG CGGGCTGTGC AGTCTTACTT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900
 GACTGGTACC ATCAGAAATT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CGCGCGCTC CAAGTGCCTC 1020
 ACAGAGACCC CCATTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
 TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCTA AGCACCACCT CTGGATGACC 1140
 TACGAGTCAG TGGTCACGGG TTCTTCCCC TTCTTCTCTA TTGCCAGGT TATACAGCTT 1200
 TTCTACCGGG GCGGCATCTG GAACATTCTC CTCTTCTCTG TGACGGTGCA GCTGGTGGGC 1260
 ATTATCAAGG CCACCTACGC CTGCTTCTCT CGGGGCAATG CAGAGATGAT CTTCATGTCC 1320
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGCTACC 1380
 ATCAACAAT CTGGCTGGGG CAACTCTGGC CGAAAAACCA TTGTGGTGAA CTTCAATTGGC 1440
 CTCAATCCCTG TGTCCATCTG GGTGGCAGTT CTCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGGC TATACTGTAT 1560
 GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 571 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
 MPVQLTTALR VVGTSLFALA VLGGILAAVY TGYQFIHTEK HYLSPGLYGA ILGLHLLIQS 60
 LPAFLHRRM RRAGQALKLP SPRRGSVALC IAAQVEDPDY LRKCLRSQR ISFPDLKVV 120
 VVDGNRQEDA YMLDIHEVL GTEQAGPFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSCIMQKW GGRKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQPFLE 300
 DWYHQKFLGS KCSFGKDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRL LNQQTWRWSKS 360
 YPREWLYNSL WFKHKLHLMWT YESVVTGFFP FFLIATVIQL FYRGRIWNIL FLFLTQVLVG 420
 IIKATYACFL RGNAMIFMS LYSLLYMSL LPAKIPAIAT INKSGWGTSG RKTIVVNFIG 480
 LIPVSIWAV LGLGLAYTAY CQDLFSETEL AFLVSGAILY GCYVWVALLML YLAIARRCG 540
 KKPEQYSLAF AEV

Seq ID NO: 572 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAAC ATTTCTCTCG CTCCTCCCTC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGCGGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCTT CGCTTGCAAT 180
 CAGCTCCTCT GTGTTTGGCG CTGGAATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTTGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300
 AAATATCCAA CATGTAATAG CCAAAACAAA TCTCCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAACTTAAA TTTCAAGGTT GGGATAAAAC ATCATTGGAA 420
 AACACATTCA TTCATAACAC TGGGAAAAA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GATTTTCAGA AATGGTGTTC AAAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCACTCGA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAAATTG 720
 GATTTCAAAG CGATTATGTA TGGAGTCGAA AGTGTAGTCT GTTTTGGGAA GCAGGCTGCT 780
 TTAGATCCAT TCATCTGTTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTATC 840
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTGTG AAGTCTTCTT AATGCAACAA 960
 TCTGGTTATG TCGAGTCTGAT GGACTACTTA CAAAACAATT TTGAGAGCA ACAGTACAG 1020
 TTCTCTAGAG AGGTGTTTTC CTCATACACT GGAAGGAAG AGATTATGA AGCAGTTTGT 1080
 AGTTTCAAGC CAGAAATATG TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTATCA 1140
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATTG TCAATAATTT GCTACCCCAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCACTAATG GCTATTATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCTGAATTA ATTGGAACCT AAGAAATAAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GGAAGGAGGA ACCCCAGATT TCTACCACA CACACTACAA TCGCATAGGG 1560
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATCTCTGGA 1620
 AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTTCTCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
 GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAACTG TTCTTAGATC TCCACATATG 1800
 AACTGTGCGG GGACTGCAGA ATCTTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATTGA CCAAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTCTG CTATCCCATC CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980
 GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACGAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTTCATCAG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAT 2100
 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGTATG AATCTGAGAA GACAACCAAG 2220
 TCCTTTCTG CAGGCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280
 CATTATTCTA CCTTTGCCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340
 TCCAGACAA AGGATTTTGGT TCCACGGTTC AACGTGGTAT ACTCGCAGAC AACCCAAACG 2400
 GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
 ACCCCTTTGT TGTCTGACAA TCAGATCTCT AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520
 TCGCCTTGC ATGCTACGCC TGTATTCTCC AGTGTGATG TGTCATTGTA ATCCATCCTG 2580
 TCTTCTATG ATGCTGACCC TTTGCTTCCA TTTTCTCTG CTTCCTTCAG TAGTGAAATTG 2640
 TTTCCGCATC TGCATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACCCAGAGT 2700
 GATAAGGTGC CCTTGCATGC TTCTCTGCCA GTGGCTGGGG GTGATTGTCT ATTAGAGCCC 2760

	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCACCC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACTTCTCTA	TGCCTTGTCT	2940
5	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACTTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
10	ACTGAACCTG	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCAACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACITTTTCAG	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTCCGCTTAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
15	TCCTCTGACC	CTGCTTCTAG	TGAAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TAAAACTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGATTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAAAACA	TGCTGCACCT	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
20	ATGCACTCTG	CTTCACCTCA	AGGTTTGACC	ATTTCCCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTGTGTTAA	AAAGTGAAAG	TTCCACCCAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCCATC	CCCCAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCCAA	AGTTCTGTTA	CTGTAAGGT	ATTTGCTGGT	4200
25	ATTCACACAG	TGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCGTCTCC	TATAGGAAAT	4260
	GGGCATGTTG	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCGTAAAC	CTCAACAAAG	4320
	TGCTGTTTTC	CTTCTAAGGC	AACCTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCTA	GCTCATCTTA	TAGAGAAATCA	4500
30	CAGGAAAAGG	TAAATGAATGA	TTCCAGACCC	CACGAAAACA	GTCTTATGGA	TCAGAAATAAT	4560
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATCC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
35	GGGCAAGGTA	CCTCAGATAG	CCCTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTTGCA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCACAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
40	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATG	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTTCAGATG	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAAATT	GAGACACTGA	AAGAGTTTTA	CCAGGAAAGTG	5340
45	CAGAGCTGTA	CTGTGCTAT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAAACAG	5400
	CACAAGATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AACTTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	5580
	TGGAGAATGA	TATGGGAACA	TAAATGTGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640
50	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	5700
	TTTCTGGTCA	TGTGCAAGTG	TGTGCAAGTG	CTTGCTTATT	ATACTGTGAG	GAATTTTACT	5760
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGGCCATG	CAGTGGGGCC	TGTTGTCTGT	5940
55	CAGTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTTCAAA	6060
	AGAAATTATT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	6120
	GGCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCCTA	TGTTAAATGCA	6180
60	CTCCTCATT	CTGGACCCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGAAAAG	6300
	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGTACATAT	CAATGCCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
	TTTCATATTA	CCAGCAGCCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATATGT	CCCAACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
65	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	GAGGAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
	CCAAATCCAG	ATAGCCCCAT	TAGTAAACT	TTTGAACCTA	TAAGTGTAT	AAAAGAAGAA	6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
70	ACTTCTGTG	CTCTGACAAC	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
	TCCACCTCTC	TGACAGTAA	TGGTGCAGCA	TTGCCTGATG	GAAATATAGC	TGAGAGCTTA	7080
	GAGTCTTTAG	TTTAAACACAG	AAAGGGGTGG	GGGGACTCAC	ATCTGAGCAT	TGTTTTCTCT	7140
75	TTCTCTAAAT	TAGGCAGGAA	AATCAGTCTA	GTTCTGTTAT	CTGTTGATT	CCCATCACCT	7200
	GACAGTAACT	TTCATGACAT	AGGATCTGCG	CGCCAAATTT	ATATCATTTA	CAATGTGTGC	7260
	CTTTTGTCAA	GACTTGTAAT	TTACTTATTA	TGTTTGAAC	AAAATGATTG	AATTTTACAG	7320
	TATTTCTAAG	AATGGAATGG	TGGTATTTTT	TTCTGTATTG	ATTTTAAACAG	AAAATTTCAA	7380
	TTTATAGAGG	TTAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAAATTTTA	7440
80	GCTGTATTGG	TAGCAATTAT	CAGGTTTGCT	AGAAATATAA	CTTTTAATAC	AGTAGCCTGT	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
	AGAAATAATC	TGTTACTTAT	TGTAATACT	GCCCTAGTGT	CTCCATGGAC	CAAAATTTATA	7620
	TTTATAATTG	TAGATTTTTA	TATTTTACTA	CTGAGTCAAG	TTTTCTAGTT	CTGTGTAATT	7680
	GTTTAGTTTA	ATAGCTGATG	TCATTAGCTG	GTCTTACTCT	ACCAAGTTTT	TGACATTGTA	7740
85	TTGTGTACCT	TAGCTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAATA	7800
	GAAATACCTT	CATTTTGAAA	GAAGTTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
	AATGGTTTTT	ATCCAAGGAA	TTGCCAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAATA	7920
	AAAAAAAATA	AAAAAAAATA	AAAA				

Seq ID NO: 573 Protein sequence:
Protein Accession #: Eos sequence

5	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
10	FKASKITPHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPEEAV	KGKGLRLALS	180
	ILFEVGTSEN	LDPKAIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVISSESQ	AVFCEVLTMQ	QSGVVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVOA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFPE	420
15	LIGTEEIIKE	EIEGKDIIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPhT	VEGTSASLND	540
	GSKTVLRSPH	MNLSPGTAESL	NTVSITEYEE	ESLLTSPKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITVD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAVFP	720
20	TEVTPHAFTP	SSRQQLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPISHASL	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLY	900
	KTLMPQSVEP	PSSDAMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
	SLFSGPSHIP	IPKSSLIITP	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
	PVSVAEFTYT	TSVFGDDNKA	LSKSEIYIGN	ETELQIPSPN	EMVYPSESTV	MPNMYDNVVK	1080
25	LNASLQETSV	SISSTKGMFF	GSLAHTTTKV	FDHEISQVPE	NNFSVQPTHT	VSQASGDTSL	1140
	KPVLANSSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLTKTVLP	1200
	AVPSDPIIVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	NHHSASLQGL	1260
	TISYASEKYE	FVLLKSESSH	QVPSLYSND	ELFQTANLEI	NQAHPPKGRH	VFATFVLSDI	1320
30	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDHVSPIG	NGHVAITAVS	1380
	PHRDGSVTST	KLLFPSPKAT	ELSHSAKSDA	GLVGGGEGDG	TDDGDGDDDD	DRGSDGLSIH	1440
	KCMSCSSVRE	SQEKVMNDS	THENSLMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDSEESG	SGQGTSDSLN	1560
	ENETSTDFSF	ADTNEKDADG	ILAGDSEIT	PGFPQSPTSS	VTSENSEVFH	VSEAEASNSS	1620
35	HESRIGLAEG	LESEKKAIVP	LVIVSALTPI	CLVLVLGILI	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGPTTE	FETLKEFYQE	VQSCVTDLGI	1740
	TADSSNHDPN	KHKRNYINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLSTAE	FWRMINEHNV	EVIVMITNLV	EKGRKCDQY	WPADGSEEEY	NFLVTQKSVQ	1860
40	VLAYITVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAA	1920
	AKRHAVGPV	VHCSAGVGR	GTIIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
	QYVFHIDTLV	EALSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIIQSDY	2040
	SAALKQCNRE	KNRTSSIIIP	ESRVRGISSL	SSEGTDYINA	SYIMGYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYWPKNDE	PINCESPKVT	LMAEHKKCLS	2160
	NEEKLIQDF	ILEATQDDYV	LEVRHFQCPK	WPNPDSPIK	TFELISVIKE	EAANRDGPMI	2220
45	VHDEHGGVTA	GTFCALTLLM	HQLEKENSVD	VYQVAKMINL	MRGPVFADIE	QYQFLYKVIL	2280
	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-4518

50	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAACC	ATTTCCTTCG	CTCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
55	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAAAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTATCTGTA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCTACT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTCCTA	GTTTGTGAGG	AGCAGTCAAA	660
65	GGAAAAGGGA	AGTTAAGAGC	TTATCCCAT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTC	GTTTGGGAA	GCAGCGTGCT	780
	TTAGATCCAT	TCATCTGTTT	GAACCTCTCT	CCAAACTCAA	CTGACAAGTA	TTACATTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTCTTGTG	AAGTCTTAC	AATGCAACAA	960
70	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCTAGA	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTTACA	1140
	TGGGAAAGAC	CTGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
75	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCTGGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
	GAGAGGGGAA	AAGACATTTA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATACA	GGAAAAGGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCATAGGG	1560
80	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTAAAT	TCCACTTCCC	AACCAAGTAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	CAGTCTCAG	ACTGTGACTG	AAGTCCACCC	TCACTAGTGT	1740
	GAAGGTACTT	CAGCTCTTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACCTGTGGG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
85	AGTTTATTGA	CCAGTTTCAA	CTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAGGAA	TCACTAAGAG	ATCCTTCTAT	GGAGGGAAAT	2100

5	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTCTCG	CAGGCCCACT	GATGTCAAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACG	2400
	GTATACAAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
	TGCTAGTAGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
10	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCCG	AGCAATTTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTAAGTTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAG	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGTT	TAAGCTAGCA	2880
15	CAGCTTGTCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAGAGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACCTCAGAA	GAGTGTGCAA	GTGCTTGCCT	ATTATACTGT	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAAAT	AAAAAAGGGC	TCCAGAGAA	GAAGACCCAG	TGGACGTGTG	3240
	GTCACACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTGTCT	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTC	AACACGGAAG	AACGTGCAAC	ATATTTGGCT	TCTTAAACA	CATCCGTTC	3480
	CAAGAAAAT	ATTGTTGATCA	AACGTAGGAG	CAATATGTCT	TCATTATGTA	TACACTGGTT	3540
25	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTCATGC	CTATGTTAAT	3600
	GCATCTCTCA	TTCTCTGGAC	AGCAGGCCAA	ACAAAGCTAG	AGAAACAAT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTGGCAT	TTATCCCTG	3780
	AGTGGAAGAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
30	GAAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCATA	ATGCCCAACT	GGTGGTTATG	ATTCTGATG	GCCAAACAT	GGCAGAAGAT	3960
	GAAATTTGTT	ACTGGGCCAA	TAAAGATGAG	CCTATAAAT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACAACA	ATGTCTATCT	AATGAGGAAA	AACCTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCAGTTTCA	GTGCTCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TCCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAAGT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTA	GCAACAAGCA	GGAAGAGAAT	4440
	CCATCCACCT	CTCTGACAG	TAATGGTGCA	GCAATGCTG	ATGGAAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCGA	GAAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTTATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAAATGT	4680
45	TGCCCTTTTG	CAAGACTTGT	AATTACTTAA	TTATGTTTGA	ACTAAATGA	TGAATTTTAA	4740
	CAGTATTCT	AAGAATGGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTATAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAATAAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACTTAA	4980
50	AGTAGAATA	ATCTGTTACT	TATTGTAAAT	ACTGCCCTAG	TGCTCTCATG	GACCAAAATTT	5040
	ATATTTATAA	TTGTATTTTA	TTATATTTTA	CTACTGAGTC	AAGTTTCTTA	GTTCTGTGTA	5100
	ATTGTTTAGT	TTAATGACGT	AGTTTATTAG	CTGGTCTTAC	TCTACCAATT	TTCTGACATT	5160
	GTATTTGTTT	ACCTAAGTCA	TTAATTTTGT	TTTACGATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCAATTTT	AAAGAAGTTT	TTATGAGAAT	AACACCTTAC	CAACATTTGT	5280
55	TCAAATGGTT	TTTATCCAAG	GAATTGCAAA	AATAAATATA	AATATTGCCA	TTAAAAAATA	5340
	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA				

Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

60	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKLL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
65	FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
	ILFVEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEBIHEAV	CSSPEPVQQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLV	QQLDGEDQTK	360
70	HEFLTDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTHYNRI	GTKYNEAKTN	480
	RSFTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NIVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPEASARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
75	TAQPDVGSGR	ESPLQNTYTE	IRVDESEKTT	KSFAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNAAESNS	SHERIGLAE	GLESEKKAIV	780
	PLVIVSALPT	ICLVVLVGLL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGAI	840
	PIKHFPHKVA	DLHASSGFTE	EPETLKEFYQ	EVQSCITVDLG	ITADSSNHPD	NKHKNRYINI	900
	VAYDHSRVKL	AQLAEKHGTL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
80	VEVIVMITNL	VEGRRKCDQ	YWPADGSEBY	GNFLVTQKSV	QVLAYYTVRN	PTLRNTRIKK	1020
	GSQGRPSGR	VVTQYHYTQW	PDMPGVEPSL	PVLTPVRKAA	YAKRHAVGPV	VVHCAGVGR	1080
	TGTYIVLDSM	LQIQHEGTV	NIFGLKHIR	SQRNYLVQTE	EQYVFIHDTL	VEAILLSKETE	1140
	VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIIQSD	YSAALKQCNR	EKNRTSSIIIP	1200
	VERSRRVGISS	LSGEGTDYIN	ASYIMGYQYS	NEFIITQHPL	LHTIKDPWRM	IWDHNAQLVV	1260
85	MIPDGNMAE	DEFVYWNKD	EPINCESFKV	TLMAEEHKCL	SNEEKLIQD	FILEATQDDY	1320
	VLEVRHFQCP	KWPNPDSPI	KTFELISVIK	EAAANRDGPM	IVHDEHGGVT	AGTFPCALTTL	1380
	MHOLEKENS	DVYQVAKMIN	LMPRGVFADI	EQYQPLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
	AALPDGNIAE	SLESLEV					

Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85

1	11	21	31	41	51	
CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
CAAAAAAACC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
CGCGCAGGGG	CCGCAGACCG	CTCGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
CTTGTGTAAG	AGATTGGCTG	GTCCATATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
AACACATTCA	TTCATACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
GTCAAGCGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
AAATGCAATA	TGTCACTCGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
GATTTCAGAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTTC	GTTTTGGGAA	GCAGGCTGCT	780
TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAACTTCAA	CTGACAAGTA	TTACATTTAC	840
AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTGTGTG	AAGTCTTAC	AATGCAACAA	960
TCTGGTTATG	TCTACTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
AGTTTCAGAAC	CAGAAATATG	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTGTACA	1140
TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGAGT	TTTGTACCAG	1200
CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
GGTGCTATTTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
TGCATAATG	GCTTATATGG	AAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCATAGGG	1560
ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACGTGCCAC	TCACACTGTG	1740
GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACGT	TTCTTAGATC	TCCACATATG	1800
AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TACAGAATA	TGAGGAGGAG	1860
AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
GCAACTCTTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
TCCTTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCAACCCG	2400
GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
CTAGTGGTTC	TTGTGGTTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
ATTTTCAGATG	ATGTCGGAGC	AATTCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
CATGCAAGTA	GTGGGTTTAC	TGAAGAAATT	GAGGAAGTGC	AGAGCTGTAC	TGTTGACTTA	2760
GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	ACAAGAATCG	ATACATAAAT	2820
ATCGTTGCCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	TTGCTGAAAA	GGATGGCAAA	2880
CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	ACAGACCCAA	AGCTTATATT	2940
GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTCT	GGAGAATGAT	ATGGGAACAT	3000
AATGTGGAAG	TTATTGTCTAT	GATAACAAAC	CTCGTGAGGA	AAGGAAGGAG	AAAATGTGAT	3060
CAGTACTGTC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAC	TTCTGGTTC	TCAGAAGAGT	3120
GTGCAAGTGC	TTGCCATTAT	TACTGTGAGG	AATTTTACTC	TAAAGAACAC	AAAAATAAAA	3180
AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGG	CGTGTGGTCA	CACAGTATCA	CTACACGCAG	3240
TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	TGACCTTTGT	GAGAAAGGCA	3300
GCCTATGCCA	AGGCCCATGC	AGTGGGGCCT	GTGTGCTGTC	ACTGCAGTGC	TGGAGTTGGA	3360
AGAACAGGCA	CATATATTGT	CTAGACAGT	ATGTTGCAGC	AGATTCAACA	CGAAGGAACT	3420
GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTCAACAA	GAAATTATTT	GGTACAACT	3480
GAGGAGCAAT	ATGTTCTCAT	TCATGATACA	CTGGTTGAGG	CCATACTTAG	TAAAGAAACT	3540
GAGGTGCTGG	ACAGTCATAT	TCATGCCCTAT	GTTAATGCAC	TCCTCATTCC	TGGACCGACA	3600
GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	AGTCAAATAT	ACAGCAGAGT	3660
GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	ATCGAACTTC	TTCTATCATC	3720
CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCCTGAGTG	GAGAAGGCAC	AGACTACATC	3780
AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	TCATCATTAC	CCAGCACCTT	3840
CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	ACCATAATGC	CCAATGGGTG	3900
GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	TTGTTTACTG	GCCAAATAAA	3960
GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACCTTCA	TGGCTGAAGA	ACACAAATGT	4020
CTATCTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	TAGAAGCTAC	ACAGGATGAT	4080
TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	CAAAATCCAG	TAGCCCCATT	4140
AGTAAACCTT	TTGAACCTTAT	AAGTGTATTA	AAAGAAGAAG	CTGCCAATAG	GGATGGGCCCT	4200
ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	CTTTCTGTGC	TCTGACAAAC	4260
CTTATGCACC	AACTAGAAAA	AGAAAAATTC	GTGGATGTTT	ACCAGGTAGC	CAAGATGATC	4320
AATCTGATGA	GGCCAGGAGT	CTTTCGTGAC	ATTGAGCAGT	ATCAGTTTCT	CTACAAAGTG	4380
ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	CCACCTCTCT	GGACAGTAAT	4440
GGTGACGATC	TGCCCTGATG	AAATATAGCT	GAGAGCTTAG	AGTCTTTAGT	TTAACACAGA	4500
AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTCCTCTCT	TCCTAAATTT	AGGCAGGAAA	4560
ATCAGTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACTTG	ACAGTAACCT	TCATGACATA	4620
GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	TTTTTGCAAG	ACTTGTAAAT	4680
TACTTATTAT	GTGTTGAAC	AAATGATTGA	ATTTTACAGT	ATTTCTAAGA	ATGGAATTGT	4740
GGTATTTTTT	TCTGTATTGA	TTTAAACAGA	AAATTTCAAT	TTATAGAGGT	TAGGAATTCC	4800

AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTGT CTGTATTGT AGCAATTATC 4860
 AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA AATAAACAC TCTTCCATAT 4920
 GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980
 GTAAATACTG CCCTAGTGTC TCCATGGACC AAATTTATAT TTATAATTGT AGATTTTTAT 5040
 ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG TTTAGTTTAA TGACGTAGTT 5100
 CATTAGCTGG TCTTACTCTA CCAGTTTTCT GACATTGTAT TGTGTTACCT AAGTCATTAA 5160
 CTTTGTTTCA GCATGTAATT TTAACCTTTG TGGAAAAATAG AATAACCTTC ATTTTGAAG 5220
 AAGTTTTTAT GAGAATAACA CCTTACCAA CATTGTTCAA ATGTTTTTAA TCCAAGGAAT 5280
 TGCAAAAATA AATATAAATA TTGCCATTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 5340
 AAA

Seq ID NO: 577 Protein sequence:
 Protein Accession #: EOS sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEKQKNG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNKKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKCNMSDGS EHSLEGQKFP LEMQIYCPDA DRPSSFEEAV KGKGLRLALS 180
 ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISEQL AVFCEVLTMO QSGVYVLMYD LQNNFREQQY KFSRQVFSSY 300
 TGKEEIEHAV CSSEFENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360
 HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPDLDFPE 420
 LIGTEEIIKE EEEGKDIEEG AIVNPGROSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QVTLEPPHT VEGTSASLND 540
 GSKTVLRSPH MNLSTGAESL NTVSITEYEE ESLTTSFKLD TGAEDSSGSS PATSAIPPIS 600
 ENISQGIYFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPMEG NVWFPSTDI 660
 TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720
 TEVTPHAFTP SSRQDLVST VNVVYSQTQ PVYNEASNSS HESRIGLAEQ LESEKKAVIP 780
 LVIVSALTFI CLVVLVGLI YNRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
 IKHFKHVDAD LHASSGFTEE FEEVQSCTVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900
 KLAQLAEKDG KLDYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMIWE HNVEVIMIT 960
 NLVEKRRRK DQWYDPDGE EYGNFLVTQK SVQVLAITYV RNFTLRNTKI KKGSKGRPS 1020
 GRVVTQYHYT QWPDGMVPEY SLFVLTFVRK AAYAKRHAVG PVVHCSAGV GRTGTIYVLD 1080
 SMLQIQHEG TVNIPGLKH IRSQRNYLVQ TEEQYVFIHD TLVEAILSKE TEVLDSHHA 1140
 YVNALLIPGP AGTKLEKQF QLLSQSNIQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200
 SSLSGEGTDY INASYIMGY QSNFIIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDQNM 1260
 AEDFVYWN KDEFINCESF KYTLMAEEHK CLSNEEKLI QDFILEATQD DYVLEVRHFQ 1320
 CPKWNPDSP ISKTFELISV IKEEAAANRDG PMIVHDEHGG VTAGTFPCALT TLMHOLEKEN 1380
 SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRO EENPSTSLDS NGAALPDGNI 1440
 AESLESVL

Seq ID NO: 578 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 501-4514

1 11 21 31 41 51
 CACACATACG CAGCGACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAGC ATTTCTCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGCGGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180
 CAGCTCCTCT GTGTTGCGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTGTGTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAT TGGGGAAAGA 300
 AATATCCAAAC ATGTAATAGC CCAAAACAA CTCTATCAA TATTGATGAA GATCTTACAC 360
 AAGTAAATGT GAATCTTAAG AAACCTTAAT TTCAGGGTTG GGATAAAACA TCATTGGAAA 420
 ACACATTCAT TCATAACACT GGGAAAAACAG TGGAAATTA TCTCACTAAT GACTACCGTG 480
 TCAGCGGAGG AGTTTCAGAA ATGGTGTGTTA AAGCAAGCAA GATAACTTTT CACTGGGGAA 540
 AATGCAATAT GTCATCTGAT GGATCAGAGC ATAGTTTAGA AGGACAAAAA TTTCCACTTG 600
 AGATGCAAT CTACTGCTTT GATGCGGACC GATTTCGAG TTTTGAGGAA GCGATCAAG 660
 GAAAGGGGAA GTTAAGAGCT TTATCCATT TGTGTGAGGT TGGGACAGAA GAAAATTGG 720
 ATTTCAAAGC GATTATTGAT GGAGTCGAAA GTGTTAGTCG TTTTGGGAAG CAGGCTGCTT 780
 TAGATCCATT CATACTGTTG AACCTTCTGC CAAACTCAAC TGACAAGTAT TACATTTACA 840
 ATGGCTCATT GACATCTCCT CCTGCACAG ACACAGTTGA CTGGATTGTT TTTAAAGATA 900
 CAGTTAGCAT CTCTGAAAGC CAGTTGGCTG TTTTGTGTA AGTTCTTACA ATGCAACAAT 960
 CTGTTATGT CATGCTGATG GACTACTTAC AAAACAATTT TCGAGAGCAA CAGTACAAGT 1020
 TCTCTAGACA GGTGTTTTCC TCATACACTG GAAAGGAAGA GATTATGAA GCGTTTGTGA 1080
 GTTCAGAAC AGAAAAATGT CAGGCTGACC CAGAGAATTA TACCAGCCTT CTGTGTACAT 1140
 GGGAAAGACC TCGAGTCGTT TATGATACCA TGATTGAGAA GTTTGCAGTT TTGTACCAGC 1200
 AGTTGGATGG AGAGGACCAA ACCAAGCATG AATTTTGTAC AGATGGCTAT CAAGACTTGG 1260
 GTGCTATTCT CAATAATTG CTACCCAATA TGAGTTATGT TCTTCAGATA GTAGCCATAT 1320
 GCCTAATGG CTATATGGA AATACAGCG ACCAAGTGT TGTGACATG CCTACTGATA 1380
 ATCTGAACT TGATCTTTTC CCTGAATTAA TTGGAAGTGA AGAAATAATC AAGGAGGAGG 1440
 AAGAGGGGAA AGACATTGAA GAAGCGCTA TTGTGAATCC TGGTAGAGAC AGTGCTACAA 1500
 ACCAAATCAG GAAAAAGGAA CCCAGATT CTACCAACAC AACTACAAAT CGCATAGGGA 1560
 CGAAATACAA TGAAGCCAAG ACTAACCGAT CCCCACAAAG AGGAAGTGAA TTCTCTGGAA 1620
 AGGTGATGTT TCCCAATACA TCTTTAAATT CCCTTCCCA ACCAGTCACT AATTAGCCAA 1680
 CAGAAAAAGA TATTTCTTGG TATCTCTAGA CTGTGACTGA ACTGCCACCT CACACTGTGG 1740
 AAGGTACTTC AGCTCTTTA AATGATGGCT CTAAACTGT TCTTAGATCT CCACATATGA 1800
 ACTTGTGCGG GACTGCAGAA TCCTTAAATA CAGTTTCTAT AACAGAAAT GAGGAGGAGA 1860
 GTTTATTGAC CAGTTTCAAG TGTGATCTG GAGCTGAAGA TTCTTCAGGC TCCAGTCCCG 1920
 CACTTCTGTC TATCCCATTC ATCTCTGAGA ACATATCCCA AGGATATATA TTTTCTCCG 1980
 AAAACCCAGA GACAATAACA TATGATGTCC TTATACCAGA ATCTGCTAGA AATGCTTCCG 2040
 AAGATTCAAC TTCAATCAGT TCAGAAAGAT CACTAAAGGA TCCTTCTATG GAGGGAATG 2100
 TGTGGTTTCC TAGCTCTACA GACATAACAG CACAGCCCGA TGTGGATGA GGCAGAGAGA 2160
 GCTTTCTCCA GACTAATTAC ACTGAGATAC GTGTTGATGA ATCTGAGAAG ACAACCAAGT 2220
 CCTTTTCTGC AGGCCAGTG ATGTACAGG GTCCCTCAGT TACAGATCTG GAAATGCCAC 2280

	ATTATTCTAC	CTTTGCTTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTGGTTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCAACCGG	2400
	TATACAAATG	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
5	AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTAC	CAGGAAGTGC	2760
10	AGAGCTGTAG	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
	ACAAGAAATG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGCTGAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTTC	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTGAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAATATGTAT	CAGTACTGGC	CTGCCGATGG	GAGTGAAGGAG	TACGGGAACT	3120
15	TTCTGGTCAC	TCAGAAAGAT	GTGCAAGTGC	TTGCTTATTA	TACTGTGAGG	AATTTTACTC	3180
	TAAGAAACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGG	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGCAG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTGCTCC	3360
20	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
	AGATTCAACA	CGAAGGAAT	GTCAACATAT	TTGGCTTCTT	AAAAACATC	CGTTCACAAA	3480
	GAAATTATTT	GGTACAAACT	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCTAT	GTTAATGCAC	3600
	TCTCATTTCC	TGGACACGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	3660
25	AGTCAAAAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAAG	3720
	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTC	TCCCTGAGTG	3780
	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTAC	CCAGCACCCCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAACCTGGT	GTTATGATTG	CTGATGGCCA	AAACATGGCA	GAAATGAAT	3960
30	TTGTTTACTG	GCCAAATAAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACCTCTA	4020
	TGGCTGAAGA	ACACAAATGT	CTATCTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAATCCAGA	TAGCCCCATT	AGTAAACTTT	TGAACTTAT	AAGTGTATA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCCT	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
35	CTTCTGTGTC	TCTGACAACC	CTTATGCACC	AACTAGAAAA	AGAAAAATCC	GTGGATGTTT	4320
	ACCAGGTAGC	CAAGATGATC	AATCTGATGA	GGCCAGGAGT	CTTGTCTGAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	4440
	CCACCTCTCT	GGACAGTAAT	GGTGAGCAT	TGCCCTGATG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TTAACACAGA	AGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTCTCTCT	4560
40	TCCTAAATTT	AGGCAGGAAA	ATCAGTCTAG	TTCTGTTATC	TGTTGATTTC	CCATCACCTG	4620
	ACAGTAACTT	TCATGCATA	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	4680
	TTTTTGCAAG	ACTTGTAAAT	TACTTATTAT	GTTTGAAC	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATTTG	GGTATTTTTT	TCTGTATTGA	TTTTAACAGA	AAATTTCAAT	4800
	TTATAGAGGT	TAGGAATTTT	AACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTAG	4860
45	CTGTATTTGT	AGCAATTTCT	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
	AATAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
	GAAATAATCT	GTACTTTATT	GTAAATAC	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTCT	GACATTGTAT	5160
50	TGTGTTACCT	AAGTCATTAA	CTTTGTTTCA	GCATGTAATT	TTAACTTTTG	TGGAAAAATG	5220
	AAATACCTCT	ATTTGTTTAA	AAGTTTAT	GAGAATAACA	CCTTACCAAA	CATTGTTCAA	5280
	ATGGTTTTTA	TCCAAGGAAT	TGCAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAATA	5340
	AAAAAAAATA	AAAAAAAATA	AAA				

Seq ID NO: 579 Protein sequence:
Protein Accession #: EOS sequence

	1	11	21	31	41	51	
60	MVFKASKITF	HWGKCNMSSD	GSEHSLEGQK	FPLEMQIYCF	DADRFSSFEE	AVKKGKGLRA	60
	LSILFVETGE	ENLDFKAIID	GVESVSRFGK	QAALDPPILL	NLLPNSTDYK	YIYNGSLTSP	120
	PCTDVTVMIV	FKDVTVSSES	QLAVFCEVLT	MQSGYVMLM	DYLNQNFREQ	QYKFSRQVFS	180
	SYTGKEEIEH	AVCSSEPENV	QADPENYISL	LVTWERPRV	YDTMIEKFAV	LYQQLDGEDQ	240
	TKHEFLTDGY	QDLGAILNNL	LPMMSYVLQI	VAICTNGLYG	KYSDQLIVDM	PTDNPELDF	300
	PELIGTEEII	KEEEEGKDIE	EGAIVNPGRD	SATNQIRKKE	PQISTTTHYN	RIGTKYNEAK	360
65	TNRSPTRGSE	FSGKGDVPT	SLNSTSQPVT	KLATEKDIDL	TSQTVTELP	HTVEGTSASL	420
	NDGSKTVLRS	PHMNLSTGAE	SLNTVSITEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIFP	480
	ISENISQGYI	FSSNPETIT	YDVLIPESAR	NASEDSTSSG	SEESLKDPSM	EGNVWFPST	540
	DITAGPDVGS	GRESFLQTN	TEIRVDESEK	TKSFSAGPV	MSQGPSVTDL	EMPHYSTFAY	600
70	FPTEVTPHAF	TPSSRQQLDV	STNVVVSQT	TQPVYNBASN	SSHESRIGLA	EGLESEKKAV	660
	IPLVIVSALT	FICLVVLVGI	LIYWRKCFQT	AHFYLEDSTS	PRVISTPPTP	IFPISDDVGA	720
	IPIKHFPKHV	ADLHASSGFT	EEFETLKEFY	QEVQSCVTDL	GITADSSNHP	DNKHKNRYIN	780
	IVAYDHSRVK	LAQLAEXDKG	LTDYINANV	DGYNRPKAYI	AAQGPLKSTA	EDFWRMIWEH	840
	NVEIVMITN	LVEKGRKCD	QYWPADGSEE	YGNFLVTQKS	VQVLAYYTVR	NFTLRNTRKIK	900
75	KGSQKGRPSG	RVVTQVHYTO	WPDNMGVPEYS	LPVLTFVRKA	AYAKRHAVGP	VVHCSAGVG	960
	RTGTYYVLDS	MLQOIQHEGT	VNIFGFLKHI	RSQRNYLVQT	EEQYVFIHDT	LVEAILSKET	1020
	EVLDSHIHAY	VNALLIPGPA	GKTKLEKQFP	LLSQSNIQQS	DYSAALKQCN	REKNRTSSII	1080
	PVRSRVRGIS	SLSGEGTDYI	NASYIMGYQ	SNEFIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
	VMIPEGQMA	EDFVYVWPNK	DEPINCESFK	VTLMABEKKC	LSNEEKLIQ	DFILEATQDD	1200
80	YVLEVRHFQC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVHDEHGGV	TAGTFCALTT	1260
	LMHQLKENS	VDVYQVAKMI	NLMRPGVFAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
	GAAEPDGNIA	ESLESVL					

Seq ID NO: 580 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4632

85	1	11	21	31	41	51
----	---	----	----	----	----	----

	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAACC	ATTTCCCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAGACAG	AGGAGCCGCA	120
5	CGGCGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AACGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
10	AACACATTCA	TTCATAACAC	TGGGAAAAAC	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCACTCGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAAGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
15	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTCT	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCTAGTCTGAT	GGACTACTTA	CAAAACAATT	TTCCGAGAGCA	ACAGTACAA	1020
20	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCAATGA	AGCAGTTTGT	1080
	AGTTTCAAGC	CAGAAATATG	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTGTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGBACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTC	TCAATATATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
25	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AGACATTTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAAAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
30	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AAGTCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
35	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAGAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCA	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCTC	AGACTAATTA	CATGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
40	TCCTTTTCTG	CAGGCCCACT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCCTTGCCTA	CTTCCCAACT	AGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTTGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGCTTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	ATGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
45	CTAGTGGTTC	TTGTGGTATG	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	2640
	ATTTTCAGATG	ATGTCGGAGC	AAATCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
	CATGCAAGTA	TGGGTTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	2760
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	2820
50	CACAAGAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	2880
	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	3000
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	3060
55	AAAGGAAGGA	GAAAAATGTA	TCAGTACTGG	CCGCGGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAAGC	TGTGCAAGTG	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGCTC	3240
	ACACAGTATC	ACTACACGCA	TGGGCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
	CATGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTG	3360
	CCTGCAAGTG	CTGGAGTTGG	TGCAACAGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
60	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTCCACA	3480
	AGAAATTATT	TGATACAAAC	TGAGGAGCAA	TATGTCCTCA	TTATGATAC	ACTGGTTGAG	3540
	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTATGCTTCA	TTGTAATGCA	3600
	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTCAACCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCTCTCTCCT	3720
65	GGCTTAACTG	ATCCTCTTAC	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CCTGAGCCAG	3780
	TCAAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAA	3840
	GGAACCTCTT	CTATCATCCC	TGTGGAAAGA	TCAAGGGTTG	GCATTTTCAT	CCTGAGTGGA	3900
	GAAGGCACAG	ACTACATCAA	TGCCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
70	CATAATGCCC	AACGTGGTGT	TATGATTCCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAAG	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTTATG	4140
	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAAACTTA	TAATTCAGGA	CTTTATCTTA	4200
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAAGTGTCC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACCTTATA	GTGTTATAAA	AGAAGAAGCT	4320
75	GCCAAATAGG	ATGGGCTTAT	GATTGTTCAAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAATC	4380
	TTCTGTGCTC	GTAAACCCCT	TGTCAACCAA	CTAGAAAAAG	AAAATTCCTG	GGATGTTTAC	4440
	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	ACAGTAAATG	TGCAGCAATG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
80	TCTTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTGT	TTCTCTCTTC	4680
	CTAAAAATAG	GCAGGAAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACTGTAC	4740
	AGTAACCTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTTATA	TCATTAACAA	TGTGTGCCCT	4800
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGAAAT	GGAAATGTGG	TATTTTTTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
85	ATAGAGGTTA	GGAAATGCCAA	ACTACAGAAA	ATGTTTGTTC	TTAGTGTCAA	ATTTTATAGT	4980
	GTATTGTGAG	CAATTATCAG	GTTTGCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
	TAAACACTCT	TTCCATATGA	TATTCAACAT	TTTACAACCT	CAGTATTCCAC	CTAAAGTAGA	5100
	AATAATCTGT	TACTTATTGT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160

ATAATTGTAG ATTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTG TGTAATTGTT 5220
 TAGTTTAATG ACGTAGTTC TTAGCTGGTC TTAGCTTACC AGTTTTCTGA CATTGTATTG 5280
 TGTACCTAA GTCAATTAAC TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAATAGAA 5340
 ATACCTTCAT TTGAAAGAA GTTTTATGA GAATAACACC TTACCAACA TTGTTCAAT 5400
 GGTTTTATC CAAGGAATG CAAAAATAA TATAAATATT GCCATTAAAA AAAAAAATA 5460
 AAAAAAATA AAAAAAATA A

Seq ID NO: 581 Protein sequence:
 Protein Accession #: EOS sequence

1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGAALNQKNWG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH GKNCMSDDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRLALS 180
 ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGVYVLMNDY LQNFREQQY KFSRQVFSY 300
 TGKEEIEHAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK 360
 HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLPPE 420
 LIGTEEIIKE EEBGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPTH VEGTSASLND 540
 GSKTVLRSPH MNLSTGTAESL NTVSITYEY ESSLTSPKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGIYFS SENPETITYD VLIPEASARNA SEDSTSSGSE ESLKDPSEMG NVWFPSSTDI 660
 TAQPDVSGSR ESPLQNTYTE IRVDESEKTT KSFAGPVMS QGSPVTDLEM PHYSTFAFFP 720
 TEVTPHAFPT SSRQQLDVST VNVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAIVP 780
 LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840
 IKHFPKHVAD LHASSGTTEE FETLKEFYQE VQSCVLDLGI TADSSNHPDN KHKNYRINIV 900
 AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAE FWRMIWEHNV 960
 EVIVMITNLV EKGRRKCDQY WPAWGSEYNG NPLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020
 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAY AKRHAVGPV VHCAGVGRV 1080
 GTYIVLDSML QQIQHEGTVN IFGFLKHRS QRNYLVQTEE QYVFIHDTLV EAILSKEDEV 1140
 LDSHIAVYN ALLIPGPAGK TKLEKQFQGL TSLPRLECRG TISAHCNLPL PGLTDPPTSA 1200
 SRVAGTILLS QSNIQSDYS AALKQCNREK NRTSSIIPE RSRVGSSLS GEGTDYINAS 1260
 YIMGYQSNF FIITQHPLH TIKDFWRMIW DHNAQLVMI PDQONMAED FVYWPKNDEP 1320
 INCESFKVTL MAEHLCLSN EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISTK 1380
 FELISVKEE AANRDGMIV HOEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM 1440
 RGVFADIEQ YQFLYKIVLS LVGTRQENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 582 DNA sequence
 Nucleic Acid Accession #: NM_002851.1
 Coding sequence: 148..7092

1 11 21 31 41 51
 CACACATACG CACGACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAATAC ATTTCTCTCG CTCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCTTAA AGCGTTTCCT CGCTTGCAAT 180
 CAGCTCCTCT GTGTGTCGCG CTGCGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTTGTTGAAG AGATTGCTCG GTCCATATAA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAATG TGAATCTTAA GAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420
 AACACATTCA TGCATAACAC TGGGAAAAAC GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GAGTTTCAGA AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTCCTA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAGGGGA AGTTAAGAGC TTTATCCATT TTGTTGAGG TTGGGACAGA AGAAAAATTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTAGTCT GTTTTGGGAA GCAGGCTGCT 780
 TTGATCCAT TCACTACTGT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTGTG AAGTCTTAC AATGCAACAA 960
 TCTGTTATG TCACTGCTGAT GGACTACTTA CAAAACAATT TTCAGAGCA ACAGTACAAG 1020
 TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTTCATG AGCAGTTTGT 1080
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCT TCTTGTTACA 1140
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCACT TTTGTACCAG 1200
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
 GGTGCTATT TCAATAATT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
 TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380
 AATCCTGAAC TTGATCTTTT CCTGAATTA ATTGGAAGTG AAGAAATAT CAAGGAGGAG 1440
 GAAGAGGGAA AAGACATTGA AGAAGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500
 AACCAATCA GAAAAAGGA ACCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCCTGGA 1620
 AAGSGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
 ACAGAAAAAG ATATTCTCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACTCTGTG 1740
 GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAACTG TTCTTAGATG TCCACATATG 1800
 AACTTGTGCG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
 AGTTTATTGA CCAAGTTTCA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
 GCAACTCTG CTATCCCAT CATCTCTGAG AACATATCCC AAGGATATAT ATTTCTCTCC 1980
 GAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040
 GAAGATTCAA CTTTCATCAG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100
 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGATC AGGCAGAGAG 2160
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
 TCCTTTCTG CAGGCCCACT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATAGCCA 2280
 CATTATTCTA CCTTGGCTA TCTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340
 TCCAGACAA AGGATTGGT CTCCACGGTC AACGTGGTAT ACTGCAGAC AACCCAACCG 2400
 GTATACATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460
 ACCCCTTGT TGCTTGACAA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520

	TOGGCCTTGC	ATGCTAGCCC	TGTATTTCCTCC	AGTGTGCGATG	TGTCATTGTA	ATCCATCCTG	2580
	TCTTCTCATG	ATGGTGCACC	TTTGCTTCCA	TTTTCTCTCTG	CTTCTTCAG	TAGTGAATTG	2640
	TTTGCCATC	TGCATACAGT	TTCTCAAAATC	CTTCCACAAG	TTACTTTCAG	TACCGAGAGT	2700
5	GATAAGGTGC	CCTTGCATGC	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGCTAGTG	AAATCGGTGT	TCCTTATATA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCAAGTTCT	TCAGGCGCTG	AACCTTCTTA	TGCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
10	GATTCGTGGG	GTGTAACTTA	TCAGGGTTCC	TTATTTAGCG	GCCTTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAAACAT	TTCTTCACT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
	TCGTGTGTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
15	ACTGAATGTC	AAATTCCTTC	TTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAGGGCAT	GTTTCCAGGG	TCCCTTGTCT	ATACCAACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCT	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTCCGTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
20	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAG	TGAAGTATTG	CTACAACCTT	CCTTTGAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACCTG	TCTTCCAGCT	GTGCCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAATAACA	TGCTGCATCT	TACATCTGTA	CCAGTTTCTG	ATGTGTGCGC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTTATG	CAAGTGAGAA	ATATGAACCA	3960
25	GTTTTGTATA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAACT	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCAATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAACT	CTCCACCAAA	AGTTCTGTGA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCACCAAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCGTGTTCC	TATAGGAAAT	4260
30	GGGCATGTTG	CCATTACAGC	TGTTTTCTCC	CACAGAGATG	GTCTGTAACT	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGACAGA	4440
	GATAGTGATG	CTTATCCAT	TCATAAGTGT	ATGTCACTGT	CATCCTATAG	AGAATCACAG	4500
35	GAAAAGGTAA	TGAATGATTC	AGACACCCAC	GAAAACAGTC	TTATGGATCA	GAATAATCCA	4560
	ATCTCATACT	CACATCTGTA	GAATCTGAA	GAAGATAATA	GAGTCACAAG	TGTATCCTCA	4620
	GACAGTCAAA	CTGGTATGGA	CAGAAGTCTC	GGTAAATCAC	CATCAGCAAA	TGGGCTATCC	4680
	CAAAAGCACA	ATGATGGAAA	AGAGGAAAAT	GACATTCAGA	CTGGTAGTGC	TCTGCTTCTC	4740
	CTCAGCCCTG	AATCTAAGCT	ATGGGCAGTT	CTGACAAGTG	ATGAAGAAAG	TGGATCAGGG	4800
40	CAAGGTACCT	CAGATAGCCT	TAATGAGAAT	GAGACTTCCA	CAGATTTTCT	TTTTGCAGAC	4860
	ACTAATGAAA	AAAGTCTGTA	TGGGATCTCT	GCAGCAGGTG	ACTCAGAAAT	AACCTCTGGA	4920
	TTCCACAGT	CCCCAACATC	ATCTGTTACT	AGCGAGAACT	CAGAAGTGTG	CCACGTTTCA	4980
	GAGGCGAGGG	CCAGTAAATG	TAGCCATGAG	TCTCGTATTG	GTCTAGCTGA	GGGTTTGGAA	5040
	TCCGAGAAGA	AGGCAGTTAT	ACCCCTTGTG	ATCGTGTCTG	CCCTGACTTT	TATCTGTCTA	5100
45	GTGGTTCTTG	TGGGTATTCT	CATCTACTGG	AGGAAATGCT	TCCAGACTGC	ACACTTTTAC	5160
	TTAGAGGACA	GTACATCCCC	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
	TCAGATGATG	TCGGAGCAAT	TCCAATAAAG	CACCTTCCAA	AGCATGTTTG	AGATTTACAT	5280
	GCAAGTAGTG	GGTTTCTGTA	ACAATTTGAG	ACACTGAAAG	AGTTTACCA	GGAAAGTGAG	5340
	AGCTGTACTG	TTGACTTAGG	TATTACAGCA	GACAGCTCCA	ACCAACCCAG	CAACAAGCAC	5400
50	AGAATTCGAT	ACATAAATAT	CGTTGCCTAT	GATCATAGCA	GGGTTAAGCT	AGCAGAGCTT	5460
	GCTGAAAAGG	ATGGCAAACT	GACTGATTAT	ATCAATGCCA	ATTATGTTGA	TGGCTACAACT	5520
	AGACCAAAAG	CTTATATTGC	TGCCCAAGGC	CCACTGAAAT	CCACAGCTGA	AGATTTCTGG	5580
	AGAATGATAT	GGGAACATAA	TGTGGAAGTT	ATTGTCATGA	TAACAAACCT	CGTGGAGAAA	5640
	GGAAAGGAGAA	AATGTGATCA	GTACTGGCCT	GCCGATGGGA	GTGAGGAGTA	CGGGAACCTT	5700
55	CTGGTCACTC	AGAAAGTGT	GCAAGTGCTT	GCCTATTATA	CTGTGAGGAA	TTTTACTCTA	5760
	AGAAACACAA	AAATAAAAAA	GGGCTCCAG	AAAGGAAGAC	CCAGTGGAGC	TGTGGTCACA	5820
	CAGTATCACT	ACACGCACTG	GCCTGACATG	GGAGTACCAG	AGTACTCCCT	GCCAGTGTCT	5880
	ACCTTTGTGA	GAAAGGCAGC	CTATGCCAAG	CGCCATGCAG	TGGGGCCTGT	TGTCGTCCAC	5940
	TGCAGTGCTG	GAGTTGGAAG	AACAGGCACA	TATATTGTGC	TAGACAGTAT	GTTGCAGCAG	6000
60	ATTCACACAG	AAGGAACTGT	CAACATATTT	GGCTTCTTAA	AACACATCCG	TTACAAAAGA	6060
	AATTATTGTT	TACAACTCTG	GGAGCAATAT	GTCTTCTATC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	AGAAACTCTG	GGTGCTGGAC	AGTCATATTC	ATGCCTATGT	TAATGCACCT	6180
	CTCATTCTCT	GACCAGCAGG	CAAAACAAAG	CTAGAGAAAC	AATTCAGCT	CCTGAGCCAG	6240
	TCAAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAAAT	6300
65	CGAAGTTCTT	CTATCTCCC	TGTGAAAAGA	TCAAGGGTTG	GCATTTTATC	CCTGAGTGGA	6360
	GAAGGCACAG	ACTACATCAA	TGCTCCTAT	ATCATGGGCT	ATTACAGAG	CAATGAATTC	6420
	ATCATTACCC	AGCAGCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	6480
	CATAATGCCC	AACGTGGTGT	TATGATTCTT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
	GTTTACTGGC	CAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTATAG	6600
70	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTCAGGA	CTTTATCTTA	6660
	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCAT	TTCAAGTGCC	TAAATGGCCA	6720
	AATCCAGATA	GCCCCATTAG	TAAAACCTTT	GAACTTATAA	GTGTTATAAA	AGAAAGAGCT	6780
	GCCAATAGGG	ATGGGCCCTAT	GATTGTTCAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAACCT	6840
	TTCTGTGCTC	TGACAACCTC	TATGCACCAA	CTAGAAAAGG	AAAATTCCTG	GGATGTTTAC	6900
75	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	6960
	CAGTTTCTCT	ACAAAGTGTAT	CCTCAGCCTT	GTGAGCACAA	GGCAGGAAGA	GAATCCATCC	7020
	ACCTCTCTGG	ACAGTAATGG	TGCAGCAATT	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	7080
	TCTTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTTG	TTTCTCTCTC	7140
	CTAAAATTAG	GCAGGAATAA	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCC	ATCACCTGAC	7200
80	AGTAACCTTC	ATGACATAGG	ATTCTGCCGC	CAAAATTTATA	TCATTAAACAA	TGTGTGCCCT	7260
	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	7320
	TTCTAAGAAAT	GGAAATTTGG	TATTTTTTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	7380
	ATAGAGGTTA	GGAAATTCAC	ACTACAGAAA	ATGTTTGTGT	TTAGTGTCAA	ATTTTATAGCT	7440
	GTATTTGTAG	CAATTTATCAG	GTTTGTCTAGA	AATATAACTT	TTAATACAGT	AGCCTGTAAA	7500
85	TAAAACACTC	TTCATATGTA	TATTTCAACAT	TTTCAAACTG	CAGTATTTCAC	CTAAAGTAGA	7560
	AATAATCTGT	TACTTATTTG	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	7620
	ATAAATTTAG	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTTGT	7680
	TAGTTTAATG	ACGTAGTTCA	TTACTGGTCT	TTACTCTACC	AGTTTCTCTG	CATTGTATTG	7740

TGTTACCTAA GTCATTAAGT TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAAATAGAA 7800
 ATACCTTCAT TTTGAAAGAA GTTTTATGA GAATAACACC TTACCAACA TTGTTCAAAT 7860
 GGTTTTATC CAAGGAATTG CAAAAATAA TATAATATT GCCATTAAAA AAAAAAATAA 7920
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

1 11 21 31 41 51
 | | | | |
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
 QSPINIDDEL TQVNWNLKKL KFQGWKTSLS ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
 FKASKITFWH FKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KKGKGLRALS 180
 ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPPILLNL LPNSTDKYYI YNGSLTSPPC 240
 15 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
 TGKEEIEHAV CSSEPENVQA DPENYTSLLV TWERPRVVD TMIEKFAVLY QQLDGEDQTK 360
 HEPLTDGYQD LGAILNLLPL NMSYVLQIVA ICTNGLYGYK SDQLIVDMPT DNPFLDLFPE 420
 LIGTEELIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYRNI GTKYNEAKIN 480
 RSPTRGSEFS KGDVDPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHT VEGTSASLND 540
 20 GSKTVLRSPH MNLGTAESL NTUSITEYEE ESLTSFKLD TGAEDSSGSS PATSAIPFIS 600
 ENISQGYIFS SENPETIYD VLIPESARNA SEDSTSSGSE ESLKOPSMEG NVWPPSSTDI 660
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGSPVTDLEM PHYSTFAYFP 720
 TEVTPHAFPT SSRQDLVST VNVVYSQTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI 780
 LNTTPAASSS DSALGHATPV PSVDVSFESI LSSYDGAPLL PFSSASFSSE LFRHLHTVSQ 840
 25 ILPOVTSATE SDKVPLHASL FVAGDLLLL PSQAQYSDVL STTHAASETL EFGSESGVLY 900
 KTLMFQVSEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG 960
 SLFSGPSHIP LKSGSLIPT ASLLQPHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020
 PVSVAEFTYT TSVFGDDNKA LKSEIIYGN ETELQIPSFN EMVVPSESTV MPNMYDNVVK 1080
 LNASLQETSV SISSTKMFP GSLAHTTTKV FDHEISQVPE NNFVSQPTHT VSQASGDTSL 1140
 30 KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200
 AVPSDILVE TPKYDKISST MLHLIVNSA SSENMLHSTS VFPVDSPTS HMHSASLQGL 1260
 TISYASEKYE PVLLKSESSH QVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320
 EPLNTLINKL IHSDEILTST KSSVTGKVFA GIFTVASDTF VSTDHSPVIG NGHVAITAVS 1380
 PHRDGSVTST KLLFPFKATS ELHSKASDA GLVGGGEDGD TDDGDDDDDD RDSGLSIHK 1440
 35 CMSCSSYRES QEKVMNDSOT HENSLMDQNN PISYLSSENS EEDNRTSVS SDSQTMDRS 1500
 PGKSPSANGL SQKHNDGKEE NDIQTGSALL PLSPESKAWA VLTSDEESGS CQGTSDSLNE 1560
 NETSTDPSFA DTNEKDDAGI LAAGDSEITP GFPSQPTSSV TSENSEVFHV SEAEASNSH 1620
 ESRIGLAEBL ESEKKAIVPL VIYSALTFIC LVVLVGILYI WRKCFQTAHF YLEDSTSPRV 1680
 ISTPTPIFP ISDDVGAIP I KHPFKHVADL HASSGFTEEF ETLKEFYQEV QSCTVDLGIT 1740
 40 ADSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGKLT YINANYVDGY NRPKAYIAAQ 1800
 GPLKSTAEAD WRMIWEHNVE VIVMITNLVE KGRRKCDQYV PADGSEYGN FLVTQKSVQV 1860
 LAYYTVRNFT LRNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVEPEYSLPV LTFVRKAAYA 1920
 KRHAVGPVVV HCSAGVGRGT TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEBQ 1980
 YVFIHDTLVE AILSKETESL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQSDYS 2040
 45 AALKQCNREK NRTSSIIPEV RSRVGISLS GEGTDYINAS YIMGYQSNE FIITQHPLH 2100
 TIKDFWRMIW DHNAQLVUMI PDGQNMAEDE FVYWPKNDEP INCBSFKVTL MAEHEKCLSN 2160
 EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISTK FELISVIEKE AANRDGPMIV 2220
 HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM RPFVFADIEQ YQFLYKVLIS 2280
 50 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 584 DNA sequence
 Nucleic Acid Accession #: NM_005688.1
 Coding sequence: 126..4439

1 11 21 31 41 51
 | | | | |
 CCGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC 60
 AGGGGCGCAG GAAITCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCGCTCAG 120
 60 AGAAGATGAA GGATATCGAC ATAGGAAAAG AGTATATCAT CCCAGTCCT GGTATAGAA 180
 GTGTGAGGGA GAGAACACAG ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240
 GGAGAACTCG ACCGTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 300
 TCTCTCTTGA TGCCCTCATG CATTCTCAGC TCAGAATCCT GGATGAGGAG CATCCCAAGG 360
 GAAAGTACCA TCATGGCTTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACCAGC 420
 65 ACCCAGTGA CAATGCTGGG CTTTTTCTCT GTATGACTTT TTGCTGGCTT TCTTCTCTGG 480
 CCCGTGTGGC CCACAAGAA GGGGAGCTCT CAATGGAAGA CGTGTGGTCT CTGTCCAAGC 540
 ACGAGTCTTC TGACGTGAAC TGCAGAAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG 600
 AAGTTGGGCC AGACGCTGCT TCCTGCGAA GGGTTGTGTG GATCTTCTGC CGCACCAGGC 660
 TCATCTGTC CATCGTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCACT GGACCAAGCT 720
 70 TCATGGTGAA ACACCTCTTG GAGTATACCC AGGCAACAGA GTCTAACCTG CAGTACAGCT 780
 TGTGTGTTAGT GCTGGGCTCT CTCTGACGG AAATCGTGGG GTCTTGGTCG CTGTCACTGA 840
 CTTGGGCATT GAATTACCGA ACCGGTGTCC GCTTGCAGGG GGCCATCCTA ACCATGGCAT 900
 TTAAGAAGAT CCTTAAGTTA AAGAACATTA AAGAGAAATC CTTGGGTGAG CTCATCAACA 960
 TTTGCTCCAA CGATGGGCGAG AGAATGTTTG AGGCAGCAGC CGTTGGCAGC CTGCTGGCTG 1020
 75 GAGGACCCGT TGTGTCCATC TTAGGCATGA TTTATAATGT AATTATTCTG GGACCAACAG 1080
 GCTTCTGGG ATCAGCTGTT TTTATCTCT TTTACCCAGC AATGATGTTT GCATCACGGC 1140
 TCACAGCATA TTTCAGGAGA AAATGCCTGG COGCCACGGA TGAACGTGTC CAGAAGATGA 1200
 ATGAAGTTCT TACTTACATT AAATTTATCA AAATGTATGC CTGGGTCAAA GCATTTTCTC 1260
 AGAGTGTTC AAAAAATCCG GAGGAGGAGC GTCCGATATT GGAAGAAAGC GGGTACTTCC 1320
 80 AGGGTATCAC TGTGGGTGTG GCTCCCATTT TGGTGGTGAT TGCCAGCGTG GTGACCTTCT 1380
 CTGTTTCATAT GACCTTGGGC TTGATCTGA CAGCAGCACA GGCTTTCACA GTGGTGACAG 1440
 TCTTCAATTC GACTTCTTTT GTTTGAAAG TAACACCGTT TTCAGTAAAG TCCCTCTCAG 1500
 AAGCCTCAGT GGCTGTGAC AGATTTAAGA GTTTGTTTCT AATGGAAGAG GTTCACATGA 1560
 TAAAGAACAA ACCAGCCAGT CCTCACATCA AGATAGAGAT GAAAAATGCC ACCTTGGCAT 1620
 85 GGGACTCCTC CACTCCAGT ATCCAGAACT CGCCCAAGCT GACCCCAAAA ATGAAAAAAG 1680
 ACAGAGGGGC TTCCAGGGGC AAGAAAGAGA AGGTGAGGCA GCTGCAGCGC ACTGAGCATC 1740
 AGGCGGTGCT GGCAGAGCAG AAAGGCCACC TCCTCTCTGA CAGTGACGAG CGGCCAGTC 1800
 CCGAAGAGGA AGAAGGCAAG CACATCCACC TGGGCCACCT GCGCTTACAG AGGACACTGC 1860

	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACCTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
5	TGAGAGACAA	CATCCTGTGT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
	GAGAGOGAGG	AGCCAACTCG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	CCCCGGGCTC	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTC	CAGTGCCTTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
10	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACCTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACTCTGTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
	AAACCATGGG	TTACACAGAAG	AAGTCACAAG	ACAAGGGTCC	TAAACACAGG	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGCTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
15	TCCTGTGTAT	TTGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GTTTGAAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCAAT	TGATCCTGA	AAGCCATTGC	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGGG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
20	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGGCG	CTGCCGTTCC	AGGCGGAGAT	GTTTCATCCG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCCCTGT	CATCCTCTTT	TCAGTCTCTG	ACATTGTCTC	CAGGGTCTCT	ATTCCGGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTTCTCTCT	CCACATCAGC	TCCAGCATAC	3300
25	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATAACGAG	3360
	AGCTGCTGGA	TGACAACCAA	GCTCCTTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GACCTCATC	ACGATCGCCC	TCATCACCAC	CACGGGCTG	ATGATCGTTC	3480
	TTATGCAACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
30	TAAACGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTTT	GGAAGCACCT	GCCAGAATTA	3660
	AGAAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGAG	3720
	AGATGAGGTA	CCGAGAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
35	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGCAGAC	CTCCGAAGCA	AACCTCTTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTCACTGG	CACCTGTGAG	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
40	TTGAATCTGA	AGTGAATGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTG	AAGAGACCAT	CCGAGAAGCA	TTTGCAAGCT	4260
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTG	TCCAACGACA	4380
	GTTCCCGATT	CTATGCCATG	TTTGTGCTG	CAGAGAACAA	GGTCCGCTGC	AAGGGCTGAC	4440
45	TCCTCCCTGT	TGACGAAGTC	TCCTTTCTTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
	CCCTCATCG	CGTCTCTCTA	CGGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCCCGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAACAA	AAATTTAGTT	TTTGTCTTTA	ATTGCACTAT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
50	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAAATA	AGCACTGTGC	TAATAACAGT	GCATATTCTT	TTCTATCAT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTGTCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTCTT	4920
	CTCTAGCTGG	TGGTTTCACG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
55	ATAGTGGGCC	CTCCGACAGC	CCCTCTGCC	GCCTCCCCAC	AGCGGCTCCA	GGGGTGGCTG	5040
	GAGAGCGGTC	GGGCGTGGGA	GACCATGCAG	AGCGCGGTGA	GTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTCTGT	GTCATCTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGGAAGC	CCAGGCCCTT	5160
	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCCCTGCT	TCTCTTTTTT	GCTGTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
60	TCCACTGCTC	TCAAGTTTCT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
	GTTGGTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTGGAGG	TGGCACTTTT	TCATTGCTCT	5400
	ATTCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TCGTGGGTCT	GTTTTCCTTT	5460
	CTCACCGCAG	TCGTCGACGA	CTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGGTTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
65	GGGGCTGGTA	GCTCAGTGG	GGCTGGTCC	TGCTGTCTAT	AGTTGAATGG	TCAGCGTTGC	5700
	ATGTCTGTAC	CAACTAGACA	TTCTGTGCC	TGAGCATGTT	TGCTGAACAC	CTTGTGGAAG	5760
	CAAAAATCTG	AAAAATGTGA	TAAAATTATT	TTGATTTTTG	TAAAAAATA	AAAAAATA	5820

Seq ID NO: 585 Protein sequence
Protein Accession #: NP_005679.1

	1	11	21	31	41	51	
75	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASHMSQLR	ILDEEHPKGR	YHHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSLLAR	120
	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLWQBELNEV	GPDAASLRRV	VWIFCRTRLI	180
	LSIVCLMITQ	LAFSPGPAPM	VKHLLEYTQA	TESNLQYSLL	LVLGLLLTEI	VRWSLSLALTW	240
	ALNYRTGVR	RGAILTMAPK	KILKLKNIKE	KSLGELINIC	SNQGQRMFEA	AAVGSLLLAG	300
80	PVVAILGMIY	NVILILPTGP	LGSAVFILFY	PAMFPASRLT	AYFRKKCVAA	TDERVQKME	360
	VLTYIKFIKM	YAWVKAPSQS	VQKIREEERR	ILEKAGYFQG	ITVGVAPIVV	VIASVVTFSV	420
	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSSEA	SVAVDRFKSL	FLMEEVHMIK	480
	NKPASPHIKI	EMKNATLAWD	SSHSSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTTEHQ	540
	VLAQKQGHLL	LDSDEPSPSE	EEBKGKHLHG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGS	600
85	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILPGKEYD	EERYNSVLNS	660
	CCLRPDLAIL	PSSDLTEIGE	RGANLGGGQR	QRISLARALY	SDRSIYILDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLTV	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNNLLGETP	PVEINSRKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEBGQL	VQLBEKGQGS	840

VPWSVYGVYI QAAGGPLAFI VIMALFMLNV GSTAFSTWNL SYWIKQSGN TTVTRGNETS 900
 VSDSMKDNPH MQYASIIYAL SMAVMLILKA IRGVFVKGT LRASSRLHDE LFRRLRSPM 960
 KFFDTTPTGR ILNRFSKMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FPWFLVAVGP 1020
 LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
 LDNDQAPFPL PTCAMRWLAV RLDLISIALI TTGLMIVLM HGOIPPAYAG LAISYAVQLT 1140
 GLFQPTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWQPE GEVTFENAEM 1200
 RYRENLPVLV KKVSFITKPK EKIGIVGRTO SGKSSLGMAL FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDL FNQYTEDQIW DALERTHMKR CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380
 MLTIAHRLHT VLGSDRIMVL AQGVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

Seq ID NO: 586 DNA sequence
 Nucleic Acid Accession #: NM_001327.1
 Coding sequence: 89..631

1 11 21 31 41 51
 | | | | |
 AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
 CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGC CGGGGCA CAGGGGGTTC 120
 GACGGGCGAT GCTGATGGCC CAGGAGGCC TGGCATTCTT GATGGCCAG GGGGCAATGC 180
 TGGCGGCCCA GGAGAGCGGG GTGCCACGGG CGCAGAGGT CCCCGGGGCG CAGGGGCAGC 240
 AAGGGCCTCG GGGCGGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
 GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCGGAG AGCGCGCTGC TTGAGTTCTA 360
 CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCGTGGCCCA 420
 GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCAGTG TGTCCGGCAA 480
 CATACTGACT ATCCGACTGA CTGTCTCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
 CTGTCTCCAG CAGCTTTCCT TGTGTATGTG GATCACGAG TGCTTCTGCG CCGTGTTTT 600
 GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCAGCCT GCGGCCCTT CTAGGTGAT 660
 GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGCCAG TTCATTGTG GGCCTGATT 720
 GTTTGTGCT GGAGGAGGAC GGCCTACATG TTTGTTCTG TAGAAATAA AACTGAGCTA

Seq ID NO: 587 Protein sequence
 Protein Accession #: NP_001318.1

1 11 21 31 41 51
 | | | | |
 MQAEGRGTTG STGDADGPGG PGIPDGPNGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
 PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EABLARRSLA QDAPPLPVFG 120
 VLLKEFTVSG NLTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLPVF LAQPPSGQRR

Seq ID NO: 588 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..459

1 11 21 31 41 51
 | | | | |
 CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
 GAAGGCCAGG GCACAGGGGG TTGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
 CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
 GGTCCCGGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCGCGGGGT 240
 CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTCGGGGCG CAGGAGGCCG 300
 GACAGCGGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTTCCTG TTGATGTGGA TCACGAGTG CTTTCTGCCC 420
 GTGTTTGTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
 TAGGTATGCG CTCCTCCCT AGGGAATGGT CCCAGCACGA GTGCCAGTT CATTGTGGGG 540
 GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAATAAAG 600
 CTGAGCTA

Seq ID NO: 589 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MQAEGQGTGG STGDADGPGG PGIPDGPNGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLFVFLAQAP SQGRR

Seq ID NO: 590 DNA sequence
 Nucleic Acid Accession #: NM_005562.1
 Coding sequence: 90..3671

1 11 21 31 41 51
 | | | | |
 ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCCG GGCAGCGACC CCGTGCAGCG 60
 AGACAGAGAC TGAGCGGGCC GGCACCGCCA TGCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGAACCTCA CAGACAACT GGTAAATGGAT 240
 TCCGCTGCTT CAAGTGCAT GACAACACTG ATGGCATTCA CTGCAGAAAG TGCAAGAATG 300
 GCTTTTACCG GCACAGAGAA AGGACCGCT GTTTCCTCTG CAATTGTAA TCCAAAGGTT 360
 CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACAGGT GTGACAGGAG 420
 CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
 ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
 ACGCGGGCGC CTGTGTCTGC AAGCCAGCTG TTAAGTGGAG ACCTGTGAT AGGTGTGAT 600
 CAGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
 GGCAATCAGC CAGCTGCGCG AGCTCTGCGA AATACAGTGT CCATAAGATC ACCTCTACCT 720
 TTCATCAAGA TGTGTATGCG TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
 AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCGTCTATT 840

	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTT	900
	TTGACTACCG	TGTGGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
	GTGCTGGTCT	ACCGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
5	TCACCAAGAC	TTACACATT	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTG	1200
	TCTCTGGAGC	CCACGACACC	TGGGTTGAAC	AGTGTATATG	TCTGTGTGGG	TACAAGGGGC	1260
	AATCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATT	AGCGAGACTG	GGGCTTTT	1320
	GCACCTGTAT	TCCTTGTAA	TGTCAAGGGG	GAGGGGCTG	TGATCCAGAC	ACAGGAGATT	1380
10	GTTATTGAGG	GGATGGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	CGACCCCGC	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTCACTGCT	1500
	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCACCGGTG	1560
	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTGTGGTAA	CATGGCCCG	1620
	TGAGGCTTGT	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
15	GTGACCGGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
	ACCAGTGCAA	AGCAGGCTAC	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTG	1800
	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATT	GGTGGCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920
	CTTGCTATAA	TCGAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
20	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	CGAGGATGCA	CGAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAGGT	GAGGAGCCAA	GAGAACAGCT	2160
	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCCGGGT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCG	CTGAGCCTGG	2280
25	CAGAAAGTGA	AGCTTCCCTG	GGAAACACTA	ACATTCTCTG	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
	CAGCCAGTAA	CTGAGGACAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGGTAGC	CCGGAACGGT	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAACCAA	GTCCCTGGCC	CAGCAGTTGA	2580
30	CAAGGGAGGC	AGGCTTAGAG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCTGGATTG	AGTGTCTCGG	CTTCAGGAG	TCAGTGATCA	GTCTTTCAG	GTGGAAGAG	2700
	CAAAGAGGAT	CAAAACAAAA	GCGGATTAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAA	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
35	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAAATGGG	3120
40	CCGGGGAGGC	CCTGGAAATC	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	GTGAGATGAG	GGAAAGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
	TGGATGTCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAACG	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCCTGCAT	CTGATGGACC	3420
45	AGCCTCTCAG	TGTAGATGAA	GAGGGCTTGG	TCTTACTGGA	GCAGAAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTCAGA	GCTGGAAGAG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TGTCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGGA	GAACTATAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTCTT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
50	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAAATGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGCTTTAT	3840
	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCTT	CATAATAGTC	GTAAGTGGAG	TCCTGGAATT	TGGACAAGTG	CTGTTGGGAT	4020
55	ATAGTCAACT	TATCTTTTGA	GTAAATGTGAC	TAAAGGAAAA	AACTTTGACT	TTGCCCAGGC	4080
	ATGAAATCTT	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCTT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCTT	CCTACTTACA	4200
	ACCCAGGGTG	TGAACATGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTCAGAGCT	ATGGTGCTTG	CTGGTGCTTG	CCACCTTCAA	4320
60	GTCTGGACCC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATATA	AAGCATTTCC	TACCAGACAA	GCAAAATGTTG	GGAAAGTATT	TACTTTTTCG	4440
	GTTTCAAGAT	GATAGAAAG	TGTGGCTTGG	GCAATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
	ATTAGTCTTA	ATTCAATCCT	ACTTTTCGAA	CACCAAAAT	GATGCGCATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTCTACT	4620
	CACACTTCAG	CTGGGTACCA	TCCATCCCTC	CATTCACTCT	TCCATCCATC	TTTCCATCCA	4680
65	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
	AGCATTTTAA	AAAAATAAAT	TAAAACTTAC	AAACTTTGTT	TGTCACAAGT	GGTGTATTAT	4860
	GCAATAACCG	CTTGGTTTGC	AACCTCTTTG	CTCAACAGAA	CATATGTTGC	AAGACCTTCC	4920
	CATGGGGGCA	CTTGAGTTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTTGTGCA	CATTTCCTTG	4980
70	CATTCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAAACACAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
	TGGTGCTGCC	TGCTTCTCTG	ATTTCTCTTG	ATTTCTCTGA	AAGTGTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 591 Protein sequence
Protein Accession #: NP_005553.1

	1	11	21	31	41	51	
80	MPALNLGCL	CFSLLLPAA	ATSRREVDC	NGKSRQCIFD	RELHRQTGNG	FRCLNNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCSKG	SLSARCDNSG	RCCKPGVGTG	ARCDRLPGF	120
	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYNNLDGGN	180
	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLDPHY	FVAPAKFLGN	QSVSYGQSL	FDYRVDGRGR	HPSAHDVILE	GAGLRITAPL	300
85	MPLOKTLPCG	LTKYTFPLRN	EHPNWNWSPQ	LSYFEYRRL	RNLALRIRA	TYGEYSTGYI	360
	DNVTLISARP	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGPF	GTCIPCNQCG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSK	PCPCNGFSC	SVMPEEEV	480

CNNCPGVTG ARCELCAADY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAFNPADKC RACNCNPMGS EPVGCERSDGT CVCKPGFGGP 600
 NCEHGAFSCP ACYNQVQKQM DQFMQQLQRM EALISKAQGG DGVPVPTDELE GRMQQAEQAL 660
 QDILRDAQIS EGASRSGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVRDTH 720
 RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSRLQGG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLG 900
 NWKEEAQQLL QNGKSGRKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL 960
 QVDNRKAEAE EAMKRLSYIS QKVSADSDKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020
 IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
 AQKVDTRAKN AGVTITQDTLN TLDGLLHLM DQLSVDEEGL VLLEQKLSRA KTQINSQRLP 1140
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

Seq ID NO: 592 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221.856

1 11 21 31 41 51
 | | | | | |
 20 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGCGC CCGGGCGCGG ACCCCAACCC 60
 CGACCCAGAG CTCTCCAGC GCGGCGCGCAG CGAGCAGGGC TCCCGCCCTT AACTTCCTCC 120
 GCGGGGCCCA GCCACCTTCG GAGATCCGGG TTGCCACCTT GCAAACTCTC CGCCTTCTGC 180
 ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CCGGGCTGCA 240
 GCTGTTGGGC TTCAATTCTG CCTTCTCTGG ATGGATCGGC GCCATCGTCA GCACCTGCCCT 300
 25 GCGCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAGTCTT 420
 TGAATCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCCTGA TGGTGGTTGG 480
 CATCTCTCTG GGAGTGATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG 540
 CTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTCTT 600
 30 TCTTGAGGT CTGGCTATT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC 720
 TGGCTGGGCT GCTGCTTCTC TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCTGTCTC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 840
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAATCA TGTGAAACA AACCGAAAT 900
 35 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAAACAAA CAAACAAACA AAAAACCCTAT GTGTTAAAT ACTCAGTGCT 1020
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCAT ATTGCTATAT ACTCAATGG GGAAGGGGT GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 40 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAAT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCTTATAT ACATATGTAA 1320
 CAGTCAATA TCATTACTC TTCTTCATTA GCTTTGGGTG CTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCCTTCAATT CTTCTGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TGTGTTTGTG 1500
 45 TTTCATTGGT CTCTATCTCC TGAATCTAAC ACATTTCATA GCCTACATT TAGTTTCTAA 1560
 AGCCAAGAAG AATTATTAC AAATCAGAAC TTTGGAGGCA AATCTTCTG CATGACCAA 1620
 GTGATAAAT CCGTTGACC TTCCACACA ATCCCTGTAC TCTGACCCAT AGCACTCTG 1680
 TTTGCTTGA AATATTGTT CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740
 50 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTTATTCTA GTTTTATATC CCCCTAACT 1800
 ACCTTTTTGT TCCCATCTC TTAATTGTAT TGTTTTCCCA AGTGTAAAT TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGCTCTGTTT GTCTGAACAA AGTGTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTCTTACC 1980
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
 55 AATATTAAT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTG 2100
 TTTATTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAACCT ACACACGTAC 2160
 CTTCACTGTA TTAAGTCTC TCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAACCTAC 2220
 ACACATACCT TCATGTGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCACTGAACA 2280
 AAACCTACG ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTC 2340
 60 ATTCTTTCAG CTGTGCTGTA CATGTTTGTG CTCTGTTCCA TTTTAAACAC TGCTCTTACT 2400
 TTCCAGTCT GTACAGAATG CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460
 GCACTGGTGT CTGGAGACTT GGATTTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCAGAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 65 GTGTTTGTG AATTGAAAA GTGCTATACT AAGGGAAGA ATTGAGGAAT TAACCTGCATA 2700
 CGTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAA TGTAAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 70 TTTTGAATCA TAATACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTG 3000
 TGTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAA 3060
 CTACACAAGG AAAGTACGCC ACCGTGTCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCTTCCAA CCTGAGATG ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT TTTTATGATG TGTGAGTGA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 75 AAAAAAATG TTTATGGCCC AAAATGACCA ACGAAATGT TACATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTTATCTCTT CTACCAACCC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTGTGATA AAGCATTAAT CTTTTCAT AAATGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAA AAA

Seq ID NO: 593 Protein sequence
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | | |
 85 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGE WMSCVSQSTG 60
 QIQCKVEDSL LNLSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLEDE DEVQKMRMAV 120
 IGGAIFFLAG LAILVATAWY GNRIVQBFYD PMTPVNARYE FGQALPTGWA AASLCLLGGA 180
 LLCCSCPRKT TSYPTPRYP KPAPSSGKDY V

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

5
10
15
20
25
30
35
40
45
50
55
60
65
70

1	11	21	31	41	51	
CCCCCATTCG	CATCTAACAA	GGAATCTGCG	CCCCAGAGAG	TCCCGGACGC	CGCCGGTCGG	60
TGCCCCGGCG	GCCCGGGCCAT	GCAGCGACGG	CCGCCGCGGA	GCTCCGAGCA	CGCGTAGCGC	120
CCCCCTGTAA	AGCGGTTTCG	TATGCCGGGA	CCACTGTGAA	CCCTGCCGCG	TGCCGGAAAC	180
CTCTTCGCTC	CGSACCAGCT	CAGCCTCTGA	TAAGCTGGAC	TCCGCACGCC	CGCAACAAGC	240
ACCGAGGAGT	TAAGAGAGCC	GCAAGCGCAG	GGAAGGCCTC	CCCACACGGG	TGGGGGAAAG	300
CGGCCGGTGC	AGCGCGGGGA	CAGGCACTCG	GGCTGGCACT	GGCTGCTAGG	GATGTCGTCC	360
TGGATAAGGT	GGCATGGAAC	CGCATGGCGG	CGGCTCTGGG	GCTTCTGCTG	GCTGGTGTGT	420
GGCTTCTGGA	GGGCGCGTTT	CGCCTGTCCC	ACGTCCTGCA	AATGCAGTGC	CTCTCGGATC	480
TGGTGAGCGG	ACCCTTCTCC	TGGCATCGTG	GCATTTCCGA	GATTGGAGCC	TAACAGTGTG	540
GATCCTGAGA	ACATCACCGA	AAATTTTCATC	GCAAACCCAG	AAAGGTTAGA	AATCATCAAC	600
GAAGATGATG	TTGAAGCTTA	TGTGGGACTG	AGAAATCTGA	CAATTGTGGA	TTCTGGATTA	660
AAATTTGTGG	CTCATAAAGC	ATTCTGAAA	AACAGCAACC	TGCAGCATAT	CAATTTTACC	720
CGAAACAAAC	TGACGAGTTT	GTCTAGGAAA	CATTTCCGTC	ACCTTGACTT	GTCTGAACTG	780
ATCCTGGTGG	GCAATCCATT	TACATGCTCC	TGTGACATTA	TGTGGATCAA	GACTCTCCAA	840
GAGGCTAAAT	CCAGTCCAGA	CAGTCAGGAT	TTGTACTGCC	TGAATGAAAG	CAGCAAGAAT	900
ATTCCCTCGG	CAAACTTGCA	GATACCCAAT	TGTGGTTTGC	CATCTGCAAA	TCTGGCCGCA	960
CCTAACCTCA	CTGTGGAGGA	AGGAAAGTCT	ATCACATTAT	CCTGTAGTGT	GGCAGGTGAT	1020
CCGGTTCCTA	ATATGTATTG	GGATGTTGGT	AACCTGGTTT	CCAAACATAT	GAATGAAACA	1080
AGCCACACAC	AGGGCTCCTT	AAGGATAAAT	AACATTTTCA	CCGATGACAG	TGGGAAGCAG	1140
ATCTCTTGTG	TGGCGGAAA	TCTTGTAGGA	GAAGATCAAG	ATTCTGTCAA	CCTCACTGTG	1200
CATTTTGCAC	CAACTATCAC	ATTTCTCGAA	TCTCCAACCT	CAGACCACCA	CTGGTGCATT	1260
CCATTCACTG	TGAAAGGCAA	CCCCAAACCA	GCGCTTCAGT	GGTTCATATA	CGGGGCAATA	1320
TTGAATGAGT	CCAAATACAT	CTGTACTAAA	ATACATGTTA	CCAATCACAC	GGAGTACCA	1380
GGCTGCCTCC	AGCTGGATAA	TCCCACTCAC	ATGAACAATG	GGGACTACAC	TCTAATAGCC	1440
AAGAATGAGT	ATGGGAAGGA	TGAGAAACAG	ATTTCTGCTC	ACTTCATGGG	CTGGCCTGGA	1500
ATTGACGATG	GTGCAAAACC	AAATTATCCT	GATGTAATTT	ATGAAGATTA	TGGAACTGCA	1560
GCGAATGACA	TCCGGGACAC	CAGGAACAGA	AGTAATGAAA	TCCCTTCCAC	AGACGTCAC	1620
GATAAAACCG	GTCGGGAACA	TCTCTCGGTC	TATGCTGTGG	TGGTGATGTC	GTCCTGGGTG	1680
GGATTTTGCC	TTTTGGTAAT	GCTGTTTCTG	CTTAAGTTGG	CAAGACACTC	CAAGTTTGGC	1740
ATGAAAGGCC	CAGCTCCGCT	TATCAGCAAT	GATGATGACT	CTGCCAGCCC	ACTCCATCAC	1800
ATCTCCAATG	GGAGTAACAC	TCCATCTTCT	TCCGAAGGTG	GCCCAGATGC	TGTCTATTAT	1860
GGAAATGACCA	AGATCCCTGT	CATTGAAAAT	CCCCAGTACT	TTGGCATCAC	CAACAGTCAG	1920
CTCAAGCCAG	ACACATTTGT	TCAGCACATC	AAGCGACATA	ACATTGTTCT	GAAAAGGGAG	1980
CTAGGCGAAG	GAGCCTTTGG	AAAAGTGTTC	CTAGCTGAAT	GCTATAACCT	CTGTCCTGAG	2040
CAGGACAAGA	TCTTGGTGGC	AGTGAAGACC	CTGAAGGATG	CCAGTGACAA	TGCACGCAAG	2100
GACTTCCACG	GTGAGGCCGA	GCTCCTGACC	AACCTCCAGC	ATGAGCACAT	CGTCAAGTTC	2160
TATGGCGTCT	GGGTGGAGGG	CGACCCCTCT	ATCATGGTCT	TTGAGTACAT	GAAGCATGGG	2220
GACCTCAACA	AGTTCCTCAG	GGCACACGGC	CCTGATGCCG	TGCTGATGGC	TGAGGGCAAC	2280
CCGCCACCGG	AAGTACGCGA	GTGCGAGATG	CTGCATATAG	CCCAGCAGAT	CGCCCGGGGC	2340
ATGGTCTATG	TGGGCTCCCA	GCATCTCGTG	CACCGCGATT	TGGCCACCAG	GAACGCTCTG	2400
GTCCGGGAGA	ACTTGCTGGT	GAAAATCGGG	GACTTTGGGA	TGTCCCGGGA	CGTGTACAGC	2460
ACTGACTACT	ACAGGGTCGG	TGGCCACACA	ATGCTGCCCA	TTGCTGGGAT	GCCTCCAGAG	2520
AGCATCATGT	ACAGGAAATT	CAGCAACGAA	AGCGACGTCT	GGAGCCTGGG	GGTCTGTTG	2580
TGGGAGATTT	TCACCTATGG	CAACAGCCCC	TGGTACCAGC	TGTCAAACAA	TGAGGTGATA	2640
GAGTGATATCA	CTCAGGCGCG	AGTCCCTGCG	CGACCCCGCA	CGTGCCCCCA	GGAGGTGTAT	2700
GAGCTGATGC	TGGGGTGCTG	CGAGCGAGAG	CCCCACATGA	GGAAGAACAT	CAAGGGCATC	2760
CATACCTCTC	TTAGAACTTT	GGCCAAAGCA	TCTCCGGTCT	ACCTGGACAT	TCTAGGCTAG	2820
GGCCCTTTTC	CCCAGACCGA	TCCTTCCCAA	CGTACTCCTC	AGACGGGCTG	AGAGGATGAA	2880
CATCTTTTAA	TGCGCGCTGG	AGGCCACCAA	GCTGCTCTCC	TTCACTCTGA	CAGTATTAA	2940
ATCAAAGACT	CCGAGAAGCT	CTCGAGGGAA	GCAGTGTGTA	CTTCTTCATC	CATAGACACA	3000
GTATTGACTT	CTTTTGGGCA	TTATCTCTTT	CTCTCTTTCC	ATCTCCCTTG	GTTGTTCTTT	3060
TTTCTTTTTT	TAAATTTTCT	TTTTTCTTCT	TTTTTCTGTC	TTCCCTGCTT	CACGATTCTT	3120
ACCCTTTCTT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACTCTGCAT	AGACAAAGGC	3180
CTTAACAAAC	GTAATTTGTT	ATATCAGCAG	ACACTCCAGT	TTGCCACCA	CAACTAACAA	3240
TGCCCTTGTG	TATTCCTGCC	TTTGATGTGG	ATGAAAAAAA	GGGAAAAACA	ATATTTCACT	3300
TAAACTTTGT	CACCTCTGCT	TACACAGATAT	CGAGAGTTTC	TATGGATTCA	CTTCTATTTA	3360
TTTATTATTA	TACTGTGTTT	TATTGTTTTT	GGATGGCTTA	AGCCTGTGTA	TAAAAAGGAA	3420
AACTTGTGTT	CAATCTGTGA	AGCCTTTATC	TATGGGAGAT	TAAAAACCAG	GAGAAAGAAG	3480
ATTTATTATG	AACCGCAATA	TGGGAGGAAC	AAAGCAACCC	ACTGGGATCA	GCTGGTGTCA	3540
GTCCCTACTT	AGGAAATACT	CAGCAACTGT	TAGCTGGGAA	GAATGTATTC	GGCACCTTCC	3600
CCTGAGGACC	TTTCTGAGGA	GTAAGAAAGC	TACTGGCCTC	TGTGCCATGG	ATGATTCTTT	3660
TCCCATCACC	AGAAATGATA	GCGTGCAGTA	GAGAGCAAAG	ATGGCTT		

Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

75
80
85

1	11	21	31	41	51	
MSSWIRWHGP	AMARLWGFCH	LVVGFWRAAF	ACPTSCCKCSA	SRIWCSDFSP	GIVAFPRLEP	60
NSVDPENITE	IFIANQKRLK	IINEDDVEAY	VGLRNLITVD	SGLKFAVHKA	FLKNSNLQHI	120
NFTRNKLTSL	SRKHPRHLDL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES	180
SKNIPLANLQ	IPNCGLPAN	LAAPNLVVEE	GKSITLSCSV	AGDPVPMYMW	DVGNLVSKHM	240
NETSHTQGS	RITNISSDDG	GKQISCVAE	LVGEDQDSVN	LTVHFAPTIT	FLESPTSDDH	300
WCIPFTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHVNTHT	EYHGCLQLDN	PTHMNGDYT	360
LIANKNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNEIPST	420
DVTDKTKGREH	LSVYAVVVIA	SVVGFCLLVM	LFLKLKLARHS	KFGMKGPASV	ISNDDDSASP	480
LHHISNGSNT	PSSSEGGPDA	VIIGMTKIPV	IENPOYFGIT	NSQLKPDFTFV	QHIKRHNIVL	540
KRELGEAGFG	KVFLAECYNL	CPEQDKILVA	VKTLKDASDN	ARKDFHREAE	LLTNLQHEHI	600
VKPYGVCEVG	DPLIMVFYEM	KHGDNLKFLR	AHGPDVFLMA	EGNPPTLTQ	SQMLHIAQHI	660
AAGMVYLASQ	HPVHRDLATR	NCLVGENLLV	KIGDFGMSRD	VYSTDYRYRG	GHTMLPIRWM	720

PPESIMYRKF TTBSDVWSLG VVLWEIFTYG KQFWYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EVYELMLGCH QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 596 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

1 11 21 31 41 51
 | | | | |
 10 GGGAGCAGGA GCCTCGCTGG CTGCTTCGCT CGCGCTCTAC GCGCTCAGTC CCCGGCGGTA 60
 GCAGGAGCCT GGACCCAGGC GCGGCGCGCG GCGTGAGGC GCCCGAGCCC GGCTCGAGG 120
 TGCATACCGG ACCCCATTCT GCATCTAACA AGGAATCTGC GCCCAGAGA GTCCCGGAGC 180
 CCGCGGCTCG GTGCCCGGCG CGCCGGGCCA TGCAGCGACG GCCCGCGCGG AGCTCGAGC 240
 15 AGCGGTAGCG CCCCCCTGTA AAGCGGTTGG CTATGCCGGG ACCACTGTGA ACCCTGCCGC 300
 CTGCGCGAAC ACTCTTCGCT CGGACCAGC TCAGCCTCTG ATAAGCTGGA CTGCGCACGC 360
 CCGCAACAAG CACCGAGBAG TTAAGAGAGC CGCAAGCGCA GGAAGGCCT CCCCGCACGG 420
 GTGGGGGAAA GCGGCGCGTG CAGCGCGGGG ACAGGCACCT GGGCTGGCAC TGGCTGCTAG 480
 GGATGTGCTC CTGGATAAGG TGGCATGGAC CCGCATGGC GCGGCTCTGG GGCTCTGCT 540
 20 GGCTGGTGT GGGCTTCGCG AGGGCCGCTT TCGCCTGTCC CACGTCTGTC AAATGCAGTG 600
 CCTCTCGGAT CTGTGTGAGC GACCCCTCTC CTGGCATCGT GGCATTTCGG AGATTGGAGC 660
 CTAACAGTGT AGATCCTGAG AACATCACCG AAATTTTCAT CGCAAAACAG AAAAGGTTAG 720
 AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780
 ATTCTGGATT AAAATTTGTG GTCATATAAG CATTTCTGAA AAACAGCAAC CTGCAGCACA 840
 TCAATTTTAC CCGAAACAAA CTGACGAGTT TGTCTAGGAA ACATTTCGGT CACCTTGACT 900
 25 TGTCTGAAGT GATCCTGGTG GGCATCCAT. TTACATGCTC CTGTGACATT ATGTGGATCA 960
 AGACTCTCCA AGAGGCTAAA TCCAGTCCAG ACACCTCAGG TTTGTACTGC CTGAATGAAA 1020
 GCAGCAAGAA TATTCCTCTG GCAAAACCTG AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080
 ATCTGCCCGC ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140
 TGGCAGGTGA TCGGTTCTCT AATATGTATT GGGATGTTGG TAACCTGGTT TCCAAACATA 1200
 30 TGAATGAAAC AAGCCACACA CAGGCTCCTT TAAGGATAAC TAACATTTCAT TCCGATGACA 1260
 GTGGGAAGCA GATCTCTTGT GTGGCGGAAA ATCTTGTAGG AGAAGATCAA GATTCTGTCA 1320
 ACCTCACTGT GCATTTTGCA CCAACTATCA CATTTCTCGA ATCTCCAACC TCAGACCACC 1380
 ACTGGTGCAAT TCCATTCTCT TCGAAAGGCA ACCCCAAACC AGCGCTTCAG TGGTTCTATA 1440
 35 ACGGGCAAT ATTGAATGAG TCCAAATACA TCTGTACTAA AATACATGTT ACCAATCACA 1500
 CGGAGTACCA CGGCTGCCTC CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560
 CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTCTGCTC CACTTCATGG 1620
 GCTGGCCTGG AATTGACGAT GGTGCAAAAC CAAATATCC TGATGTAATT TATGAAGATT 1680
 ATGGAAGTGC AGCGAATGAC ATCGGGGACA CCAAGAACAG AAGTAATGAA ATCCCTTCCA 1740
 40 CAGACGTGAC TGATAAAAACC GGTGCGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800
 CGTCTGGTGT GGGATTTTGG CTTTTGGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860
 CCAAGTTTGG CATGAAGATG TTCTCATGGT TTGGATTGGG GAAAGTAAAA TCAAGACAAG 1920
 GTGTTGGCCC AGGCTCCGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCCATCACA 1980
 TCTCCAATGG GAGTAACACT CCATCTTCTT CGGAAGGTGG CCCAGATGCT GTCAATTATTG 2040
 45 GAATGACCAA GATCCCTGTC ATTGAAAATC CCCAGTACTT TGGCATCACC AACAGTCAGC 2100
 TCAAGCCAGA CACATTTGTT CAGCACATCA AGCGACATAA CATTTGTTCTG AAAAGGGAGC 2160
 TAGGCGAAGG AGCCTTTGGA AAGTGTGTTCC TAGCTGAATG CTATAACCTC TGTCTGAGC 2220
 AGGACAAGAT CTGTGTGACA TGAAGACCC TGAAGGATGC CAGTGACAAAT GCACGCAAGG 2280
 ACTTCCACCG TGAGGCGGAG CTCCTGACCA ACCTCCAGCA TGAGCACATC GTCAAGTTCT 2340
 50 ATGGCGTCTG CGTGAGGGGC GACCCCTCTA TCATGGTCTT TGAGTACATG AAGCATGGGG 2400
 ACCTCAACAA GTTCTCTCAG GCACACGGCC CTGATGCCGT GCTGATGGCT GAGGGCAACC 2460
 CGCCACGGA ACTGACGAG TCGCAGATGC TGCAATAGC CCAGCAGATC GCCGCGGGCA 2520
 TGGTCTACCT GCGCTCCGAC CACTTCGTGC ACCGCGATT TGGCCACAGG AACTGCCTGG 2580
 TCGGGGAGAA CTGTCTGTG AAAATCGGGG ACTTTGGGAT GTCCCGGGAC GTGTACAGCA 2640
 55 CTGACTACTA CAGGTCGGT GGGCACAA TGTGCCCCAT TCGCTGGATG CCTCCAGAGA 2700
 GCATCATGTA CAGGAAATTC ACGACGSAAA GCGACGCTCG GAGCCTGGGG GTCGTGTTGT 2760
 GGGAGATTTT CACCTATGGC AAACAGCCCT GGTACCAGCT GTCAAAACAT GAGGTGATAG 2820
 AGTGTATCAT TCAGGGCCGA GTCTCTGAGC GACCCCGCAC GTGCCCCAG GAGGTGTATG 2880
 AGCTGATGCT GGGGTGCTGG CAGCGAGAGC CCCACATGAG GAAGAACATC AAGGGCATCC 2940
 60 ATACCTCTCT TCAGAACTTG GCCAAGGCAT CTCCGGTCTA CCTGGACATT CTAGGCTAGG 3000
 GCCTTTTCC CCAGACCGAT CCTTCCCAAC GTACTCTCA GACGGGCTGA GAGGATGAAC 3060
 ATCTTTTAA TGCCTGTGGA GGGCACCAAG CTGCTCTCCT TCACTCTGAC AGTATTAAAC 3120
 TCAAGACTC CGAAGAAGCT TCGAGGGAAG CAGTGTGTAC TTCTTCATCC ATAGACACAG 3180
 TATGACTTCT TTTTGGCAT TATCTCTTTC TCTCTTCCA TCTCCCTTGG TTGTTCTTTT 3240
 65 TTCTTTTCTT AAAATTTCTT TTCTTCTT TTCTTCTT TTTTCTGCTC TCCCTGCTTC ACGATCTTCA 3300
 CCCTTTCTTT TGAATCAATC TGGCTTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360
 TTAACAAACG TAATTTGTTA TATCAGCAGA CACTCCAGTT TGCCACCAC AACTAACAAAT 3420
 GCCTGTGTGT ATTCTGCCT TTGATGTGGA TGAAAAAAG GGAACAACAA TATTTCACTT 3480
 70 AAATTTGTC ACTTCTGCTG TACAGATATC GAGAGTTTCT ATGGATTAC TTCTATTTAT 3540
 TTATTATTAT TACTGTTCTT ATTGTTTTTG GATGGCTTAA GCCTGTGTAT AAAAAGAAA 3600
 ACTTGTGTTT AATCTGTGAA GCCTTATCT ATGGGAGATT AAAACAGAG AGAAAGAAAG 3660
 TTTATTATGA ACCGCAATAT GGGAGGAACA AAGACAACCA CTGGGATCAG CTGGTGTACG 3720
 TCCTACTTA GGAATACTC AGCAACTGTT AGCTGGGAAG AATGTATTCT GCACCTTCCC 3780
 CTGAGGACCT TTCTGAGGAG TAAAAAGACT ACTGGCCTCT GTGCCATGGA TGATTTCTTT 3840
 75 CCCATACCA GAAATGATAG CGTGCACTAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900
 ATGGCGCATA GTGTGCTCGG ACACAGTTTT GTCTTGTAG GTTGTGATGA TAGCACTGGT 3960
 TTGTTTCTCA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAAG AGGTGGATTG 4020
 ATGTCCAGAG CTCATTTCCG GGTGAGGTGG GAAAGCC

Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

1 11 21 31 41 51
 | | | | |
 85 MSSWIRWHP AMARLWGFV LUVGFWRAP ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKPVAKKA FLKNSNLQHI 120
 NPTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLP SAN LAAPNLVVEE GKSITLSCSV AGDPVPNMWY DVGNLVSKHM 240

NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
WCIPFTVKGN PKPALQWFFN GAILNESKYI CTKIHVNTHT EYHGCLQLDN PTHMNGDYT 360
LIAKNBYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPT 420
DVTDKTGRH LSVYAVVVIA SVVGFCLLV LFLKLARHS KFGMDPSWF GFGKVKSRQG 480
5 VGPASVISND DNASPLHII SNGSNTSPSS EGGPDAAVIG MTKIPVIE NP QYFGITNSQL 540
KPDTFVQHIK RHNIVLKREL GEGAFGRVFL ABCYNLCPEQ DKILVAVKTL KDASDNARKD 600
FHREAE LLTN LQHEHIVKPY GVCVEGDPLI MVPEYMKHGD LNKPLRAHGP DAVLMAEGNP 660
PTBLTQSQML HIAQQAAGM VYLAHQHVFH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
10 DYYRVGGHTM LPIRMWPPES IMYRKFTTES DVWSLGVVLM EIFTYKQFPW YQLSNNEVIE 780
CITQGRVLQR PRTCEVYE LMLGCWQREP HMRKNIKGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 598 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74..814

1 11 21 31 41 51
| | | | |
AAAACCTTGA GGTGATTCAT CTCCAGGCT CTCCTTCCAT CAAGTCTCTC CTCCTAGCG 60
CTCTGGGTCC TTAATGGCAG CAGCCGCCGC TACCAAGATC CTTCTGTGCC TCCCGCTTCT 120
20 GCTCCTGCTG TCCGGCTGGT CCGGGCTGG GCGAGCCGAC CCTCACTCTC TTGTCTATGA 180
CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTT AAGGCCAGGT 240
GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTCACAC CTGTCACTCC 300
CCTGGGGAAG AAACATAATG TCACAACGGC CTGGAAAGCA CAGAACCCAG TACTGAGAGA 360
GGTGGTGGAC ATACTTACAG AGCAACTGCG TGACATTGAG CTGGAGAATT ACACACCCAA 420
25 GGAACCCCTC ACCCTGCAGG CCAGGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480
TGGATCTTGG CAGTTCACTG TCAGTGGGCA GATCTTCTCT CTCTTTGACT CAGAGAAGAG 540
AATGTGGACA ACGGTTTATC CTGGAGCCAG AAAGATGAAA GAAAAGTGGG AGAATGACAA 600
GGTTGTGGCC ATGTCTCTCC ATTACTTCTC AATGGGAGAC TGTATAGGAT GGCTTGAGGA 660
CTTCTTGATG GGCATGGACA GCACCCCTGA GCCAAGTGCA GGAGCACCAC TCGCCATGTC 720
30 CTCAGGCACA ACCCAACTCA GGGCCACAGC CACCACCTC ATCCTTTGCT GCCTCTCTCAT 780
CATCTCTCCC TGCTTCACTC TCCTTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTTA 840
AAGCTGATAC CAAAAGGCTC CTGTGAGCAC GGTCTTGATC AAACCTCGCC TTCTGTCTGG 900
CCAGCTGCCC ACGACCTACG GTGTATGTCC AGTGGCCTCC AGCAGATCAT GATGACATCA 960
TGGACCCAAT AGCTCATCA CTGCCTTGAT TCCTTTTGCC AACAAATTTA CCAGCAGTTA 1020
35 TACCTAACAT ATTATGCAAT TTCTCTTGG TGCTACCTGA TGGAAATCCT GCACCTAAAG 1080
TTCTGGCTGA CTAACAAGA TATATCATTT TCTTCTTCT CTTTTGTGTT GGAAATCAA 1140
GTACTTCTTT GAAATGATAT CTCTTCTTG CAAATGATAT TGTGAGTAAA ATAATCACGT 1200
TAGACTTCAG ACCCTCGGGG ATTCTTTCG TGCTCTGAAA GAGAATTTT AAATTATTTA 1260
40 ATAAGAAAAA ATTTATATTA ATGATTGTTT CCTTTAGTAA TTTATTGTTT TGTACTGATA 1320
TTTAAATAAA GAGTCTATT TCCCAAAAAA AAAAAAAAAA AA

Seq ID NO: 599 Protein sequence
Protein Accession #: BAB61048.1

1 11 21 31 41 51
| | | | |
MAAAAATKIL LCLPLLLLL GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
FLHYDGNKT VTPVSPLGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120
50 LQARMSCEQK AEGHSSGSWQ FSPDGGIFLL FDSEKRMWTT VHPGARKMKE KWENDKVAM 180
SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
FILPGI

Seq ID NO: 600 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

1 11 21 31 41 51
| | | | |
GGCTCTCACC CTCTCTCTCT CGAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG 60
CCCAGTATCT GAGTACCTCG CTGCTCTCTG TGGCCACCTC AGCTGTGGCC CTGGCCTGGA 120
60 GCCCAAGGA GGAGGATAGG ATATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
65 ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCC TGTAGTGCTC 540
CCACCCCTGG ACTGGTGGCC CCCACCTGCG GGGAGGCCTC CCCATGTGCC TGGCCCAAGA 600
70 GACAGACAGA GAAGGCTGCA GGAGTCTCTT GTTGCTCAGC AGGGGCTCT CCCTCCCTC 660
CTTCTTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
AAACAGTAGC ATCGCC

Seq ID NO: 601 Protein sequence
Protein Accession #: NP_001889.1

1 11 21 31 41 51
| | | | |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
80 DDYRRRLRV LRARQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF 120
EIYVWPWENR RSLVSRQCE S

Seq ID NO: 602 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299.961

1 11 21 31 41 51
| | | | |

CTCTGAGCTT CTCTGAGCCT TGTITGCTCA TCTGGA AAAA GGGGATTAAA CCATTTACCT 60
 CATGGAGTTG TGAAGAATA GCTGCAAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
 CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCTCTG TTCCTCACCT GGAGAACTG 180
 GGGTGGCAGG CCGGTCCCCC ACAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
 CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGTGGTG TGATAGAGAT 300
 GGAAC TTGGA CTGTGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGGGCGAGCC 360
 TGGCTGTGG CCCAGCCTGG CCGCTCTGGC TCTGCTGAGC AGCGTGCAG AGGCCTCCCT 420
 GGGCTCCGCG CCCCAGAGCC CTGCCCCCG CGAAGGCCCG CCGCTGTCC TGGCTGCC 480
 CGCGGCCAC CTGCGGGGG GACGCAAGCG CCGCTGGTGC AGTGAAGAG CCGGGGGCC 540
 GCGCGCGCAG CCGCTCTGGC CCGCGCCCC GCGCGCTGCA CCCCCCTG CTCTTCCCCG 600
 CGGGGGCCCG GCGCGCGGG CTGGGGGCCC GGGCAGCGCG GCTCGGGCAG CCGGGGCGCG 660
 GGGCTGCCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTGCGCTGG GCCACCGCTC 720
 CGACGAGCTG TGGCTTTTCC GCTTCTGCAG CCGCTCTGCG CCGCGCGCGC GCTCTCCACA 780
 CGACCTCAGC CTGGCCAGCC TACTGGGCGC CCGGGCCCTG CGACCGCCCC CCGGCTCCCG 840
 GCCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
 CAACAGCACC TGGGAAGCCG TGGACCGCT CTCCGCAACC GCCTGCGGCT GCCTGGGCTG 960
 AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCTGGGAC 1020
 CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
 AGGCCCTAC CCGTGGTGA TGGATATCAT CCCCAGACAG GTGAAGGGAC AACTGACTAG 1140
 CAGCCCCAGA GCCCTCAGCC TGGGATCCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT 1200
 GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCGCTG AACCTGGGAC 1260
 CCTCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCAGG CCCTGTAGGG 1320
 ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGGTTGAA AGTGCCTGTG CTGGAAGTGG 1380
 CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
 | | | | |
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRLRSQIV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

1 11 21 31 41 51
 | | | | |
 ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
 GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC 120
 TCGCTCCCG CCTTCACTCA CTCTTCCCG CCCTCGGCC GGCCTCCAG CTCTCTACTT 180
 CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCTCTC CACGCTCGA GTTCTCTACT 240
 CTCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCT CCAACCTCGG GGGACCTAGC 300
 CAACTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG 360
 CGGGGCGAGG GCGCTCCAG CCCACCCCG GGATCTGGTG ACGTGGGGC TGAATTTGA 420
 CACCGGACGG CTGCGGGCG GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGCCCC 480
 CAGACAAGGC CCGGGGGGCT CGCCAGCAGC AGGTCCCTCG GGGCCAGCC CTGCTGCCA 540
 CCGGGGCTG GAGCCCCACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGGC ACTGCCAGGT GTACAGTCTT GGCATGCGC TGTTTGAGCT TCGGGGAGA 660
 GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCCTCCTG GTGTTGATAG 780
 AGATGGAAT TGGACTTGA GGCCTCTCCA CGCTGTCCA CTGCCCTGG CCTAGGCGGC 840
 AGCTGCCCC GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCTTGGGCTC CGCCCGCGC AGCCCTGCCC CCGCGGAAG CCCCCCGCT GTCTTGGCT 960
 CCCCCGCGG CCACCTGCCG GGGGGAACGA CCGCCGCTG GTGCACTGGA AGAGCCCGGC 1020
 GGCGCGCGCC GCAGCCTTCT CCGCCCGCGC CCGCGCGCC TGCACCCCA TCTGCTCTT 1080
 CCGCGGGGG CCGCGCGCG CCGGCTGGG GCGCGGCGC CCGCGCTCG GCAGCGGGG 1140
 CGCGGGGCTG CGCTCTGCGC TCGCAGCTGG TGCCGGTGG CCGCTCGG CTGGGCCACC 1200
 GCTCCGACGA GCTGGTGGCT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG CCGCGCTCT 1260
 CACACGACCT CAGCTTGACC AGCTACTGG GCGCGGGGC CCTGCGACCG CCGCGGGCT 1320
 CCGCGCCCGT CAGCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCG CACCGCTGC GGTGCTCTG 1440
 GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCTTA CCGGTGGCTC TTCTGCTCTG 1500
 GGACCTCCC GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
 TGAGAGGCC CTACCGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA 1620
 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG 1680
 CTATGGAGCC CTTGAGCCC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTGAACTCTG 1740
 GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT 1800
 AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGGC TGTGCTGGAA 1860
 CTGGCTGTA CTCACATG GGAGCTGGCC CC

Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

1 11 21 31 41 51
 | | | | |
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRLRSQIV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

Coding sequence: 1..714

```

1      11      21      31      41      51
5  ATGCCCCGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCCTTC TCCCCAAGCC 60
   CACCTGGGTG CCCCTCTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
   TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGCTC CAGAGGCCTC CCTGGGCTCC 180
   GCGCCCGGCA GCGCTGCCCC CCGGGAAGGC CCCCAGCTG TCTGGGCTC CCCCAGCGGC 240
   CACCTGCGCG GGGGACGCAC GGCCCGCTGG TGCACTGGAA GAGCCCGGCG GCCGCGCGCG 300
   CAGCCTTCTC GGGCCGCGCC CCGCGCGCCT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
   CGCGCGGCGC GGGCTGGGGG CCGGGGCAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
   CGCCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
   CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
   AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCGCGGGCTC CCGGCCCGTC 600
   15 AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
   ACCTGGAGAA CCGTGGACCG CCTCTCGGCC ACCGCTCGCG GCTGCTGGG CTGAGGGCTC 720
   GCTCCAGGCG TTTCAGACT GGAACCTTAC CGGTGGCTCT TCCTGCGTGG GACCTCTCCG 780
   CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC 840
   20 TACCGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
   AGAGCCCTCA CCCTGCGGAT CCAGACCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
   TTGGACCCA CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT 1020
   CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
   TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCTT GTGCTGGAAC TGGCCTGTAC 1140
   TCACTCATGG GAGCTGGCCC C

```

Seq ID NO: 607 Protein sequence

Protein Accession #: NP_476501.1

```

1      11      21      31      41      51
30 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
   APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRRARRPP QPSRPAPPPP APPSALPRGG 120
   RAARAGGPGS RARAGAGRC RLRSQVLPVR ALGLGHRSD ELVRFRCSSG CRRARSPHDL 180
   35 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

```

Seq ID NO: 608 DNA sequence

Nucleic Acid Accession #: NM_057090.1

Coding sequence: 29..715

```

1      11      21      31      41      51
40 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTTGGAGGCC TCTCCACGCT 60
   GTCCCACTGC CCCTGGGCTA GCGGCGAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
   45 GTGGCCACCC CTGGCCGCTC TGCTCTGCTG GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
   CGCGCCCGGC AGCCCTGCCC CCGCGGAAGG CCCCAGCTG GTCCTGGCGT CCCCAGCGGC 240
   CCACCTGGCG GGGGAGCGCA CGGCCGCTG GTGCAGTGGG AGAGCCCGGC GGCCCGCGCC 300
   GCAGCCTTCT CGGCCCGCGC CCCCAGCGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
   CGCGCGGCGC CGGCTGGGG GCGCGGCGC CGCGCTCGG GCAGCGGGG CCGGGGGCTG 420
   50 CCGCTGCGC TCGCAGCTGG TGCCGCTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
   CTGGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGGCTCTC CACACGACCT 540
   CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CCTGCGACCG CCCCAGGGCT CCGCGCCCGT 600
   CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660
   CACCTGGAGA ACCGTGGACC GCCTCTCGCG CACCGCCTGC GGCTGCGCTG GCTGAGGGCT 720
   CGCTCCAGGG CTCTGACAGC TGACACCTTA CCGGTGGCTC TTCTGCGCTG GGACCTCTCC 780
   55 GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCC 840
   CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
   CAGAGCCCTC ACCCTGCGGA TCCACGCTTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
   CTTGCGACCC ACTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC 1020
   60 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
   TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCTGTGA 1140
   CTCACCTCAT GGAGCTGGCC CC

```

Seq ID NO: 609 Protein sequence

Protein Accession #: NP_476431.1

```

1      11      21      31      41      51
65 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
   GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
   70 SRARAAGARG CRLRSQVLPV RALGLGHRSD ELVRFRCSSG SCRRARSPHD LSLASLLGAG 180
   ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

```

Seq ID NO: 610 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1746

```

1      11      21      31      41      51
80 ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG 60
   GCCTACCATG GCTGCCCTAG CGAGGTGTACC TGCTCCAGGG CCTCCAGGT GGAGTGCAAC 120
   GGGGACGCA TGTGGCGGT GCCCACCCCT CTGCGCTGGA ACGCCATGAG CCTGCAGATC 180
   CTCACACGC ACATCACTGA ACTCAATGAG TCCCGTTCC TCAATATCTC AGCCCTCATC 240
   GCCTGAGGA TTGAGAAGAA TGAGCTGTGC CGCATCACGC CTGGGGCCTT CCGAAACCTG 300
   85 GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAGCTGCG AGGTCTGCTC CATCGGCTC 360
   TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTCTGTCCA GTAACAGCT GTTGACAGATC 420
   CAGCCGGCCC ACTTCTCCCA GTGCAGCAAC CTCAGGAGC TGCAGTTGCA CGGCAACCAC 480
   CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCAGGAA GCTCAATCTG 540

```

	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCTCTCCGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACTCTG	AGGAACTGGC	TCTACAGCAG	AACAGAGATT	GACTGCTCTC	CCCTGGTCTC	720
5	TTCCAACAAC	ACCAACACCT	CCAGAGACTC	TACCTGTCCA	ACAACCAAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCTGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAAOC	ACAICTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TAGCCGCAA	TGAGATCAGC	TTCATCTCCC	GGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
10	TTCCGCATGT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACACCCAG	1200
	CTGGAGAACT	TGCCCTCTCG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
	TATGACAAAT	CTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCTGTCTC	1320
15	AACCAAGCTA	GGTAGGGAC	GGCACTGTGA	CCTGTGTGTT	TCAGCCAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCAITATCAT	CAATGTCAAC	GTGCTGTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCTAGATT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCATGTA	GCTAACACAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTCAAGTCA	CTAGTACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
20	ATTGCGGCA	TGTAAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGC	1680
	TGTTGTCTGT	GCAAGAGAG	GAGCCAGGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTCTGTGGC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTCTCTGA	CTTGCTGTAT	TCTCCGCTAG	AGAAGCAGGT	1920
25	CGTCCGAGC	CTTCTACAA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTCATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCCA	AATCTCTCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
30	ACCCAGCATG	TCCCTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGTCTCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAGAA	GACTTCAAA	CATTAACTG	GTTCCTTAAG	AGCCGCTCAAT	2340
	CAGCCTGGTT	TGCGGATGCG	TATGAAGAG	AGAAGGAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAGA	GCGGTCTATC	GTGTCTCACT	TGTGATTTTT	ATCTGGAATA	GGAAGAAAAC	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AACCTTGCTT	2520
35	TGAAAAGTTT	AGCCCTTAA	GGATGAGAA	AGAAATCTGG	TGCTGGGGG	TCCTGTGTTT	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGG	TCCTGTGTTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCAACA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ATCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTGGGC	TTTTCCAGAA	2820
40	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGA	GCCAGGACGG	2880
	TCCCCCACA	GTACGCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCCTG	3000
	AGAGACCCCT	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGACG	CCACACCTCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCTC	3120
45	TCCGCTGGA	GCTTCTATG	GAGGTGATAT	GCCTGTATCT	GTTTTAAATT	TTTATCTTCT	3180
	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	TGTGTAATA	TCTCCATCAA	CATCAGATC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCAACTGCG	3360
	GTCTGGGGGC	TCCCTGAGC	TCTCTCTGCG	TGTGCTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
50	TCCAGGGTTA	TCTTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCTTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATGACA	TGCGGCTCAA	GAAATGAGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGACAAA	CTGGCCAGT	TTACAGTGAA	ATGGAGAAAT	TCAGGTCTCC	ACGTCTGCC	3600
	AGGAAAGAAC	TTCAGCTGAC	TCCACGGGGA	TCTGAAATC	CACGACCAAT	CCGATCGGC	3660
55	TCTTATTAGC	TCCCGCTTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGCGCTCTTA	TGAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTTCC	TTTCCCTTC	CAGTTCCTGC	ACAAAAGTG	3840
	CAGGAGCAGG	TGCTGACCCG	TTTCCCTTC	CAGTTCCTGC	ACAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CAGTAGTGCA	CTTTGTAGCT	TTTCACTCTC	TGTCCAGGG	AATCTAGGAG	3960
60	AGATGAGGCC	CGTCAGATG	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGTTGGCC	TGCTGTGCTT	GGTGCCAACA	4140
	GGGGCATCCC	GCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTCTGCCCCA	AGACCTGTGG	4200
	GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCTAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TGATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCCTTA	4320
65	GGTATTCTCT	GCATAGGCCA	TGACATTGGA	GCACCTTCTC	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCTAGAT	GACACACCC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGA	GTCTCTTTC	CAACAGGATG	ATGCATTGCT	TCAATTCTCA	4620
70	GGGCTGGAAT	GAGCCGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGTACAGA	GTTCAGTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCATCT	GGAGTGGGAG	TGCGGAGTTA	4740
	GTGTTGGAGA	AGAAACAACA	AAAGCCAATT	AGAACCATA	TTTTTAAAAA	GTGCTTACTG	4800
	TGCACAGATA	CTCTTCAAGC	ACTGGAACST	GATTCTCTCT	CTAGCCCTCA	GCACCCCTGC	4860
	GGTAGGAGTG	CGCCCTCTAC	CCACTTGTGA	TGGGGTACAG	AGGCACCTGC	TCTCTGCAT	4920
75	GGTGTTCAT	AGGCTGGGAG	TTTTATTAT	CTCTTCAAA	TTTGTACAAG	AGCTCATGGC	4980
	TTGTCTTGGG	CTTCTGTCAT	TAAACCAAAG	GAAATGGAAG	CCATTCCCTG	GTGCTCTCC	5040
	TTAGTCTTGG	TCATCAGAAC	CTCACTTGGT	ACCATATAGA	TCAAAAGCTT	TGTAACCACA	5100
	GGAAAAATA	AATCTTCCA	TCCCTTAAAG	AATAGAATAG	TTTGTCCCTC	TCATGGGAAT	5160
	TGGCTGTAT	CTTCTGTGTT	CTTCTCTCT	AGAATTAGA	GATACAAGAG	TTTACTTAG	5220
80	AACCTTTTCAT	GGACACAATT	TCCACAACCT	TTCAGATGCT	GATGTAGAGC	TATTGGGAAA	5280
	GAATTTCCAA	ACTCAGGAAG	TTTGACAGAG	GCAGACAGCT	AGAGATAACT	CGGAGCCAG	5340
	AGTTGGTCCA	CAGATGTTAG	ATGTATCCTA	GCTTTTAGCC	ATAAACCACT	CAAAGATTCA	5400
	CCCCCAGAT	CCCACAGTCA	GAATGAATC	TGCGTTGTTG	GGAAGCCAGC	AGTGGCCTTG	5460
	GGAGGAGAGC	CATGGCTGTG	GTTCAGAGAG	GGTGGGCTGG	CAAGCCACTT	CCGGGGAAAA	5520
85	CTCCTTCCGC	CCAGGTTTTC	TCTTCTCTT	AAGGAGAGAT	TGTTCTCACC	AACCCGCTGC	5580
	CTTCATGCTG	CCTTCAAGC	TAGATCATGT	TTGCCTTGCT	TAGAGAATTA	CTGCAATCA	5640
	GCCCCAGTGC	TTGGCGATGC	ATTTACAGAT	TTCTAGGCCC	TCAGGGTTT	GTAGAGTGTG	5700
	AGCCCTGGTG	GGCAGGGTTG	GGGGGTCTGT	CTTCTGCTGG	ATGCTGCTTG	TAATCCATT	5760

GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

5
10
15
20

1	11	21	31	41	51	
MPLKHYLLLL	VGCQAWGAGL	AYHGCPSSECT	CSRASQVECT	GARIVAVPTP	LPWNAMSLQI	60
LWTHITELNE	SPFFINISALI	ALRIEKNELS	RITPGAFRNL	GSLRYLSLAN	NKLQVLPIGL	120
FQGLDSLES	LLSSNQLLQI	QPAHFSQCSN	LKELQLHGNH	LEYIPDGAFD	HLVGLTKLNL	180
GKNSLTHISP	RVFQHLGNLQ	VLRLYENRLT	DIPMGTFDGL	VNLQELALQQ	NQIGLLSPGL	240
FHNHNLQRL	YLSNNHISQL	PPSIFMQLPQ	LNRLTLFGNS	LKELSLGIFG	PMPNLRLEWL	300
YDNHISLSPD	NVFSNLRQLQ	VLILSRNQIS	FISPGAFNGL	TELRELSLHT	NALQDLQGNV	360
FRMLANLQNI	SLQNNRLRQL	PGNIPANVNG	LMAIQLNQNO	LENLPLGIFD	HLGKLCLELRL	420
YDNPWRCDS	ILPLRNWLLL	NQPRLGTDV	PVCFSPANVR	GQSLIINNVN	VAVPSVHVPE	480
VPSYPETPWY	PDTSPYPTT	SVSSTELTS	PVEDYDLTT	IQVTDERSVW	GMTQAQSGLA	540
IAAIVIGIVA	LACSLAACVG	CCCKKRSQA	VLMQMKAPNE	C		

Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

25
30
35

1	11	21	31	41	51	
ATGATGCATT	TGCTCAATTC	TCAGGGCTGG	AATGAGCCGG	CTGGTCCCCC	AGAAAGCTGG	60
AGTGGGGTAC	AGAGTTCACT	TTTCCTCTCT	GTTTACAGCT	CCTTGACAGT	CCCAGCCCCA	120
TCGTGAGTGG	GAGCTGGGAG	TCAGTGTGGG	AGAAGAAACA	ACAAAAGCCA	ATTAGAACCA	180
CTATTTTAA	AAAGTGCTTA	CTGTGCACAG	ATACTCTTCA	AGCACTGGAC	GTGATTTCTC	240
TCTCTAGCCC	TCAGCACCCC	TGGCGTAGGA	GTGCCGCCTC	TACCCACTTG	TGATGGGGTA	300
CAGAGGCACT	TGCTCTTCTG	CATGGTGTTC	AATAGGCTGG	GAGTTTATT	TATCTCTTCA	360
AACTTTGTAC	AAGAGCTCAT	GGCTTGTCTT	GGGCTTTCGT	CATTAAACCA	AAGGAAATGG	420
AAGCCATTC	CCTGTTGCTC	TCCTTAG				

Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

40

1	11	21	31	41	51	
MMHLLNSQGW	NEPAGPPESW	SGVQSSVFLS	VYSSLTVPRP	SGVGAGSQCW	RRNKSQLEP	60
LFLKSAYCAQ	ILFKHWTWIL	SLALSTPAVG	VPPLPTCDGV	QRHLLFCMVF	NRLGLVFIS	120
NFVQELMACL	GLSSLNQRKW	KPPFCCSP				

Seq ID NO: 614 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

50
55
60
65
70
75
80
85

1	11	21	31	41	51	
GTCCCGCAG	CGCCGTCGCG	CCCTCCTGCC	GCAGGCCACC	GAGGCCGCCG	CCGTCTAGCG	60
CCCCGACCTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	TCTTGTCGT	120
GAGCGACTCC	AAAGGCAGCA	ATGAAGTCTA	TCAAGTTCCA	TCGAAGCTGT	ACTGTCTAAA	180
TGGAGGAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CACTGGTGCA	ACTGCCCAA	240
GAAATTCGGA	GGGAGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
TCATTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
CTCTGCCACT	GTCCTTCAGC	AAACGTACCA	TGCCCCACAGA	TCTGATGCTC	TTCAGCTGGG	420
CCTGGGGA	CATAATTACT	GCAAGAACCC	AGACAACCCG	AGGCGACCC	GGTGCTATGT	480
GCAAGTGGGC	CTAAGCCGCG	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGA	540
AAAGCCCTCC	TCTCCTCCAG	AAGAATTAAA	ATTTCAGTGT	GGCCAAAGA	CTCTAGGCC	600
CGCTTTAAG	ATTATTGGGG	GAGAATTAC	CACCATCGAG	AACCAGCCCT	GGTTTGCGGC	660
CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	GCCTCATCAG	720
CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAGA	AGGAGGACTA	780
CATCGTCTAC	CTGGGTGCGT	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
GGTGGAA	CTCATCTAC	ACAAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAACGA	900
CATTGCCTTG	CTGAAGATCC	GTTCRAAGGA	GGGCAGGTGT	GCGCAGCCAT	CCCGACTAT	960
ACAGACCATC	TGCCCTGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACAA	GCTGTGAGAT	1020
CACCTGGCTT	GGAAAAGAGA	ATTCTACCGA	CTATCTCTAT	CCGGAGCAGC	TGAAAATGAC	1080
TGTTGTGAAG	CTGATTTCCC	ACCGGGAGTG	TCAGCAGCCC	CACCTACTAG	GCTCTGAAGT	1140
CACCACCAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCTC	GCCAGGGAGA	1200
CTCAGGGGGA	CCCCTGCTCT	GTTCCCTCCA	AGGCCGCATG	ACTTTGACTG	GAATTGTGAG	1260
CTGGGGCCGT	GGATGTGCC	TGAAGGACAA	GCCAGGCGTC	TACACGAGAG	TCTCACACTT	1320
CTTACCCTGG	ATCCGCGATC	ACACCAAGGA	AGAGAATGGC	CTGGCCCTCT	GAGGGTCCCC	1380
AGGGAGGAAA	CGGGCACCAC	CCGCTTTCTT	GCTGGTTGTC	ATTTTTGCAG	TAGAGTCATC	1440
TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCCTGTGG	1500
CACCACCAGG	GTGAACGACA	ATAGCTTTAC	CCTCAGCGAT	AGGCCTGGGT	GCTGGCTGCC	1560
CAGACCCTCT	GGCCAGGATG	GAGGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
TGTCTTTTTC	TGGACTGAGG	CCTGCAGGAG	TTAAAAAGGG	CAGGGCATCT	CCTGTGCATG	1680
GGCTCGAAGG	GAGAGCCAGC	TCCCCCGACC	GGTGGGCATT	TGTGAGGCCC	ATGGTTGAGA	1740
AATGAATAAT	TCCCCAATTA	GGAAGTGTA	GCAAGCTGAGG	TCTCTTGAGG	GAGCTTAGCC	1800
AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	GGGCTCTGAT	1860
ATTCCATGAA	TGTATCAGGA	AAATATATATG	TGTGTGTATG	TTTGCACT	TGTTGTGTGG	1920
GCTGTGAGTG	TAAGTGTGAG	TAGAGCTGG	TGCTGATTG	TTAAGTCTAA	ATATTTCTCT	1980
AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACTC	2040
CTGGGGCCTC	TTGGTCCCC	CAGTGCAGAG	TGCCTGGGAA	TGTACTTATT	CTGCAGCATG	2100
ACCTGTGACC	AGCATGTGCT	CAGTTTCACT	TTACATAGAG	TGTCCTTTC	TTGGCCAGTT	2160
ATCCCTTCCT	TTAGCCTTAG	TTATCCCAAT	CCTCACTGGG	TGGGGTGAGG	ACCACTCCTT	2220
ACACTGAATA	TTTATATTTC	ACTATTTTAA	TTTATATTTT	TGTAATTTTA	AATAAAAGTG	2280
ATCAATAAAA	TGTGATTTT	CTGA				

Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ 60
HCEIDKSKTC YENGNGHYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN 120
YCRNPDNRNR PWCVVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII 180
10    GGEFTTIENQ PWFPAIYRRH RGSVTVYVCG GSLISPCWVI SATHCFIDYP KKEDYIYVLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHENDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFVK ENSTDYLYPE QLKMTVVKLI SHRECQPHY YGSEVTTKML 360
CAADPQWKTD SCQGDSSGGPL VCSLQGRMTL TGIWSWGRGC ALRDKPGVYT RVSHFLPWIR 420
SHTKEENGLA L

```

Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

```

20    1      11      21      31      41      51
|      |      |      |      |      |
CGCCAAAGGA AAAGCCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
CTCTCCGCGC GCCCCACCTC CTCCGCTCTG CGTCTCTCCT GAGCAGCGGG CCCAGACTGC 120
GCTCCGCGCG CGGCCCTCGC CCGCGGAGC CCTCCTACCC CGGCCGACG CTCGCCCGCG 180
25    GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CCGGCTCCTG GAACGGAGCC 240
CTCTGCCGCG TGCTCCTGCT GACCCCTCGC ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC 360
CTGAAGAGT GCTTTACAGC TGCAATCTA ATTCAATCAA GTGATCCTGA CTTCCAAATT 420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCTCTCGA GAAGAGAAGT 480
30    TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
GAGCATCAA CAAGAGTCCT AAAGAAAAGA CATACTAAAG AAAAGTTCT AAGCGCGGCC 600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTGG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCCTTC AACAGGTTC AATCTGACAG GCCCAAAACT ATACCATATA CTATTCCATA 720
AGAGGTCTCG GAGTGGACCA AGAACCTCGG AATTATTTTT ATGTGGAGAG AGACACTGGA 780
35    AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
TTTGCAACAA CTCACAGATG GTATACTCCA GAACCTCCAC TGCCCCCTAAT AATCAAAATA 900
GAGGATGAAA ATGATACTA CCCAATTTTT ACAGAAAGAA CTTATACTTT TACAATTTTT 960
GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
GACACGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACC 1080
40    CTATTTTCTA TGCATCCAAC TACAGCGCTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
GAGTTAAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACTTGCCA 1260
ACATTACTCT GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATC 1320
TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACCTGGG AGCTAATTAT 1380
45    ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAATTTG TAACAGATGC CAAACCAAT 1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
CAAAATTGGTG GAGTCTAATG AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
AGCACAGCAA CAGTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCTT 1620
CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAAGTG GAACAACAAG CAATGGATAT 1680
50    AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTAT 1740
CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAAGTTT CAGAAGCCTG 1800
GATAGAGAGG CAGAGACCAT CAAAAATGCG ATATATAATA TTACAGTCTT TGCATCAGAC 1860
CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
AGCCCATTTA TACCTAAAAA GACAGTGATC ATCTGCAAA CCAACATGTC ATCTGCGGAG 1980
55    ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCAC CTTTGACTT TAGTCTGGAG 2040
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
CGTCTTCTCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 2280
60    AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCA CTGTTTACG 2340
CTGTTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTAGCC 2400
CAGCAGAACCT TAATGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
AATGGCTTCA CAACCCAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520
TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGAGGAG ACACAGACC 2580
65    TCGGAATCCT GCCGGGGGGC TGCCACCAT CACACCTGG ACTCCTGCAG GGGAGGACAC 2640
ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCGGT 2700
CTTGGTGAAG AAGTGATCT GTGTAATCAA GATGAAAATC ACAAGCATGC CCAAGACTAT 2760
GTCCTGACAT ATAATATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820
70    GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880
CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTCTAATA AGTCTCTGAA AGCCAGTGGC 2940
TTTATGACTT TTAATAAAAA TTACAAACCA AGAATTTTTT AAAGCAGAAG ATGCTATTGG 3000
TGCGGGTTTT TCTCTCATT TTTGGATGGA ATCTCTTTGG TCAATGCAC ATTTACAGAG 3060
AGACACTATA AACAAGTACA CAAATTTTTC AATTTTACAA TATTTTAAAT TTACTTATCT 3120
75    TCTATCCAAG GAGGTCTACA GAGAAATTA AGTCTGCCTT ATTTGTACA TTTGGGTATA 3180
ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTA TTCAAGTCTT TATTATAGAC 3240
TATTTGAAGC ACAACCTAAT GGAATAATGT AGAGACCTTG CTTTAACATT ATCTCCAGTT 3300
AATTAAGTGT TCATGTGTGT CTTGGAACCT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
ACTGCATTCT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGAGAG 3420
TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

```

Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

```

85    1      11      21      31      41      51
|      |      |      |      |      |
MEARPSGSW NGALCRLLLL TLAILPASD ACKNVLHVP SKLDAEKLVG RVNLKECFDA 60
ANLIHSSDPD FQILEDGSVY TTNITLLSSE KRSFTILLN TENQKKKIF VFLEHQTKVL 120

```


KKRHTKEKVL RRARRRWAPI PCSMLENSLG PFPLFLQVQV SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLPYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY 240
 PIFTEETYPF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFMSHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPTFTRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNB NGNFKIVTDA KTNBGLVLCVV 420
 KPLNYEERQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREASTI 540
 KNGIYNITVL ASDQGGRTCT GTLGILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFQSYVVPV TVRDLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIQGGGV QLGKMAILAI LLGIALLFPI LFTLVCGASG 720
 TSKQPKVIFD DLAAQNLLVS NTAAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVRGG HQTSSECRGA GHHTLDSCR GHTEVDNCR YTYSEWHSFT QPRLGEKVYL 840
 CNQDENHKA QDYVLTYNYE GRGSVAGSVG CCSERQEDDG LEFLDNLEPK FRTLAEACMK 900
 R

Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

1 11 21 31 41 51
 CGCCAAAGGA AAAGCCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
 CTCTCCGCGC GCCCCACCTC CTCCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
 GCTCCGGGCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGAGC CTCCGCCCGC 180
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTT CCGGCTCCTG GAACGGAGCC 240
 CTCTGCCGCG TGCTCCTGCT GACCCCTCGG ATCTTAATAT TTGCCAGTGA TGCTGCAAA 300
 AATGTGACAT TACATGTTC CTCCAAACTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360
 CTGAAAGAGT GCTTTACAGC TGCAAACTTA ATTCAATCAA GTGATCCTGA CTCCAAAT 420
 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGCTCTCGGA GAAGAGAAGT 480
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTG 540
 GAGCATCAAA CAAAGGTCTT AAAGAAAAGA CATACTAAAG AAAAGATTCT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 CTTTTCCTTC AACAGGTTC AATCTGACAG GCCCAAATCT ATACCATATA CTATTCCATA 720
 AGAGGTCTCT GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
 AACTTGTATT GTACTCGTCC TGATAGTCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA CTCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
 GAGGATGAAA ATGATACTA CCAATTTTTT ACAGAAAGAA CTATACTTTT TACAATTTTT 960
 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACACGATGC ACACACGCTT GAAGTACTCC ATCATTTGGC AGGTGCCACC ATCACCCACC 1080
 CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
 GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAATTTTTT 1200
 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACTTGCCA 1260
 ACATTACTCT GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATC 1320
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACCTGGG AGCTAATTAT 1380
 ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAATTTG TAACAGATGC CAAACCAAT 1440
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
 CAAATTGGTG TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
 AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCTT 1620
 CCAATACAGA CTGTTCCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680
 AAAGCATATG ACCCAGAAAC AGGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTAT 1740
 CCAACAGGCT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAGATTTT CAGAAGCCTG 1800
 GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860
 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAC 1920
 AGCCCATCTA TACCTAAAAA GACAGTGATC ATCTGCAAAC CCACCATGTC ATCTGCGGAG 1980
 ATTGTTGCGG TTGATCTTGA TGAGCCTATC CATGGCCAC CCTTTGACT TAGTCTGGAG 2040
 AGTTCTACTT CAGAAAGTACA GAGAAATGGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
 CGCTTTCTCT ATCAGAAATG TCCTCCATT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
 GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGG 2280
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGG ATAGCATTGC TCTTTTGCAT CCTGTTTACG 2340
 CTGGTCTGTG GGGCTTCTGG GAGCTCTAAA CAACCAAAAG TAATTCCTGA TGAATTAGCC 2400
 CAGCAGAAC TAATTGTATC AAACACAGAA GCTCTCGGAG ATGACAAAGT GTATTCTGCG 2460
 AATGGCTTCA CAACCCAAAC TGTGGGCGCT TGTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520
 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGAGAGG ACACAGACC 2580
 TCGGAATCCT GCCGGGGGGG TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC 2640
 ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCGGT 2700
 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAAAA ATTAACAAT GAAAGAAAGT 2760
 GTATCTGTGT AATCAAGATG AAAATCACAA GCATGCCCAA GACTATGTCC TGACATATAA 2820
 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGTTGT TGCAGTGAAC GACAAGAAGA 2880
 AGATGGGCTT GAATTTTGG ATAATTGGA GCCCAAATTT AGGACACTAG CAGAAGCATG 2940
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
 AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTCTC 3060
 TCATTATTG GATGGAATCT CTTTGGTCAA ATGCACATTT ACAGAGAGAC ACTATAAACA 3120
 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTCTA TCCAAGGAGG 3180
 TCTACAGAGA AATTAAGTC TGCCTTATT GTTACATTG GGTATAATGA CAACGCCAA 3240
 TTTATAGTGC AATAAAATGT AATTAATTC AGTCTTATT ATAGACTATT TGAAGCACAA 3300
 CCTAATGGAA AATGTAGAG ACCTTGCTTT AACATTATCT CAGTTAATT AAGTGTTCAT 3360
 GTGGTGCTTG GAACTGTGT TTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 ATTATTTTAT TCTGTGAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

1 11 21 31 41 51
 MEARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECPFA 60

ANLIHSSDPD FQILEDGSDVY TTNTILLSSE KRSPTILLSN TENQEKKKIF VFLEHQTKVL 120
KKRHTKEKVL RRAKRRNAPI PCSMLENSLG PFPLPLQVQ SDTAQNYTIY YSIRGPGVDQ 180
EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTEPLPLPLI IKIEDENDNY 240
PIFTEETYTF TIFENCVRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
5 TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY 360
VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNBGLCVV 420
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
KENAEVGTTS NGYKAYDPET RSSSGIRYK LTDPGTWVTI DENTGSIKVF RSLDREAETI 540
10 KNGIYNTVL ASDQGGRTCT GTLGIILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600
EPIHGPPDFP GLEASSTSEVQ RMWRLKAIND TAARLSYQND PPFSGYVVP I TVRDLRGMS 660
VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWLAI LLIALLFCI LFTLVCGASG 720
TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
QETIEMVKGK HQTSESCRGH GHHTLDSCR GGHTVDNCR YTYSEHNSFT QPRLGEESIR 840
GHTLIKN

Seq ID NO: 620 DNA sequence

Nucleic Acid Accession #: NM_032545.1

Coding sequence: 46..718

1 11 21 31 41 51
AAACTGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60
CCATGTCAAG CTCTCTGTTA CGGTCAAGTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
25 CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
CGAGGGCTGG GGGCGGAGG AGCCGCTCCC TACTCTCCGG GCTTTCGGAG AGGGTGCGTC 300
CGCGCGGCGG CGCTGTCTGA GGAACGCGCG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360
CCCGGCCAC TTACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
CCTGGAGCAC GGAGCCTGGA CCTCCGCGC CTGCCACCTC TGCAGTGCA TCTTCGGGCG 480
30 CCTGCACTGC CTCCCTCTCC AGACGCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCTC 540
CCAGCTCAC GGGCGGAGG CGGGGGGCGC GCCCAGCTG CTACTCTTG TGCCCTGCGC 600
ACTCCTGCAC CGCCTCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC 660
CGTCTCTCAG CGGGAGCGCG GCCCTGCGG AAGCCCGGGA CTGGGCGATC GCCTTTAATT 720
TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780
35 TTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

Seq ID NO: 621 Protein sequence

Protein Accession #: NP_115934.1

1 11 21 31 41 51
MTWRHHVRLI FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHFE 60
45 VTGSAEGWGP EEPPLYSRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR 120
SECGALHEGA WTRACHLCR CTFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPGRPLGL HRL

Seq ID NO: 622 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..390

1 11 21 31 41 51
ATGAGGTTC A GTGTCTCAG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60
55 TATGTGTGAG TCTGTCTCCT CTTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120
GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTTGGAG 180
CAGTGTCTTT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCGCCCAATG TGGTCCCCC 240
TGCACCTTCT GGCCTCTGCT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
60 TTTGTTGTGA AGCTGAAGGT TCAGGGTGTG AATCCCAGT GCCACTCATC TCCCATCTCC 360
AGTAAATGTG AAGAGGCGG GATATGTTAG

Seq ID NO: 623 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
MRFSVSGMRT DYPRSVLAPA YVSVCLLLL PREVIAPAGS EPWLCQAPAP CGDKIYNPLE 60
70 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120
SKCERGRIC

Seq ID NO: 624 DNA sequence

Nucleic Acid Accession #: M18728.1

Coding sequence: 51..1085

1 11 21 31 41 51
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
75 CCTCAGCCCC TCCTCTGAGA TTGCATGTCC CCTGGAAGGA GGTCCGTGCTC ACAGCCTCAC 120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
80 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCAAA CCTGCCCCAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCGGAGC 480
85 TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGTA AATGGTCAGA 600
GCCTCCCGGT CAGTCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTC ACTCTACTCA 660

	GGGTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
	ACCGCAGTGA	CCCGATCACC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCT	780
	CCTCAAAAGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
5	ACCCACCTGC	ACGACTACTCT	TGGTTTATCA	ATGGGAAGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
	TCCTCTCAGC	TGTGGCCACC	GTGGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTAAT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCTT	1140
	GAATTCTTCT	AGCTCTCTCA	ATCCCATTCT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
10	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCCTCAGGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAAC TAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACTATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTGTCTCT	TGCTTATGCC	1440
	TGCCCTCTTC	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
15	GGGTAACCTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TGACTGACAT	TAGCAGCATC	TTTAACACAG	CCGTGTGTTC	1620
	AAATGTACAG	TGGTCTCTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
20	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATGG	CTCACTCAT	1860
	CTGACTCATT	CTTTATCTTA	TTTGTATGG	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
25	ATAAAGGCC	CAATGGTGG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TGGTCAACAC	2160
	TCTCACCTAG	GTGAGCGCAT	TGAGCCAGTG	GTGCTAAATG	CTACATACTC	CAACTGAAAT	2220
	GTTAAGGAAG	AAGATAGATC	CAATTAAAAA	AAATTAAAAA	CAATTAAAAA	AAAAAAGAGA	2280
	ACACAGGAGA	TTCCAGTCTA	CTTGAGTTAG	CATAATACAG	AAGTCCCTCT	TACTTTAACT	2340
	TTTACAAAAA	AGTAACCTGA	ACTAATCTGA	TGTTAAACCA	TGTATTATT	TCTGTGGTTC	2400
30	TGTTTCTCTG	TTCCAAATTG	ACAAAACCCA	CTGTTCTTGT	ATTGTATTGC	CCAGGGGAG	2460
	CTATCACTGT	ACTGTAGAG	TGGTGCTGCT	TTAATTCTATA	AATCACAAT	AAAAGCCAA	2520
	TAGCTCTATA	ACT					

Seq ID NO: 625 Protein sequence
Protein Accession #: AAA59907.1

	1	11	21	31	41	51	
40	MGPPSPAPPCR	LHVPWKEVLL	TASLLTFWNP	PTTAKLTIES	TPFNVAEGKE	VLLLAHNLPO	60
	NRIGYSWYKG	ERVDGNSLIV	GYVIGTQOAT	PGPAYSGRET	IYPNASLLIQ	NVTQNDTGFI	120
	TLQVTKSGLV	NEEATQGFHV	YFELPKPSIS	SNNSNPVEDK	DAVAFTCEPE	VQNTTYLWWV	180
	NGQSLPVSPR	LQLSNGNMTL	TLLSVKRND	GSYECEIQNP	ASANRSDPVT	LNVLYGPDVP	240
	TISPSKANYR	PGENLNLSC	AASNPPAQYS	WFINGTFQQS	TQELFIPNIT	VNNSGSYMCQ	300
45	AHNSATGLNR	TTVTMITVSG	SAPVLSAVAT	VGITIGVLAR	VALI		

Seq ID NO: 626 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

	1	11	21	31	41	51	
50	GGAGCTCAAG	CTCCTCTACA	AAGAGGTGGA	CAGAGAAGAC	AGCAGAGACC	ATGGGACCCC	60
	CCTCAGCCCC	TCCTCTGAGA	TGCAATGTCC	CCTGGAAGGA	GGTCTGTCTC	ACAGCCTCAC	120
	TTCTAACCTT	CTGGAACCCA	CCCACCACTG	CCAAGCTCAC	TATTGAATCC	ACGCCATTCA	180
55	ATGTCGACAG	GGGGAAGGAG	GTTCTTCTAC	TGCCCCACAA	CCTGCCCCAG	AATCGTATTG	240
	GTTACAGCTG	GTACAAAGGC	GAAAGAGTGG	ATGGCAACAG	TCTAATTGTA	GGATATGTAA	300
	TAGGAATCTA	ACAAGCTACC	CCAGGGCCCG	CATACAGTGG	TGAGAGACAC	ATATACCCCA	360
	ATGCATCCCT	GCTGATCCAG	AACGTACACC	AGAATGACAC	AGGATTCTAT	ACCCTACAAG	420
60	TCATAAAGTC	AGATCTTGTC	AATGAAGAAG	CAACCGGACA	GTTCCATGTA	TACCCGGAGC	480
	TGCCCAAGCC	CTCCATCTCC	AGCAACAAC	CCAACCCCGT	GGAGGACAAG	GATGCTGTGG	540
	CCTTCACTCG	TGAACCTGAG	GTTCAAGACA	CAACCTACCT	GTGGTGGGTA	AATGGTCAGA	600
	GCCTCCCGGT	CAGTCCCAGG	CTGCAGCTGT	CCAATGGCAA	CATGACCCCT	ACTTACTCTA	660
	GGCTCAAAAG	GAACGATGCA	GGATCCTATG	AATGTGAAAT	ACAGAACCCA	GCGAGTGCCA	720
65	ACCGCAGTGA	CCGAGTCAAC	CTGAATGTCC	TCTATGGCCC	AGATGTCCCC	ACCATTTCCT	780
	CCTCAAAGGC	CAATTACCGT	CCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	840
	ACCCACCTGC	ACAGTACTCT	TGGTTTATCA	ATGGGAGGTT	CCAGCAATCC	ACACAAGAGC	900
	TCTTTATCCC	CAACATCACT	GTGAATAATA	GCGGATCCTA	TATGTGCCAA	GCCCATAACT	960
	CAGCCACTGG	CCTCAATAGG	ACCACAGTCA	CGATGATCAC	AGTCTCTGGA	AGTGCTCCTG	1020
70	TCCTCTCAGC	TGTGGCCACC	GTGGGCATCA	CGATTGGAGT	GCTGGCCAGG	GTGGCTCTGA	1080
	TATAGCAGCC	CTGGTGTAAT	TTCGATATTT	CAGGAAGACT	GGCAGATTGG	ACCAGACCTT	1140
	GAATTCTTCT	AGCTCTCTCA	ATCCCATTCT	ATCCCATGGA	ACCACTAAAA	ACAAGGTCTG	1200
	CTCTGCTCCT	GAAGCCCTAT	ATGCTGGAGA	TGGACAATC	AATGAAAATT	TAAAGGGAAA	1260
	ACCCCTCAGC	CTGAGGTGTG	TGCCACTCAG	AGACTTCACC	TAAC TAGAGA	CAGTCAAACT	1320
	GCAAACCATG	GTGAGAAATT	GACGACTTCA	CACTATGGAC	AGCTTTTCCC	AAGATGTCAA	1380
75	AACAAGACTC	CTCATCATGA	TAAGGCTCTT	ACCCCTTTT	AATTGTCTCT	TGCTTATGCC	1440
	TGCCCTCTTC	GCTTGGCAGG	ATGATGCTGT	CATTAGTATT	TCACAAGAAG	TAGCTTCAGA	1500
	GGGTAACCTA	ACAGAGTGTC	AGATCTATCT	TGTCAATCCC	AACGTTTAC	ATAAAATAAG	1560
	AGATCCTTTA	GTGCACCCAG	TAGCTGACAT	TGACAGCATC	TTTAACACAG	CCGTGTGTTC	1620
80	AAATGTACAG	TGGTCTCTTT	CAGAGTTGGA	CTTCTAGACT	CACCTGTTCT	CACTCCCTGT	1680
	TTTAATTCAA	CCAGCCATG	CAATGCCAAA	TAATAGAATT	GCTCCCTACC	AGCTGAACAG	1740
	GGAGGAGTCT	GTGCAGTTTC	TGACACTTGT	TGTTGAACAT	GGCTAAATAC	AATGGGTATC	1800
	GCTGAGACTA	AGTTGTAGAA	ATTAACAAAT	GTGCTGCTTG	GTTAAATGG	CTCACTCAT	1860
	CTGACTCATT	CTTTATCTTA	TTTGTATGG	TTTGTATCTT	GCCTAAGGTG	CGTAGTCCAA	1920
85	CTCTTGGTAT	TACCTCTCTA	ATAGTCATAC	TAGTAGTCAT	ACTCCCTGGT	GTAGTGTATT	1980
	CTCTAAAAGC	TTTAAATGTC	TGCATGCAGC	CAGCCATCAA	ATAGTGAATG	GTCTCTCTTT	2040
	GGCTGGAATT	ACAAAACCTA	GAGAAATGTG	TCATCAGGAG	AACATCATAA	CCCATGAAGG	2100
	ATAAAGGCC	CAATGGTGG	TAAGTGATAA	TAGCACTAAT	GCTTTAAGAT	TGGTCAACAC	2160

TCTCACCCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTA AAC CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAAACCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGTCTGT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

Seq ID NO: 628 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTCGCGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAATCTA ACAAGCTACC CCAGGGCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GGTGATCCAG AACGTACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCAGG GTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCACTGA CCGATCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTCTG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGTCTCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCCGATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGATT TTGATATT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
 GAATCTTCT AGCTCTCTCA ATCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAATC AATGAAATTT TAAAGGGAAA 1260
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACATAGAGA CAGTCAAAT 1320
 GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGATC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCTT TGCTTATGCC 1440
 TGCTCTTTT GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAATAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620
 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTAGACT CACCTGTCTT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATGAATTT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800
 CGTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCAT CTCTTATCTA TTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGPAT TACCCTCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGAGCC CAAATGGTGG TAAGTATGTA TAGCACTAAT GCTTTAAGAT TGGTTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTA AAC CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAAACCA CTGTTCTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGTCTGT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
 Nucleic Acid Accession #: NM_016639.1
 Coding sequence: 40..429

1 11 21 31 41 51
 GCGGCGGGG CAGACAGCGG CGGGCGCAGG ACGTGCATA TGGCTCGGG CTCGCTGCGC 60
 CGGTGCTGC GGTCTCTGTG GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG 120
 GAGCAAGCGC CAGGCACCGC CCCCTGCTCC CGCGGAGCT CCTGGAGCGC GGAACCTGGAC 180
 AAGTGCATGG ACTGCGGCTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CTGGGGCTGC 240
 GCTGCAGCAC CTCTGCCCC CTTCGGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
 CTGACCTTCG TGCTGGGGCT GCTTCTGGC TTTTGGTCT GGAGACGATG CCGCAGGAGA 360
 GAGAAGTTC CACCCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGCGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCG GGGCTCGCCC ACTCATCATT CATTTCATCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGAGCG GGGGGAGGCC AAGCTCCTCC AACCACAAGG 540
 GGGGTGGGGG GGGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTCG ACAGGGGAGG GGGGTGCCCT 720
 CCTTCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACTCAGAT GTCTGAAAT TCACCAACGG GGGTCAACCT GGGGGGTTAG GGACCTATT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCTACTC 900
 CCAAGAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
 AATAAAAGAA TCTTTAACTT TAAAAAATAA AAAAAAAA

Seq ID NO: 631 Protein sequence
 Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLLWP ILGGALS LTF VLGLLSGLFLV WRRCRRRREKF TPIEETGGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAAATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTCG TGTTGCTTGG CCTGGTGGGC CCAGTCTCTG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATACTC CTTGGAGATT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCACCT GGAAAGGAAC AAAGACCTTT TGCTGAAGA TTTTGTGGTT 360
 TATACCTTCA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTTG 420
 CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTCATCCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCAT TTGAGCACAT CATTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720
 GAGCTGTTCA TTGTGCTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAA AGATGATTCT CCTGGCAAACT TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTCGAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGGTGTCT GTGATGTGCT GGGGAACCTC GTGCAGTGGC GGGAAAAGTT TCTTATCACA 960
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAGAAAG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTGG TGGGAACAGT GTGTTCAAGG AGCCACGCGAG GCGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCAGC ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTAGCAGT TGCAGTGCAG AGGACTTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAAACTG CTTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCCTGTG GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTGG TACTCCTAAG 1380
 GAATGTGAAT TGACACCTTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTTG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCGGA 1500
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTCAGAA TGATATCCT TGCCAGATA ACAGGCTTA TTGCTACAA 1620
 GGATGTGCC AGTATTATGA TGCTCAATGT CAAGTCACTT TTGGCTCAA AGCCAAAGGCT 1680
 GCGGCAAGG ATTGTTTCAT TGAAGTGAAT TCTAAGGTG ACAGATTGG CAATTGTGGT 1740
 TTCTCTGGCA ATGAATACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAAAG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAACGCT 1860
 AGTCGAGGCA CCAATGTGTT GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGGTTA ACCAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCCAGTGT 1980
 GTAGATGCTT CTGTTCTGAA TTATGACTGT GATGTTTCTA AAAAGTGTCA TGGACATGGG 2040
 GTATGTAAAT GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATTGTGAG 2100
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAT GAATACTGCA 2160
 TTGAGGGAGC GACTTCTGGT CTCTCTTCTC CTAATTGTTC CCTTATTGT CTGTGCTATT 2220
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCAGAA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTCTCT 2340
 CGACATGTTT CTCCAGTGAC ACCTCCCGAG GAAAGTCTCA TATATGCAAA CAGATTGCA 2400
 GTACCAACCT ATGCAAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACAA 2460
 CCGAAAGTAT CATCTCAGGG AAACCTTAAT CCTGCCCGTC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTTCCC TCACTTGATT TTTTAAACCT TCTTTTGTCA AATGCTTCTA GGGAACTGAG 2580
 CTAATACTTT TTTTCTTCT TGATGTTTTC TGAAAAGCC TTTCTGTTGC AACTATGAAT 2640
 GAAACAAAA CACCACAAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760
 CATCATTGAA TAAGTCTTAT TCAGTTCATG GTGAGGTTAA TGCACTAATC ATGGATTTT 2820
 TGAACATGTT ATTGCAGTGA TTCTCAAATT AACTGTATTG GTGTAAGATT TTTGTCTATT 2880
 AGTGTTTAAG TGTATTCTG AATTTCTTAC CTTAGTTATC ATTAATGTAG TTCCTCATTT 2940
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGACGAAAT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATA AGATGTCATA 3120
 TTTATTTGAA AGTACAAAAA ATACTAAAAA AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180
 TCCATTTTAT TGACCTTTCA ACTATAGGTA ATAACCTCTA GAGAAATTAA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATTATAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAATAT GTTGATTCTAT 3360
 GGCATAATAA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAAAT TCATGAGCAC TTTAAAAATC GAACCTTCAA AGCTTGCTAT TAAATCATTT 3480
 AGAATGTTTA CATTACTATA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAAT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTAAATACC TACAAAAAAG 3600
 TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTAA AAATGAATTT TTACTATGGC 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
AAAGTTTAAT AATAGGTTTA TTAACCTGAAT TTCATTAGTT TTTTAAAGT GTTTTGGTT 3780
TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
AAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
Protein Accession #: NP_003807.1

1 11 21 31 41 51
| | | | |
MGSGARFPSP TLRVRWLLLL GLVGPVLGAA RPFQQTSHL SSYEIITPWR LTRERREAPR 60
PYSKQVSVVI QAEGKEHIIH LERNKDLLPE DFVVTYNKE GTLITDHPNI QNHCHYRGYV 120
EGVHNSIAL SDCFLRLGLL HLENASYGIE PLQSSSFEH IIRMDVYK EPLKCGVSNK 180
DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELFIVV DKERYDMMGR NQTAVREEMI 240
LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELQ HNLGMNHDDG 360
RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGKN CLNIPKPDE AYSAPSCGNK 420
LVDAGEECDC GTPKECELD P CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLRGKTSEC 480
DVPEYCNSSS QFCQPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCP 540
IEVNSKGRDF GNCGPGSNEY KKCATGNALC GKLCENVQE IPVFGIVPAI IQTPSRGTKC 600
WGVDFQLGSD VPDPGMVNEG TKCGAGKICR NFQCVDAVSL NYDCDVQKKC HGHGVCNSNK 660
NCHCENGWAP PNCETKYGGS SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TPPREVPIYA NRFAPVTYAA 780
KQPQFPSPRP PFPQPKVSSQ GNLIPARPAP APPLYSST

Seq ID NO: 634 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

1 11 21 31 41 51
| | | | |
AGTCTCTGCT CTTCCAGACC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
CGGCAGTGAG CTCCCGCTGG TCTGCTGGC GCTGGTCTCT TGCCTAGCGC CCCGGGGGCG 120
AGCGGTCCCG CTGCTGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTC 240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCACCCAA 360
GGCCTTGGCG AATCAGCAGC CTTCTGGGGA TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
AGGTTCAAAA GGCAGATTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
CCCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
CTTCTGTTT AAATCTGTTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
TTTTTATATC TAGGCTACTT GTTGTTAGA TTCAAGGCCC CGAGCTGTTA CCATTACAAA 780
TAAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
Protein Accession #: NP_002082.1

1 11 21 31 41 51
| | | | |
MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTKMYPR GNVHVAVGHM GKKTGESS 60
VSEKGLKQK LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQQPS WDSSEDSNFK 120
DVSGSKGVGR LSAPGSQREG RNPQLNQ

Seq ID NO: 636 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

1 11 21 31 41 51
| | | | |
GCGGAAGCAG CGAGAGGGGA GCCCCTTTG GCGCTCTCC GTGGAACCGG TTTTCCGAGG 60
CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
TTTTCTCCTC CCCGCGCCTC CCGGTCGCG CCGGTTTACC GCTCAGTCCC CGCGCTCGCT 180
CCGACCCCA CCCACTTCCT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
TCGGGGAAGT TGTGGCTGTC GAGAAATGGG GTCTGTGGGT ACCTGTTCCT GCCCTGGAAG 300
TGCCCTCGTG TCGTGCTCT CAGGCTGCTG TTCCTTGATC CCACAGGAGT GCCCGTGCGC 360
AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CCGTCCGCGA GGGGAGAGC 420
GCCACCTCA GGTCACTAT TGACAACCGG GTCAACCGGG TGGCCTGGCT AAACCGCAGC 480
ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCCCTGGATC CTCGCTGGT CTTCTGAGC 540
AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
TACACCTGCT CGGTGCAGAC AGACAACCA CCAAGACCT CTAGGGTCCA CCTCATTTGT 660
CAAGTATCTC CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAATGA AGGGAACAA 720
ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTTACTTG GAGACACATC 780
TCTCCAAAG CGGTGTGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
CGGGAACAGT CAGGGGACTA CAGTGCACT GCCTCCAATG ACCTGGCCGC GCCCGTGGTA 900
CGGAGAGTAA AGGTACCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGT 960
GTCCCGGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
TTCCAGTGGT ACAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGA 1080
AACAGACCTT TCCTCTCAA ACTCATCTC TTCATGTCT CTGAACATGA CTATGGGAAC 1140
TACACTTGG TGGCCTCAA CAAGCTGGG CACACCAATG CCAGCATCAT GCTATTTGGT 1200
CCAGGCGCGT TCAGCAAGGT GACCAACGG ACCTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
CTGCCCTCTC TGGTCTTGCA CCGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCCCCACC 1320
CGGGAAGGCG TGCCGCCACC ACCACCAACA ACACAACAGC AATGGCAACA CCGCAGCAA 1380
CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
GGGAGGGGAA CAAAGATAC TTTGGGGGGA AAAGAGTTT AAAAAAGAAA TTGAAAATTG 1500
CCTTGACAGT ATTTAGGTAC AATGGAGTTT TCTTTTCCA AACGGGAAGA ACACAGCACA 1560

CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTCAATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG CGTGGCGCTG CSASNDVAAP VVRRVKVTN YPPYISEAKG TGVFVGQKGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAATA AAAAAAATA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 MGVCVGLFLP WKCLVUVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTRVAVLN RSTILYAGND KWCLDPRVVL LSNTQTOYSI EIQNVDVYDE GPYTCVQTD 120
 NHPKTSVRHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISP KAVGFV 180
 SDEYLEIQG ITRQSGDYB CSASNDVAAP VVRRVKVTN YPPYISEAKG TGVFVGQKGT 240
 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VERNPFLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGGAVSEVS NGTSRRAGCV WLLPLLVHL LLLK

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 GATTGTCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAAATACG CGCTCCCTCC CTCCCTCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTGCG GGCAGTCGCA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300
 GGAAATCTCT TCAGGCTTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TGCGGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATGTGTACCTT ATGATGTGTG 420
 GGCCAGCAAC TACGTAGATC TGATCAGAGA ACAGGCCGAT ATCGCATTGA CCGGGGAGC 480
 TGAGGTGAAG GGGCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
 GCGGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA GTCAGTGTCT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
 CACCCCGCTG GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGAGC AAGCTGAGCA CATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAAGAAAC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTGCTCATCA TGGTAACACT 960
 CGCGATTTAC CAGTCCACC ACAAAATGAC TGCCAAACCAG GTCAGATCC CTCGGGACAG 1020
 ATCCCACTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAGCA CTTTTCATC TTGTACACGA GATACACCAA 1140
 CATAGTACA ATCAAAAGG CTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
 TTGAAACAT GCTTCTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGTCT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAC 1500
 TCATGCTCCC TGACGCAAGA CCCCAGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAATAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRG HSQSELQVFW VDRAYALKML 120
 FVKESHNMMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKRMG

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCCTTCGGG CTCCTTGTGC 120
 GCGCTGCTCG CGCTGCTGCT CCGCTGAGC CCGCGGGGCG CCCTCGCCAG CGCTGGTCTC 180
 GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC GCGTTACGCT GAGAGTAAAC 240
 CCAAAACGTA TTGGTAAACT GCAGGTGTTT CCGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCCTGAAGAA GGTGTGCTGG ACCCGGAAGC CCCTTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGACAGT GGAACAAGA AAACTGAGT AACAAAAAAG 420
 ACCATGCATC ATAAATTTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAAT AAGAAGGAAG GGTGTGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAGGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCTTTTGG 660
 CAATTGACCA TATTGTGAGC AAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG 780
 ATTCGTATG GAAATAATGT TTTATTAGTG TGCTGTGAG GGAGGTATCC TGTGTGTTCT 840
 ACTCACTCT CTCATAAAAT AGGAAATATT TAGTTCTGT TTTCTTGGG AATATGTTAC 900

TCTTTACCCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCAACCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
 CATGATTAC TCATTAACT TTGATTTGT ATGCTATTTT TTCACTATAG GATGACTATA 1140
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATCC 1200
 TGATTGCTAA TTTACATAGA AATGTATTCT CTGGTTTT TAAATAAAAG CAAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCCT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCA AAAAAA AAAAAA

Seq ID NO: 641 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLPSSRAAR VPGPSGLCA LLALLLLLP PGPLASAGPV SAVLTELRCR CLRVTLRVNP 60
 KTIGKLQVP AGPQCSKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKQN

Seq ID NO: 642 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

1 11 21 31 41 51
 TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCTTTTGT GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC 120
 TCTGCGCGCG GCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
 AGACTGGGCG TCCTCGCGCG TTCCGGCGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
 TGCAGGAGCT GCGCGCGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCA GAGCGGGCGC 300
 GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGCGCGCGGT CCTGGCGCAG CTGCTGCGCG 360
 TCTGGGGGCG CCCCCGCAAC TCTGATCCGG CTCTGGGCTT GGACGACGAC CCGACGCGC 420
 CTGAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCGCGCGCCG GTCCCGCGCG CGCGCTCCG ACCCGGGCCC CCGGTCTACG 540
 ACGACGGCCC CGCGGGCGCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC CGCGCGCTC CGCGGTGCCG CCGACACGGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCCT AGAGACCCCG GCGCCCCAGG 780
 TGCTTGACG CCGCTCTTGT CCACCTTGAG CACTGCGCGG ATCCGTGCA CCCTGGGACC 840
 CAGAAGTGCC CCGCGCATCC CGCCACGAG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence
 Protein Accession #: NP_037403.1

1 11 21 31 41 51
 MAGSPLLWGP RAGVGLLVL LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLEAERQER ARAEAQEAED QQARVLAQLL RVWGAAPRNSD 120
 PALGLDDDDP APAQLARAL LRRLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAFGDA 180
 EAGDETFDPV DPELLRYLLG RILAGSADSE GVAAPRRRLR AADHDVGSSEL PPEGVLGALL 240
 RVKRLTEPAP QVPARRLLPP

Seq ID NO: 644 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

1 11 21 31 41 51
 CCCAGAGCCG CTCCCCCTG TTGCTGGCAT CCCAGCTTC CTCCCTTGCC AGCCAGGACG 60
 CTGCGGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGGCCTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
 TCCCTCGAC CTGCGCGGCG TACCCTCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTAATGACGA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCCGC GCCGGGCCCT 420
 TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CGGCGGTGCC GAGCCGGGAG 480
 GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCCGCG GGGTCGCGCT GCTAGGCTCG CGGAAACGCT CCTAGCGACA CTCGCCCGCG 600
 GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC 660
 GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTATTACC GCTGCATTG 720
 TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCTT CTGGGCGAGC TGGGTGTTT 780
 CACTTGTCTT TGCACTGGGC CRAAGTGAAG ACAATAGATG TGCACTCTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCTTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTICA 900
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTGTTAT AATACCCACT GAAATGAATA 1020
 TTAATACCCA GGTACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCGTGACT TTCGCTTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTCGATGCCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
 AAGGAGGTTT TGACGCCATG CTTGAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

5
10
15
20
25
30
35
40

```

GCAAAATGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
ACAAACAACAT TAATGTGATC TTGTCAGTTC AAGGAAAAACA ATTTTCATTG TATAAGGATC 1740
TTCTACCCCT CTGGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
ATAAATTTGGT AGTGGAAAGCC TATCAGAAGC TCATTTTCTAGA AGTGAAAGTT CAGGTGGAAA 1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAAACAG 1980
TTACAATGAA AAAATGTGAT GTACACAGGAG GAAAAAACTA TGCAATTAATC AAACCTATTG 2040
GTTTAAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTTC AGATTCCAAG TGTTTCCAGT 2160
GTGATGAGAA TAAATGTGAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
ACAAGGATCA GCCGTGTTGC AGTGGTCSAG GAGTTTGTGT TGTGGGAAA TGTTCATGTC 2280
ACAAAATTAA GCTTGGAAAA GTGATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
CATATCACC A TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
TCAATTCAA GGGCCAAAGT TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACAACA GCATTATGTC GACCAAACTT 2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAAATATTTT CATCATTTTC ATAGTTACAT 2760
TCTTGATTGG GTTGCTTAAA GTCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
ATAAAATTAA GTCTCATCA GATTACAGAG TGTGAGCTCT AAAAAAGGAT AAGTTGATT 2880
TGCAAAAGTG TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
TGGATATCAG CAATTAATGT GCTCATGAAA CTTTCAGTGT CCACTCTCAA AAAAAGATT 3000
TTAAACACTT AATGGGAAAC TGAATTGTT AATAATTGCT CCTAAAGATT ATAAATTTAA 3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC 3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAAATGTGT TTACTACTGT TTGAGACTAG TGTGTTGTA GCACCTTACT GTAATATATA 3240
ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTTAT CCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
CACTACAAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG 3420
TATATTCTAA GGTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTGCTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
AAAGATTATT GCTTTTAAA GTGTGTAGTT TTATGATGT GTGTTTATGG TTTGCTTATT 3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660
TTTTTACAGG ATAAATTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
GAATGTTAA

```

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

45
50
55

```

1 11 21 31 41 51
MCGSALAPFT AAFVCLQND RGPASFLWAA WVFSLVLGLG QGEDNRCASS NAASCARCLA 60
LGPECGWCVQ EDFISGSSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
GEVSIQLRPG AEAANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLRKMMAFF 180
SRDFRLGPGS YVDKTVSPYI SHPERIHNO CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK MNVYVKSSTM EHPSLGQLSE KLIDNNINVI FAVQGGQFHW YKDLLPLLP 360
TIAGEIESKA ANLNLNVEEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMEGCR 420
NVTNSDEVLF NVTVMKCD VTGGKNYAI KPIGFNSTAK IHIHRNCSCQ CEDNRGPKGK 480
CVDETFLDSK CFQCDENKCH FDEDFSSSES CKSHKQDQVC SGRGVVCVCK CSCHKIKLKG 540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCPSGWE GDRQCPSAAA QHCVNSKGQV 600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL S QAILDQCKTS 660
CALMEQQHYV DQTSCEPSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNLIKSSS 720
DYRVSASKID KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRCNF

```

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

65
70
75
80
85

```

1 11 21 31 41 51
ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAAATG ATTCCATAAT GAACAAAGTG 60
AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA 120
ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC 180
AACCACAGAG ACTGGTTGAG TTTGTTGCTC AAACCTAGAGA AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAAAT GATTGGTCTG TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAAATGA GAGTTTGTCT AGAATTCAAG TGAGATTTCG TGAATTAAAA 360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACCTGCAAG 420
AAATTTGCTT TTGTTTATAT ATCTTTTGCA CAATTGAAC TGTCACAAGG TAATGTCAAA 480
AAAAGTAAAC AACTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG 540
GAAATTGCCC TGGCGAATTT AAGCTCCCAA AAAAGCAGC TGCTTTTCAA GGAGGAAAAAG 600
AAGAATTAT CAGCATCTAC GGTATTAACT GCCCAAGAAT CATTTCCGG TCACTTGGG 660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720
TTATATGGAG AGAATCATGC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780
CAAACCTAAC AACTAAACA GTCATGCCA TTTGGAAGAG TCCCAAGTAA CCTTCTAAAT 840
AGCCAGATG GTGATGTGAA GACAGATGAT TCAGTTGTAC CTGTTTATAT GAAAAGACAA 900
ACCTCTAGAT CAGAAATGCC AGATTGTTG GTGCTTGGAT CTAACCAAG TGGAAATGAT 960
TCTCTGTAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG 1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCTGAA GAATAAAACG 1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTTCA 1140
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGATTAA CCAGAAATCCT 1200
GCTGATCTTT CAATCATCTG GCAGATTCGG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260
AAACATACCA CTTTGGAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320
ACATCTAAAT GGTTTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGAT 1380

```

5 GATTACATGA GCTGTTTTAG AACTCCAGTT GTAAAGAATG ACTTTCCACC TGCTTGTCTAG 1440
 TTGTCAACAC CTTATGGCCA ACCTGCCTGT TTCCAGCAGC AACAGCATCA AATACTTGCC 1500
 ACTCCACTTC AAAATTTTACA GGTTTTAGCA TCTTCTTCAG CAATGAATG CATTTGGGTT 1560
 AAAGGAAGAA TTTATTCAT TTTAAAGCAG ATAGGAAGTG GAGGTTCAAG CAAGGTATTT 1620
 CAGGTGTTAA ATGAAAAGAA ACAGATATAT GCTATAAAAT ATGTGAACCT AGAAGAAGCA 1680
 GATAACCAA CTCTTGATAG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA 1740
 CACAGTGATA AGATCATCCG ACTTTATGAT TATGAAATCA CGGACCAGTA CATCTACATG 1800
 GTAATGGAGT GTGGAAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT 1860
 10 CCATGGGAAC GCAAGAGTTA CTGGA AAAAT ATGTTAGAGG CAGTTCACAC AATCCATCAA 1920
 CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAAATGCTA 1980
 AAGCTAATTTG ATTTTGGGAT TGC AAAACCA ATGCAACCAAG ATACAACAAG TGTGTGTTAA 2040
 GATTCTCAGG TTGGCAGCT TAATTATATG CCACCAAGAG CAATCAAGA TATGTCTTCC 2100
 TCCAGAGAGA ATGGGAATC TAAGTCAAAG ATAAGCCCCA AAAGTGATGT TTGGTCTCTA 2160
 GGATGTATTT TGTAATATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAAATCAG 2220
 15 ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTC CGATATTCCA 2280
 GAGAAAGATC TTCAGATGT GTTAAAGTGT TGTTTAAAAA GGGACCCAAA ACAGAGGATA 2340
 TCCATTCCTG AGCTCCTGGC TCATCCCTAT GTTCAAATTC AAACCTCATCC AGTTAAACCA 2400
 ATGGCCCAAGG GAACCACTGA AGAAATGAAA TATGTTCTGG GCCAACTTGT TGGTCTGAAT 2460
 20 TCTCTAACT CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA 2520
 AGTCATAATT CTTTCATCTC CAAGACTTTT GAAAAAAA GGGGAAAAA ATGA

Seq ID NO: 647 Protein sequence
 Protein Accession #: NP_003309.1

25 1 11 21 31 41 51
 MESEDLSGRE LTIDSIMNKV RDIKNKFKNE DLTDELSLNK ISADTTDMSG TVNQIMMMAN 60
 NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAI EALPP DKYQGNESFA RIQVRFAELK 120
 30 AIQEPDDARD YFQMARANCK KPAFVHISPA QFELSQGNVK KSKQLLQKAV ERGAVPLEML 180
 ETALRNLLWQ KKQLLSSEEEK KNLASSTVLT AQESFSGSLG HLNRRNNSCD SRGQTTKARF 240
 LYGENMPQD AEIGYRNSLR QTNKTKQSCP FGRVPVNLN SPDCDVKTDD SVVPCFMKRO 300
 TSRSECDRLV VPGSKPSGND SCELRLNLSKV QNSHFKEPLV SDEKSELII TDSITLKNKT 360
 ESSLLAKLEE TKBYQEPFEPV ESNQKQWQSK RKSECINQNP AASSNHWQIP ELARKVNTAQ 420
 KHTTFEQPVF SVSKQSPPI SSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPFACQ 480
 35 LSTPYGQPAC FQQQHQHILA TPLQNLQVLA SSSANECISV KGRIYSILKO IGSQSSKVF 540
 QVLEKQKIY AIKYVNLLEA DNQTLDSYRN EIAYLNKLQO HSDKIIRLYD YEITDQYIYM 600
 VMECCNIDLN SWLKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLPK ANFLIVDGML 660
 KLIDFGIANQ MQPDTTSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL 720
 40 GCILYMTYG KTFPQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI 780
 SIPELLAHFY VQIQTHPVNQ MAKGTTEEMK YVLGLVLGLN SPNSILKAAK TLYEHYSGGE 840
 SHNSSSKTF EKRRGKK

Seq ID NO: 648 DNA sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241..1902

45 1 11 21 31 41 51
 CGCAGAGGA GCGCTCGGCC GGCTAGCCAG GCGCGCCCCA GCGCCTCCCC AGGCCGCGAG 60
 CGCCCTGCGC GCGGTGCGCT GCGCTCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACCTG 120
 CGAGTGGAGC GGAGGACCGG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 GGGTCCGGCC GCGCGCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 50 ATGCTCTGCG CTGGAGCCT TCGCTCCCG CTGCTGCTCT CCGTGGTGGC AGGTGGTTTC 300
 GGGAAACGGG CCACTGCAAG GCATCACGGG TTGTAGTAGT CGGCACGTCG GCCTGGGGTC 360
 55 TGCTACTATG GAATCAACT GCGCTGCTGC TACGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
 AGATGCTTTC CAGGATACAC CGGAAAAACC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAG GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 60 ATAACTGTCT AGTACAGCTC TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
 AAATGTCACA TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 65 AATGAATGTA CTATGATAG CCATACGTGC AGCCACCATG CCAATGCTT CAATACCCAA 960
 GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTGCT 1020
 ATCCCTGAAA ATTCTGTGAA GGAAGTCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAATTTAA AAATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
 70 ATAGTTTCCA GAGCGGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
 CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAA TATCTCGGTT 1440
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 75 TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTCC GGCCTTGGCA 1560
 GTGCACAAGA AAGACATTGG CCGATTGAAA CTTCTCTTAC CTGACCTGCA ACCCAAAGC 1620
 AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA CAGATAACAA TGCCCTGGCA TGGGAGAAGA CCACAGTGA GGATGAAAAA 1740
 TGGAAAGACG GAAAATTTCA GTGTATCAAA GGAAGTGAAT CTACCAAAG CATCATTTT 1800
 80 GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 TTGACTTTGT ATGTCAGTTC CTTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
 TCTTGATATA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
 85 TTCTGGAATC TTTCCCACTT ATATTATAAA ATATGGAAT GTCAAGTTAT CTCCCTCCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
 TAGAAAAAAA AGCAGAGAGA AATGTTTAACT TGTGTGACTC TTATGATACT TCTTGGAAAC 2280
 TATGCATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGCTCTTCA TAGCCAAACT 2340

TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAA AAAA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	PGECVGNPKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRCV	NTHGSYKCF	120
LSGHMLMPDA	TCVNSRTCAM	INQYSCEDT	BEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYIC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTFK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFLGI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPLA	GHKDKIGRLK	LLLPDLQPQS	NFCLLFDYRL	AGDKVQKLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERGKGTG	EIAVDGVLLV	540
SGLCPSLLS	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

1	11	21	31	41	51	
GCAGCTCCAG	TCCCGGACGC	AACCCCGGAG	CGGTCTCAGG	TCCCTGGGGG	GAACGGTGGG	60
TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
CTCATTTTCA	GGAAAGCCTG	AAATAGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
ATCTTTGGAT	GGGGATCTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
ATCAGGAATT	TGAAGAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
CTCCTAAGAG	GGCAGAGTCT	CTTCACTGTG	GAACCAATTA	CTGTTCCAG	ATGTATGAAA	360
ATGGCCTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
CGCGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCTG	AATGTTCAAC	AAACATTGAA	480
ACTTTCCTCT	GCAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCACCT	540
TGTCGTAAAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACCTTTGGG	600
ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCTT	660
GTAACCTTTG	ATCCACACAC	AGAAATTTCT	GGTCTCAGA	AGAAAACAGA	ACAAGTCCAA	720
AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
TTTCTGGGAA	TTGACCAAGT	TGCGCCTCCA	TGCCCCAACA	TGTATTTTAA	AAGTGATGAG	840
CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
TTCACTATCC	TACTTTTTTT	AATTGATGTT	AGAAAGATTCA	GATACCCAGA	GAGACCAATT	960
ATATATTACT	CTGCTGTGTA	CAGCATTGTA	TCTCTTATGT	ACTTCATTGG	ATTTTGTCTG	1020
GGCGATAGCA	CAGCCTGCAA	TAAAGGCAGT	GAGAAGCTAG	AACCTGGTGA	CACCTGTTCT	1080
CTAGGCTCTC	AAAATAAGGC	TTGCACCGTT	TTGTTTCATG	TTTTGTATTT	TTTCACAATG	1140
GCTGGCACTG	TGTGGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
TGGAGTTTGG	AAGCCATCGA	GCAAAAGACA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGAACA	1260
CCAGGTTTCC	TGACTGTGAT	GCTTCTTGCT	CTGAACAAAG	TTGAAGGAGA	CAACATTAGT	1320
GGAGTTTGCT	TGTTTGGCCT	TATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
CTGTGCCTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTTAAAT	1440
CATGTTTCGAC	AAGTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
ATTGGAATTG	GAGTCTTCAG	CGGCTTGTAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
TACGCTCATG	AGCAAGTGAA	CAGGATTACC	TGGGAGATAA	CTTGGGTCCT	TGATCATTGT	1620
CGTCAGTACC	ATATCCCATG	TCCCTTATCAG	GCAAAAGCAA	AAGCTCGACC	AGAATTGGCT	1680
TTATTTATGA	TAAATACCTT	GATGACATTA	ATTGTTGGCA	TCTCTGCTGT	CTTCTGGGTT	1740
GGAAGCAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
CCAATCAGTG	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCACAA	1860
TCTAAGTTTA	AACACAAAAA	GAAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCATT	1920
TCCAAATCCA	TGGGAACCCG	CACAGGAGCT	ACAGCAATC	ATGGCACTTC	TGCAGTAGCA	1980
ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
ACATCAATGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTAAAG	AGAACAGGAC	2100
TGTGGTGAAC	TCGCTCTGAT	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTCGAC	2160
GGGAAGGGCC	AGGCAGGCG	TGTATCTGAA	AGTGGCGGGA	GTGAAGGAAG	GATTAGTCCA	2220
AAGAGTGATA	TTACTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTTCAGAGT	CCCCAGTTCT	2280
TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAGGAGTG	2340
AGAAAAGAGC	AGGGAGGTGG	TTGTCAATCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
CAGAAGCAAA	TTTGTGTTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
TACGTTCTTC	TTTTGCACTT	AAAGTTGCAT	TGCCTACTGT	TATACTGGAA	AAAATAGAGT	2520
TCAAGAATAA	TATGACTCAT	TTCAACAAAA	GGTTAATGAC	AACAATATAC	CTGAAACACG	2580
AAATGTGCAG	GTTAATAATA	TTTTTTTAA	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
CTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCTCT	2760
GTATCTTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
ATTCAAGTAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
ATTTCTAAGA	AAATTTGAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTATTG	ATACCTTACC	ATCTAAAAATG	3000
TGTGATTTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTATGTA	ACTGAAATAA	3060
GGTGCTTACT	CAAGAGGTGT	CCACTATTGA	TTGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
ATATTTAAAA	TAAATGTGCC	TAAAGGGTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
GGCCAAGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTCATGA	CCACCCATTG	ATTGTATTAT	3240
AACCACTTAC	AGTTGCTTAT	ATTTTGTGTT	TTAACCTTTG	TTTCTTAAAC	TTTAGAATAT	3300
TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

1	11	21	31	41	51

MEMFTPLLTCT IFLPLLRGHS LFTCEPITVP RCMKAMYNMT FFPNLMGHYD QSIAAVEMEH 60
 FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRWPBE 120
 LECDRLLQYCD ETVPVTPDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSKG QGYKFLGIDQ 180
 CAPPCCPMYF KSDPELEFAKS FIGTVSIFCL CATLFTFLTP LIDVRRFRYP ERPIIYYSVC 240
 YSIVSLMYFI GFLGLDSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FPMAGTVMW 300
 VILITITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKEVG DNISGVCFVG 360
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVROVI QHDGRNQEKI KKFMRIGVFP 420
 SGLYLVLPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALPMIKY 480
 LMTLIVGISA VFVWGSKKTCT TEWAGFFKRN RKRDPISBSR RVLQESCEFF LKHSKVKHK 540
 KGHYKPPSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLITEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNMLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

1 11 21 31 41 51
 20 TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA CGCCGTACCA 60
 GCCGCGTCTC TCAGGACAGC AGGCCCTGT CCTTCTGTGG GCGCGCGCTC AGCCGTGCCC 120
 TCCGCCCTCT AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAC TCTCAATAT TATGAATTAC ATGAACTAT TGGGACAGGT GGCTTTGCAA 240
 AGGTCAAACT TGGCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 25 AAAACACACT AGGGAGTGAT TTGCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAAC 360
 TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
 TGGTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTC CAGGATCGCC 480
 TGTGAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC 540
 ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC 600
 30 ATAAATTAAA GCTGATTGAC TTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC 660
 ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAA 720
 CATATCTTGG ATCAGAGGCA GATGTTTGGG GCATGGGCAT ACTGTTATAT GTTCTTATGT 780
 GTGGATTCTT ACCATTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
 GAAAATATGA TGTTCCTCAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC 900
 35 TGCAGGTGGA CCGAAAGAAA CGGATTCTTA TGAATAATCT ATTGAACCAT CCTGGATCA 960
 TGCAAGATTA CAACTATCCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG 1020
 ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAACA ATGGAGGATT 1080
 TAATTTCACT GTGGCAGTAT GATCACTTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA 1140
 AGGCTCGGGG AAAACAGGTT CGTTTAAGGC TTTCTTCTTT CTCCTGTGGA CAAGCCAGTG 1200
 40 CTACCCCATT CACAGACATC AAGTCAAATA ATTGGAGTCT GGAAGATGTG ACCGCAAGTG 1260
 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGCTAC TCCCGGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 45 AAAATGTATA TACTCTTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTGTAGC 1500
 CAAAGACTCC AGTTAATAAG AACAGCATA AGAGAGAAAT ACTCACTACG CCAATCGTT 1560
 ACACATACAC CTCAAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620
 TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCTT TAGCCCTGAG AGCGGTGCC 1680
 GCTCAGTGA ATTTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAA AGAAAGGGAG 1740
 50 CCAAAGTGT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAAGGAA GGGTCTGTCC AGAGACGGGC CCAGAAAGCT AAGGCTTAC TATAATGTGA 1860
 CTACAACATG ATTAGTGAAT CCAGATCAAC TGTGAAATGA AATAATGTCT ATTCTTCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAACA CAGTCAGATT 1980
 TTGGGAAAGT GACAAATGCA TTTGAATTAG AAGTGTGCCA GCTTCAAAA CCCGATGTGG 2040
 TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCTGGGT TTAACAAA TTAGTGAAG 2100
 55 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTT CATCCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220
 CTACCAACTT GTTCTTAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATTATT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTT 2340
 60 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 65 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETA KIFMVLEYCP GGELFDYIIS QDRLSEETR VVFRQIVSAV 120
 70 AYVHSQGYAH RDLKPENLLE DEYHKLKLD FGLCAKPKGN KDYHLQTCG SLAYAAPELI 180
 QGKSYLGSEA DVNSMGLILY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNFFI HLDDDCVTEL SVHRRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSPSCG QASATPFTDI KSNNWSLEDV 360
 75 TASDKYVYAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTFANKL 420
 KNKENVYTPK SAVKNKPYFM FPEPKTFVNN NOHKREILT PNRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKLH YNVTTTLVN PDQLLNEIMS ILPKKHVPV QKGYTLKQCT 600
 QSDFGKVTMQ FELEVQCQLQK PDVVGIRQR LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 85 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAAACCT CACTACCATG AGAATTGCAG TGATTGCTT TTGCTCTCTA 120

GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180
 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
 CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
 TCTGATGAAT CTGATGAAGT GGTCACTGAT TTTCCACCGG ACCTGCCAGC AACCGAAGTT 480
 TFCCTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
 GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
 GACGAGGACA TCACCTCACA CATGGAAGC GAGGAGTTGA ATGGTGCTA CAAGGCCATC 660
 CCCGTTGGCC AGGACCTGAA CGCGCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
 GAAACGAGTC AGCTGATGTA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840
 CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900
 GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCTGAT TTCTCATGAA 960
 TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACTTTGC 1020
 ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
 ATTAGTTTAT TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
 CTATGTTTAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260
 TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
 ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TGTGTGTGAT 1380
 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAAAT TGGTGTGTCT 1440
 AATTGCTTAT TTGTTTTCCT ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTTACT 1500
 GCCTAAAAAA AAAAAAATA AAAAA

Seq ID NO: 655 Protein sequence
 Protein Accession #: NP_000573

1 11 21 31 41 51
 | | | | |
 MRIAVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL 60
 PSKSNESHDD MDDMDDEDD DHVDSQDSID SNDSDDVDDT DSHQSDSHS HSDSDDELVT 120
 DFPTDLPAE VFTPVVFTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NEHSDVIDSQ ELKSVSRFPH SHEFHSHEDM LVVDPKSKEB DKHLKFRISH ELDSASSEVN

Seq ID NO: 656 DNA sequence
 Nucleic Acid Accession #: NM_003108.1
 Coding sequence: 76..1401

1 11 21 31 41 51
 | | | | |
 GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA 60
 GCCCTGCAAC GGATCATGTT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCCC 120
 CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GCCCTGGAC 180
 GAGAGCGACC CAGACTGGTG CAAGACGGCG TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
 TTCTATGGTAT GGTCCAAGAT CGAACGCAGG AAGATCATGG AGCAGTCTCC GGACATGCAC 300
 AACGCGGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAATA TGCTGAAGGA CAGCGAGAAG 360
 ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
 TACAAGTACC GGCCCGCGAA AAAGCCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
 CAGAGCCGAG AGAAGAGCGC GGCCCGCGGC GCGCGGCGGA GCGCGGGCGG AGGCGCGGGC 540
 GGTGCCAAGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCGCGGCC 600
 GCGGGCGCCA AGCGCGGCGC GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC 660
 GACGACTACG TGTGTGGGAG CTTGCGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG 720
 ACGGTCAAGT GCGTGTCTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG 780
 CAGCTGCAGA TCAACACAGG GCCCGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC 840
 CTGCAGCGCG CGGGGACGCA GCCGTGCGAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG 900
 CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCTCG AGGGAGCGAG CCTCTACGAC 960
 GAGGTGCGGG CGCGGCGGAC CTCGGGCGCC GGGGGCGGCA GCGGCTCTA CTACAGCTTC 1020
 AAGAACATCA CCAAGACGCA CCGCGCCGCG CTCGCGCAGC CCGCGCTGTC GCCCGCGTTC 1080
 TCGCGCTCGG TGTCACCTCT CTGTCACGAG AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC 1140
 GAGGACGCGG ACGACCTGAT GTTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC 1200
 GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGCGCGGGA ACCTGTCCCT GTCGCTGGTG 1260
 GATAAGGATT TGATTCTGTT CAGCGAGGGC AGCCTGGGCT CCCACTTCGA GTTCCCGCAG 1320
 TACTGCACGC CGGAGCTGAG CGAGATGATC GCGGGGAGCT GGCTGGAGGC GAACTTCTCC 1380
 GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG 1440
 AGCTGGGTTT CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG 1500
 ATGATGGTGG TGTGTATGTT GCGGTGGTGA GGGTGGAGGG GAGAGAAGAA GATGCTGATG 1560
 ATATTGATAA GATGTCGTGA CGCAAGAGAA TTGGAAAAACA TGATGAAAT TTTGGTGGAG 1620
 TAAAGTGAA ATGATGATTT TTTAAACATT TTTCTGTCC TTTTCTGTC CCCCTCCCT 1680
 TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1740
 AAAATGTGTT TTTGTAATTA CTATTCTTTT TTCCTGAAAT TCGTGATTGC AACAAAGGCA 1800
 GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
 GTCGGTCTTT GAGGCTGGA AGACGTCTGC AGAGGACCCCT TTTGGCAGCA CAACTGTTAC 1920
 TCTAGGGAGT TGGTGGAGAT ATTTTCTTTT CTTAAGAGAA CTTAAGAAAC TGGTGATTTT 1980
 TTTTAAACAA AAAAAGGG

Seq ID NO: 657 Protein sequence
 Protein Accession #: NP_003099.1

1 11 21 31 41 51
 | | | | |
 MVQQAESLEA ESNLPREALD TEEGEFMACS FVALDESDDP WCKTASGHIK RPMNAPMVWS 60
 KIERRKIMEQ SPDMHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYDPYKYRP 120
 RKPKPMPSA KPSASQSPFK SAAGGGGSSA GGGAGGAKTS KGSKKCKGL KAPAAAGAKA 180
 GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDELQLQIK 240

QEPDEDEEP PHQQLLPFG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVRA 300
ATSGAGGGRS LYYSFKNITK QHPPPLAQA LSPASSRSVS TSSSSSGSS SGSSGEDADD 360
LMFDLSLNFQ QSARSASEQ LGGAAAGNL SLSLVDKDL SFSEGLSGH FEFPDYCTPE 420
LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGGCACAG CTTCGTGGCG CTCTGGGCAC 180
15 CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
GCTTCATCCA CCGCGGCTTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCTCTT 300
CCATTTTGGG CTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT CTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
20 GCCTGCAAGA TAGCCATTTT CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TOGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
ACATCCGGGA ACCTTCGAC AATGAGACGT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
25 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
GGCAACAACCT GGGCTGCGAG CTCTCGGTGG AGACGTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA CGAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGAGGTC CACTTCGCA GCATCCGGTC CACGGGAGC AAACAGGCA 1020
GCCAGAACCG CTCCAAGAG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
30 AGAACAGCAG CAGGACCGAG AGCAGGCCCT GTAAGAAGCA CGAGCTGTAT GTCACTTCC 1140
GAGACTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
AGGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGTGTG GCGCCACGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACTGCATC CTGAAGAAAT 1380
35 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT 1440
TTGGGGCCAA GTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCTTTTGG TGAGACCTTC CCTCCCTAT CCGCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGCG TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
40 TCTTACAAGC TGTGACGGCA AAACCTAGCA GGAACAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTTGGT GGGAAAGTCT AGCCATGCAC GGAATCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG

Seq ID NO: 659 Protein sequence
Protein Accession #: NP_001710

1 11 21 31 41 51
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQREILS 60
ILGLPHRRPR HLQCKINSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRYIKDY 180
IRERFDNETF RISVYQVLQE HIGRESDLFL LDSRTLWASE EGWLVDITTA TSNHWVNNPR 240
55 HNGLQLQSVL TLDGQSNPKP LAGLIGRHGP QNKQPFMVAF FKATEVHFPS IRSTGSKQRS 300
QNRSKTPKQK EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGNQDWIIA PEGYAAYYCE 360
GECAFPPLNSY MNATNHAIVQ TLVHFIPNET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H

Seq ID NO: 660 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 211..1895

1 11 21 31 41 51
GGATCTGAGG GGGCGCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTCCGA 120
GAGGAATTAT CTGATAAAAT TCCTGGGTAA ATATTTTAA AAACGGAGAG TTTTAAAAA 180
TGATTTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGT CACAGCATA 240
70 GTGCTTTTTC TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
CACAGGTTCC TTGAACAGCT GGATCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
CTTGCTGCTG AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCACT CCAGGAGGGA 420
GAAGGTAATT GTTTCCTGTA ATGGGATGGA CTCATTGTT GGCAGGAGG AACAGTGGGG 480
AAAAATATCG CTGTTCCATG CCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
75 TTCCGACACT GTAACCCCAA TGAACATGG GATTTATGC ACAGCTTAAA TAAACATGG 600
GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAGCAAGAA 660
TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCTTGT 720
GCTGTGGCTA TTCTCATCAT TGGTACTTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
CACATGCACT TATTGTGTC TTTTATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
80 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
CAAAATTCAC TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
GTTGTGATGT TTAATTACTT CTTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAATAACCT GTGGGCTTTC 1080
ATCTTGATAG GCTGGGGGTT TCAGCAGCA TTTGTTGAG CATGGGCTGT GGCACGAGCA 1140
ACTCTGGCTG ATGGGAGGTG CTGGGAACCT AGTGCTGGAG ACATCAAGTG GATTATCA 1200
85 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
AAACTGGCCA AATCGACACT GGTCTGGTCT CTAGTCTTGT GAGTGCAATTA CATCGTTTTC 1380

GTATGCCTGC CTCACCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTCTTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAGAG 1560
 ACACCGCCAT GTGGCAGCGG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCTTCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGGAACTTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSSTSI VLFLFSSPST INESSISSRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNIITAQLEB EGNCFFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
 DPMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGSISFGLS AVAILIIGYF 180
 RRLHCTRNYI HMHLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSV 240
 KSQYIGCKIA VVMFIYFLAT NYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPA 300
 FVAAMAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKINETNA 360
 VGHDRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FNSFQGFV 420
 SIYCYCNGE VQAEVKMWS RWNLSVDWKR TPCGSRRCG SVLTTVTHTS SSQSQAAS 480
 RMVLISGKAA KLASRQPDH IITLPGYVWSN SEQDCLPHSF HEETKEDSGR QGDILMEKP 540
 SRPMESNPDT EGCQGETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CCGGGCCCGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTTAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCACATCAC 300
 AGCTCACTC CAGGAGGGAG AAGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTTG 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCACTGCTA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGCAG GATGACCCAC AAAATTCAT TGAAGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTACTCT CTGGCTACAA ATTATTATG 900
 GATCCTGGTG GAAAGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TGTGTGCAGC 1020
 ATGGGCTGTG TCACGAGCAA CTCTGGCTGA TGGGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260
 AGTGCAATAC ATCGTGTTCG TAGTCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGCT TCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATGCCGCT CAGTGCTCAC 1500
 CACCGTGAGC CACAGCACA GCAGCCAGT ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTTACC 1620
 TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCTGCCA CACTCTTTCC ACGAGGAGAC 1680
 CAAGGAAGAT AGTGGGAGC AGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTT TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAG 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCCTTT TAGAAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CTTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACCTCTTC 2460
 TTCTTTGTAA ACCATGTGAT GTGGAAGAT TTCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TGTGAATGTA TTTTATAGC AAATCATGCT GCATCTATAT CTTTCTCTG 2580
 TTTGAGCTGT TGTACATTG TACATGGCAT GTGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLGASLHV GWLMLGSL LARAQLSDG TITIEEQIVL VLKAKVQCEL NITAIQLEGE 60
 GNCFFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW FMHSLNKTWA 120
 NYSDCLRFLQ PDISIGKQEP FERLYVMYT VGSISFGLS VAILIIGYFR RLHCTRNYIH 180
 MHFLFVSFMLR ATSIFVKDRV VHAHIGVKE LESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

5 VMEIYFLATN YYWILVSGLY LHNLIIVAFV SDTKYLWGFII LIGWGFPAAP VAANAVARAT 300
LADARCWELS AGDIKIWIYA PILAAIGLNF ILPLNTVRVL ATKIWSTNAV GHDTRKQYRK 360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS IYCYCNGEV 420
QAEVKIMWRS WNLKSDWKR PPGRSRRCS VLTITVTHSTS SQSQVAASR MVLISGKAAC 480
IASRQPDHSI TLPGYVWSNS EQDCLPHSFH BETKEDSGRO GDDILMEKPS RPNESNPOTE 540
GCGGETEDVL

Seq ID NO: 664 DNA sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

10 1 11 21 31 41 51
CTTCTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
15 GACAAGCACA TGGACTTTTT TTATAATAG AGCAACACTG ATACTGTGGA TGAAGTGGCA 120
GGAAACAAAGC TTGTGATTGT TTGTGTGTGT GGGACGTTTT TCTGCTGTGT TATTTTTTTT 180
TCTAATTTCTC TGGTCATCGC GGCAGTGATC AAAACAGAAA AATTTTCATT CCCCTTCTAC 240
TACCTGTGTGG CTAATTTAGC TGTCTGCGAT TTCTTGTCTG GAATTCGCTA TGTATTCTGT 300
20 ATGTTTAAAC CAGGCCCACT TTCAAAAAC TTGACTGTCA ACCGCTGTGT TCTCCGTGAG 360
GGGCTTCTGG ACAGTAGCTT GACTGTCTCC CTCACCAACT TGCTGTTTAT CGCCGTGGAG 420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
CTGCTCATTG TGCTGTCTGT GGCATCGGCC ATTTTATATG GGGCGTCCC CACACTGGGC 540
TGAATTTGCC TCTGCAACAT CTCTGCTGTC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT 600
TACCTGTGTG TCTGGACAGT TGCCAACTTC ATGGCCTTCC TCATCATGTT TGTGGTGTAC 660
25 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720
TCCATCAGCC GCGCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
GCGTTTGTGG TATGCTGGAC CCGGGCCTGT GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
GTGCTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGAC CATGAAGAAG 960
30 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGCGCTC CCTCTCGAT CCCCTCCACA 1020
GTCTCAGCA GAGGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
GTCTGCAATA AAAGCACTTC CTAACTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140
GTCTTAGG

35 Seq ID NO: 665 Protein sequence
Protein Accession #: NP_036284

40 1 11 21 31 41 51
MNECHYDKHM DFFYNRSNTD TVDDWTGTLK VIVLCVGTFF CLFIFFSNLS VIAAVIXNRK 60
FHFPFYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
LVIAVERHMS IMRMVHNSL TKKRVTLIL LVWAIAPMG AVPTLGWNL CNISACSSLA 180
PIYSRSLYVF WTVSNLMAFL IMVVYLRIY VYVKKRKNVL SPHTSGSISR RRTPKMLMKT 240
VMTVLGAFVW CMTPLGVLL LDGLNCRQCG VQHVIRWFL LALLNSVNVN IYISKDEDM 300
45 YGTMKKMICC PSQENPERR SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

50 1 11 21 31 41 51
AACTCCCGCC TCGGGACGCC TCGGGGTGCG GCTCCGGCTG CGGCTGCTGC TCGGGCGCCC 60
GCGCTCCGGT GCGCTCCGCT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCCGTGCGC 120
55 CCTCAGCTCC TTTTCTGTAG CCGCGCGCGA TGGAGCTGTC GCGGGGATCC CCGGCCAGAC 180
CCGCGCGGTT GCTCTGTCTC AGCGTCTGTC TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240
CCATTGTCTT CATCAAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
TTGCTGTGGA GTTGTAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
60 CTGTCCAGGA CACGGAGCGG CGTTTCCGCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG 420
ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
AAGCCGCGAG TGCCAAGGCC TCCTTCAACA TCAATGGAT TGAGGCAGGT CCTGTGGTCC 540
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACT CTCTGTTGCC 600
ACATTGATGG GACCCCTCGG CCCACCTACC AATGGTTCCG AGATGGGACC CCCCCTTCTG 660
ATGGTCAGAG CAACCCAGCA GTGAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720
65 GTCTGAGCA TAGTGGGCTG TATTCTGTCT GCGCCACAG TGCTTTGGC CAGGCTTGCA 780
GCAGCCAGAA CTTACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGCTG GTGCTGGCAC 840
CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
AGCCACCCCG GAGCCTGCGC TGGCTCTTG AGGATGAGAC TCCCATCACT AACCGCAGTC 960
70 GCGCCCCACA CCTCCGAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
TCCGGCCACG CAATGACGGG ATCTACCGCT GCATTGGCCA GGGGAGAGG GGGCCACCCA 1080
TCATCTGGA AGCCACACT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTGAGCCAC 1140
GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
AGCCAGCGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
75 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320
GCCACGCGGC CAACCTGGCT GTGACGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
TGCCCTCTCT GCTGAAGAAG CCCCAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
TGGATTGCCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGATACAGA AACCATGTC 1500
TCATCTCAGA GGACTCAGG TTGAGGTCT TCAAGAATGG GACCTTGCCT ATCAACAGCG 1560
80 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
AGGCGCAAGC CCGTGTCCAA GTGCTGGAAA AGCTCAAGTT CACACCAACA CCCCAGCCAC 1680
AGCAGTGCAT GGAGTTTAC AAGGAGGCCA CGGTGCCCTG TTCAGGCCA GGGCCAGAGA 1740
AGCCCACTAT TAAGTGGGAA CCGGAGATG GAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
ACGCTGGGAC CCTGCTATTT GCCCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA 1860
85 TTGCTCCAA CGGGCCGAGC GGGCAGATTG GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
TTATCACTTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
TGCACTGCGA GGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA 2040
TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGATGGC TCCTGGTGA 2100

WO 02/086443

	TCCATCAAGCT	GGCCCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCGAGC	ACACGCTGCA	2160
	ACCATCAAGCA	CACGAGGAGG	CCCTCTATGT	TGCTGGACAA	GCTGTGCGC	GAGGAGTCCG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
	CGCGCTGTGC	CTACATCAATT	GCOCGTGCTG	GGCCTATGTT	CTACTGCGAG	ARGCGCTGCA	2340
5	AAGCCAAGCG	GCTGCAGAA	CACGCCGAGG	GGCGAAGACC	AGAGATGGAA	TGCGTCAACG	2400
	GAGGGCCCTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTTGGGCT	CGGCCCGCGC	GCACCAACAA	ACACGCCAGC	CACAAGTGAT	ARGATGCATC	2520
	TCCCAAGGTC	TAGCTCTGAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGGTG	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTTGSTA	CTTGTGAAGA	2640
10	GGCTCGAGAC	GAGAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAACTGTAA	CCACGCCAAC	CTGTGTGGCG	TCTCTGGGCT	GTGGCGGGAG	CGTAGACCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGAATCTG	GAGACCTCAA	GCAGTTCTCG	AGGATTTTCA	2820
	AGAGCAAGGA	TGAAAAATTT	AAGTCAACGC	CCCTCAGCAC	CACGACGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGAGGACCA	TGTCCACAA	CCGCTTTGTG	CATAAGGACT	2940
15	TGGCTGCGCG	TAACTGCCTG	GTCAGTCCCC	AGAGACAAGT	GAAGGTCGCT	GCCCTGGGGC	3000
	TCAGACAGGA	TGTGTACAA	AGTGAGTACT	ACCACCTCCG	CCAGGCGCTG	TGTCCGCTGG	3060
	GCTGGATGTA	CCCCGAGGCC	ATCTCTGAGG	GTGACTTTCT	TACAAGGTCT	GATGTCTGGG	3120
	CCTTTCGGTG	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCCAT	GGTGGGCAGG	3180
	CAGATGATGA	AGTATCTGGCA	GATTTCGAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	GCTGCCCTCT	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCACGCCCC	TGGGAGACAG	CACCGTAGAG	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCCGCTCAG	ATGGCCTGGG	CGGGGAGGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CAGCATGATG	GGCAAGATTC	CTGTCTCTCT	GGGCCCTGAG	TGCGCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGGT	CTGAGCAGGG	CCCTGGCCTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAACT	GGGCGACATT	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTCTCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACCTCTGCC	CTCATCTGCC	AACCTTGCCT	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTTAATA	TTCTCAAGTT	CTGGGACAC	3780
	AGGGTATAAG	AGTCTCTTGC	CCACTCTGTC	ACTTGGGGGT	CTAGACAGG	ATTATAGAGG	3840
30	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	GATACCCAGA	CCCAAGCTCT	3900
	CCCCACCCCT	CTCTCCTTTC	CTCATCTTAA	GTGCGTGGCA	GTAGAGGAGG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GCOCCTTTTG	TATGCACACC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGC	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
	GCCATCTCTA	CCCCACCTGG	TTATTTGTTG	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTTTT	4140
35	TGTTTTTGTT	TTTACACTCG	CTGCTCTCAA	TAATAAGCC	TTTTTTTA		

Seq ID NO: 667 Protein sequence
Protein Accession #: NP_002812

40	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGGTQT	AIVFIKQPSS	QDALQGRRAL	LRCEVEAPGP	60
	VHVYWLDDGA	PVQDTERRFA	QGSSLSFAAV	DRLQDSGTFQ	CVARDDVTGE	EARSANASFN	120
	IKWIEAGVPV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DQGSNHTVSS	180
45	KERNLTLRPA	GEHSGLYSC	CAHSAFGQAC	SSQNFTLSIA	DESFARVLLA	PQDVVVARYE	240
	EAMFHQCQSA	QPPPSLQWLF	EDETPITNRS	RPPLRLRATV	FANGSLLLQT	VRPRNAGIYR	300
	CIGGQGRGPP	IILEATHLHA	EIEDMPLFEP	RFTTAGSEER	VTCLPPKLGK	EPSVNWWEHAG	360
	VRLPETHGRVY	QKGHELVLAN	IAESDAGVYT	CHAANLAGQR	RQDVNITVAT	VPWSLKKPQD	420
	SQLEEGKPGY	LDCLTQATPK	PTVVWYRNQM	LISEDSEFVE	FKNGTGLRNS	VEBYDGTWYR	480
50	CMSSTPAGSI	EAQARQVQLE	KLKFTPPPPQ	IQCMEFDKEA	TVPCSATGRS	KPTIKWERAD	540
	GSSSLPEWVT	NAGTLHFARV	TRDDAGNYTC	IASNGPQQGI	RAHVQLTVAV	FITFKVEPER	600
	TTYVQGHGHTL	QCEAQQGDPK	PLTVQKWKGR	ILDPTKLGRP	MHTFGNSVL	HAIDVAPDSG	660
	RYTICAGNSL	NIKHTEAPLY	VLDKVPPEES	EGPGSPPPYK	MIQTIGLSVG	AAYVYIAVL	720
	GLMFYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEEVALT	SLGSGPAATN	780
55	KRHSDDKMH	PRSSSLQVIT	TLGKSEFEAV	FLAKAAGLEE	GVASTLVLVK	SLQTKDEQQQ	840
	LDPRREELME	GKLNHANPVR	LLGKCEAEAP	HYMVLEYVDL	GDLKLQFLRS	KSXDEKLRSQ	900
	PLSTKQKVAL	CTQVALGMEH	LSNINRFKSD	LAARNCLVSA	QRQVKVSALG	LSKDVYNSEY	960
	YHFRQANVPL	RWMSPEALIE	GDFSTKSDVW	AFGVSLMVEVF	THGMPPHGQ	ADDEVLADLQ	1020
60	AGKARLQVPE	GPCSLYRLM	GRCWALSPKD	RPSFSEIASA	LGDSVTDSKP		

Seq ID NO: 668 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

	1	11	21	31	41	51	
65	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGCAGA	GAGATTTAGA	TGACAGAGAA	60
	ACCCCTGTTT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTTTAAT	120
	GTGTGCAACT	CGAATTATAG	ATCTGGGTATA	TAGGATTGCG	CTTATTCAAT	GAAGCAAGCT	180
70	GGGTTCCTTT	TGGGAATATT	GCCTTTTATTC	TGGGTTTCAAT	ATGTTACCGA	CTTTTCCCTTT	240
	GTTTTATTGA	TAAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAGTC	TTTGGTCAAT	300
	AAAACCTTCG	GCTTTCGACG	GTAATCTGCTC	CTCTCTGTCT	TCGAGTTTTT	GTATCCCTTTT	360
	ATAGCAATGA	TAAGTATCAA	TATAATAGCT	GAGAGATACT	TGAGCAAAGT	TTTTCAAAGA	420
75	ATCCCAAGAG	TTGATCCTGA	AAACGTGTTT	ATTGGTCGCC	ACTTCATTAT	TGGACATTTCC	480
	ACAGTTACCT	TTACTCTGCG	TTTTATCCTTG	TACCCGAAATA	TGCAAAAGCT	TGGAAGAGCT	540
	TCCTCATCTC	TCACAGGTTT	AAACAATCTG	ATTCTTGGAA	TATGTAAGGC	AAGGGCAATT	600
	TCACTCGGCT	CACACATACC	AAAAACAGAA	GACGCTTGGG	TATTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TCGGGGTATG	GTCTTTTGCA	TTTATTGGCC	CACTTATCTC	CTTCTTAGTT	720
	TACAGTTCTC	TAGAAGAACC	CACAGTAGCT	AAAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
80	GTGATTTCTG	TATTTATCTG	TATATTCCTT	GCTACATGTG	GATACCTTGG	ATTTACTGGC	840
	TTTCACCAA	GGGACTATTT	TGAATAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGTT	ATGGTGTCTAC	TGTCATTTTG	ACATACCCTA	TGGAATGCTT	TGTGACAAGA	960
	GAGGTAAATG	CCAAATGTGTT	TTTTTGGTGGG	ATATCTTCACT	CGGTTTCCA	CATTGTGTGA	1020
	ACAGTGTATG	TCATCAGTGT	AGCCAAGCTT	GTGCTATTGC	TGATTGATGT	CCTCGGGATA	1080
85	GTCTCTAGAC	TCAATGGTGT	GCTCTGTGCA	ACTCCCCCTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTTATCTGA	AACTGTCCTGA	AGAACCAAGG	ACACACTCCG	ATAGGATATT	GTCTTGTGTC	1200
	ATGCTCTCCA	TGTGGTCTGT	GGAATGTTT	TTTGGATTCT	TCATGGCTAT	TACAATATCT	1260

CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCATGA

Seq ID NO: 669 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRDLDDRE	TLVSEHEYKE	KTCQSAALFN	VVNSIIGSGI	IGLPYSMKQA	60
GFPLGILLFL	WVSYVDFSL	VLLIKGGALS	GTDTYQSLVN	KTFGFPYGLL	LSVLQFLYPP	120
IAMISYNIIA	GDILSKVFOR	IPGVDPENVF	IGRHFIIGLS	TVTFTLPLSL	YRNIAKLGKV	180
SLISTGLTTL	ILGIVMARAI	SLGPHIPKTB	DAWVFAKENA	IQAVGVMSFA	FICHNSFLV	240
YSSLEEPVA	KWSRLIHMSI	VISVFICIFP	ATCGYLTFPG	FTQGDLFENY	CRNDDLVTFG	300
RFCYGVTVIL	TYPMECFVTR	EVIANVFFPG	NLSSVPHIVV	TVMVITVATL	VSLLDCLGI	360
VLELNGVLCA	TPLFIIPSA	CYLKLSSEPR	THSDKIMSCV	MLPIGAVVMV	FGFVMAITNT	420
QDCTHGQEMF	YCFPDNFSLT	NTSESHVQQT	TQLSTLNISI	FQ		

Seq ID NO: 670 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCAGA	GAGGATTGCC	TTATTCAATG	60
AAGCAAGCTG	GGTTTCCTTT	GGGAATATTG	CTTTTATCT	GGGTTTCATA	TGTTACAGAC	120
TTTTCCCTFG	TTTTATTGAT	AAAAGGAGGG	GCCCTCTCTG	GAACAGATAC	CTACCAGTCT	180
TGGTCAATA	AAACTTTCGG	CTTTCAGGG	TATCTGCTCC	TCTCTGTTCT	TCAGTTTTTG	240
TATCCTTTTA	TAGCAATGAT	AAGTTACAAT	ATAATAGCTG	GAGATACTTT	GAGCAAAAGT	300
TTTCAAGAA	TCCAGGAGT	TGATCCTGAA	AACGTGTTTA	TGTCGCGCA	CTTCATTATT	360
GGACTTTCCA	CAGTTACCTT	TACTCTGCCT	TTATCCTTGT	ACCGAAATAT	AGCAAAGCTT	420
GGAAAGGCTC	CCCTCATCTC	TACAGGTTTA	ACAACCTCTG	TTCTTGGAAT	TGTAATGGCA	480
AGGGCAATTT	CACGTGGTCC	ACACATACCA	AAAACAGAAG	ACGCTTGGGT	ATTTGCAAAG	540
CCCAATGCCA	TTCAAGCGGT	CGGGGTTATG	TCTTTTGCAT	TTATTTGCCA	CCATAACTCC	600
TTCTTAGTGT	ACAGTTCTCT	AGAAGAACC	ACAGTAGCTA	AGTGGTCCCG	CCTTATCCAT	660
ATGTCCATCG	TGATTCTGT	ATTTATCTGT	ATATCTTTG	CTACATGTGG	ATACTTGACA	720
TTTACTGGCT	TCACCCAAGG	GGACTTATTT	GAAATTTACT	GCAGAAATGA	TGACCTGGTA	780
ACATTGGAA	GATTTTGTTA	TGGTGCTACT	GTCATTTTGA	CATACCCTAT	GGAAATGCTT	840
GTGACAAAG	AGGTAATTGC	CAATGTGTTT	TTTGGTGGGA	ATCTTTCATC	GGTTTTCCAC	900
ATTGTTGTAA	CAGTGATGGT	CATCACTGTA	GCCACGCTTG	TGTCATTGCT	GATTGATTGC	960
CTCGGGATAG	TTCTAGAACT	CAATGGTGTG	CTCTGTGCAA	CTCCCCCTCAT	TTTTATCATT	1020
CCATCAGCCT	GTATCTGAA	ACTGTCTGAA	GAACCAAGGA	CACACTCCGA	TAAGATTATG	1080
TCTGTGTGTA	TGCTTCCCAT	TGGTGCTGTG	GTGATGGTTT	TTGGATTGCT	CATGGCTATT	1140
ACAAATACTC	AAGACTGCAC	CCATGGGCAG	GAAATGTTCT	ACTGCTTTCC	TGACAATTTT	1200
TCTCTCAAA	ATACCTCAGA	GTCTCATGTT	CAGCAGACAA	CACAACCTTC	TACTTTAAAT	1260
ATTAGTATCT	TTCAACTCGA	GTAA				

Seq ID NO: 671 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQRGLPYSM	KQAGFPLGIL	LLFWVSVYTD	FSLVLLIKGG	ALSGTDTYQS	60
LVNKTFFGPG	YLLSLVQLPL	YPIAMISYN	IIAGDTLSKV	FORIPGVDP	NVFIQRHPII	120
GLSTVTFTLP	LSLYRNIAKL	GKVSLLSTGL	TLILGLVMA	RAISLPHIP	KTEDAWVFAK	180
PNAIQAVGVM	SFAFICHNS	FLVYSSLEEP	TVAKWSRLIH	MSIVISVVIC	IFPATCGYLT	240
FTGFTQGDLF	ENYCRNDLV	TFRFCYGV	VILTYPMECF	VTREIVANVF	PGNLSVVFH	300
IVTVVMVITV	ATLVSLIDC	LGIVLELNGV	LCATPLIFII	PSACYLKLSE	EPRTHSDKIM	360
SCVMLPIGAV	VMVFGFVMAI	TNTQDCTHGO	EMFYCFPDNF	SLTNTSESHV	QTTQLSTLN	420
ISIFQLE						

Seq ID NO: 672 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCATC	CCGCCGCAGT	TTTCCCTTGT	TTTATTGATA	60
AAAGGAGGGG	CCCTCTCTGG	AACAGATACC	TACCACTCTT	TGGTCAATAA	AACTTTCGGC	120
TTTCCAGGGT	ATCTGCTCCT	CTCTGTCTTT	CAGTTTTTGT	ATCCTTTTAT	AGCAATGATA	180
AGTTACAATA	TAATAGCTGG	AGATACTTTG	AGCAAAGTTT	TTCAAAGAAT	CCCAGGAGTT	240
GATCCTGAAA	ACGTGTTTAT	TGGTCGCCAC	TTCAATTATG	GACTTTCAC	AGTTACCTTT	300
ACTCTGCCTT	TATCCTTGTA	CCGAAATATA	GCAAAGCTTG	GAAAGGTCTC	CCTCATCTCT	360
ACAGGTTTAA	CAACTCTGAT	TCTTGGAATT	GTAATGGCAA	GGGCAATTTT	ACTGGGTCCA	420
CACATACCAA	AAACAGAAGA	CGCTTGGGTA	TTTGCAAGC	CCAATGCCAT	TCAAGCGGTC	480
GGGGTTATGT	CTTTTGCAAT	TATTTGCCAC	CATAACTCCT	TCTTAGTTTA	CAGTTCTCTA	540
GAAGAACCAC	CAGTAGCTAA	GTGGTCCCGC	CTTATCCATA	TGTCCATCGT	GATTTCGTGA	600
TTTATCTGTA	TATTTCTTGC	TACATGTGGA	TACTTGACAT	TTACTGGCTT	CACCCAAGGG	660
GACTTATTTG	AAAATTACTG	CAGAAATGAT	GACCTGGTAA	CATTGGAAG	ATTTTGTAT	720
GGTGTCAGTG	TCATTTTGAC	ATACCCTATG	GAATGCTTTG	TGACAAGAGA	GGTAATTGCC	780
AATGTGTTT	TTGGTGGGAA	TCCTTCATCG	GTTTTCCACA	TTGTTGTAA	AGTGATGGTC	840
ATCACTGTAG	CCAGCTGTGT	GTCATTGCTG	ATTGATTGCC	TCGGGATAGT	TCTAGAACTC	900
AATGTGTGTC	TCTGTGCAAC	TCCCCTCATT	TTTATCATTC	CATCAGCCTG	TTATCTGAAA	960
CTGTCTGAAG	AACCAAGGAC	ACACTCCGAT	AAGATTATGT	CTTGTGTGTC	GCTTCCCAT	1020
GGTGCTGTGG	TGATGGTTT	TGATGCTGTC	ATGGCTATTA	CAAATACTCA	AGACTGCACC	1080
CATGGGCAGG	AAATGTTCTA	CTGCTTTCCT	GACAATTTCT	CTCTCACAAA	TACCTCAGAG	1140
TCTCATGTTT	AGCAGACAAC	ACAACTTTCT	ACTTTAAATA	TAGTATCTT	TCAACTCGAG	1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQPSLVLLI	KGGALSGTDT	YQSLVNKTFG	FPGYLLLSVL	QPLYPFIAMI	60
SYNIIAGDTL	SKVFQRIPIG	DPENVFIGRH	FIIGLSTVTF	TLPLSLYRNI	AKLGKVSLSIS	120
TGLTTLILGI	VMARISLGP	HIPKTEDAWV	FAKPNAIQAV	GVMSPAFICH	HNSFLVYSSL	180
EEPTVAKWSR	LIHMSIVISV	PICIFFATCG	YLFTPTGPTQG	DLFENYCRND	DLVTFGRFCY	240
GVTVILTYPM	ECFVTREIVIA	NVFFGGNLS	VFHIVVTVMV	ITVATLVSL	IDCLGIVLEL	300
NGVLCATPLI	FIIPSACYLK	LSEEPRTSD	KIMSCVMLPI	GAVVMVFGFV	MAITNTQDCT	360
HQEMFYCFP	DNFSLTMTSE	SHVQQTQLS	TLNISIFQLE			

Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

1	11	21	31	41	51	
ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGCAGG	TCAATAAAAC	TTTCGGCTTT	60
CCAGGGTATC	TGCTCCTCTC	TGTTCTTCAG	TTTGTGATC	CTTTTATAGC	AATGATAAGT	120
TACAAATATA	TACCTGGAGA	TACTTTGAGC	AAAGTTTTC	AAAGAATCCC	AGGAGTTGAT	180
CCTGAAAACG	TGTTTATGG	TGCCACTTC	ATTATTGGAC	TTTCCACAGT	TACCTTTACT	240
CTGCCCTTAT	CCCTGTACCG	AAATATAGCA	AAGCTTGGAA	AGGTCTCCCT	CATCTCTACA	300
GGTTTAAACA	CTCTGATTCT	TGGAATTGTA	ATGGCAAGGG	CAATTTCACT	GGGTCCACAC	360
ATACAAAAA	CAGAAGACGC	TTGGGTATT	GCAAGGCCA	ATGCCATTCA	AGCGGTCCGG	420
GTTATGTCTT	TTGCATTAT	TTGCCACCAT	AATCCTTCT	TAGTTTACAG	TTCTCTAGAA	480
GAACCCACAG	TAGCTAAGTG	GTCCCGCCTT	ATCCATATGT	CCATCGTGAT	TTCTGTATTT	540
ATCTGTATAT	TCTTTGCTAC	ATGTGGATAC	TTGACATTTA	CTGGCTTCAC	CCAAGGGGAC	600
TTATTTGAAA	ATTACTGACG	AAATGATGAC	CTGGTAACAT	TTGGAAGATT	TGTTTATGGT	660
GTCACGTGTA	TTTGTACATA	CCCTATGGAA	TGCTTTGTGA	CAAGAGAGGT	AATTGCCAAT	720
GTGTTTITTT	GTGGGAATCT	TTTCATCGGT	TTCCACATTG	TTGTAACAGT	GATGGTCATC	780
ACTGTAGCCA	CGCTGTGTC	ATTGCTGATT	GATTGCCTCG	GGATAGTTCT	AGAACTCAAT	840
GGTGTGCTCT	GTGCACTCC	CCTCATTTTT	ATCATTCCAT	CAGCCTGTTA	TCTGAACTCG	900
TCTGAAGAAC	CAAGGACACA	CTCCGATAAG	ATTATGTCTT	GTGTCATGCT	TCCCATTTGGT	960
GCTGTGGTGA	TGCTTTTGG	ATTGCTCATG	GCTATTACAA	ATACTCAAGA	CTGCACCCAT	1020
GGGCAGGAAA	TGTTCTACTG	CTTCTCTGAC	AATTTCTCTC	TCACAAATAC	CTCAGAGTCT	1080
CATGTTTCAGC	AGACAACACA	ACTTTCTACT	TTAAATATTA	GTATCTTTCA	ACTCGAGTAA	

Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGYQRQEPVI	PPQVNKTGFG	PGYLLLSVLQ	FLYPFIAMIS	YNIAGDTLS	KVFQRIPIGVD	60
PENVFIGRHF	IIIGLSTVTF	LPLSLYRNIA	KLGVSLIST	GLTTLILGIV	MARISLGP	120
IPKTEDAWVF	AKPNAIQAVG	VMSFAFICH	NSFLVYSSLE	EPTVAKWSRL	IHMSIVISVF	180
ICIFFATCGY	LTFTGFTQGD	LFENYCRND	LVTFRFCY	VTVILTYPM	CFVTRIVIAN	240
VFFGGNLSV	FHVVTVMVI	TVATLVSLI	DCLGIVLELN	GVLCATPLIF	IIPSACYLKL	300
SEEPRTSDK	IMSCVMLPIG	AVVMVFGFVM	AITNTQDCTH	GQEMFYCFPD	NFSLTNTSES	360
HVQQTQLST	LNISIFQLE					

Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

1	11	21	31	41	51	
AGGAATCTGC	GCTCGGGTTC	CGCAGATGCA	GAGGTGAGG	TGGCTGCGGG	ACTGGAAGTC	60
ATCGGGCAGA	GGTCTCACAG	CAGCCAAGGA	ACCTGGGGCC	CGCTCCTCCC	CCCTCCAGGC	120
CATGAGGATT	CTGCAGTTAA	TCTGCTTGC	TCTGGCAACA	GGGCTGTAG	GGGGAGAGAC	180
CAGGATCATC	AAGGGTTCG	AGTGAAGCC	TCACTCCAG	CCCTGGCAGG	CAGCCCTGTT	240
CGAGAAGACG	CGGCTACTCT	GTGGGGCGAC	GCTCATCGCC	CCCAGATGGC	TCTGTACAGC	300
AGCCCACTGC	CTCAAGCCCC	GCTACATAGT	TCACCTGGGG	CAGCACAACC	TCCAGAAGGA	360
GGAGGGCTGT	GAGCAGACCC	GGACAGCCAC	TGAGTCTTC	CCCCACCCCG	GCTTCAACAA	420
CAGCCTCCCC	AACAAGACC	ACCGCAATGA	CATCATGCTG	GTGAAGATGG	CATCGCCAGT	480
CTCCATCACC	TGGGCTGTGC	GACCCCTCAC	CCTCTCCTCA	CGCTGTGTCA	CTGCTGGCAC	540
CAGTGCCTCT	ATTTCCGGCT	GGGGCAGCAC	GTCCAGCCCC	CAGTTACGCC	TGCCTCACAC	600
CTTGCGATGC	GCCAACATCA	CCATCATTGA	GCACCAGAAG	TGTGAGAAGC	CCTACCCCGG	660
CAACATCACA	GACACCATGG	TGTGTGCCAG	CGTGCAGGAA	GGGGGCAAGG	ACTCCTGCCA	720
GGGTGACTCC	GGGGGCCCTC	TGGTCTGTAA	CCAGTCTCTT	CAAGGCATTA	TCTCTGGGG	780
CCAGGATCCG	TGTGCGATCA	CCGAAAGCC	TGGTGTCTAC	ACGAAAGTCT	GCAAAATATGT	840
GGAGTGGATC	CAGGAGACGA	TGAAGAACAA	TAGACTGGA	CCCAACCCAC	ACAGCCCATC	900
ACCTTCATT	TCCACTTGGT	GTTTGGTTCC	TGTTCACTCT	GTAAATAAGA	AACCCTAAGC	960
CAAGACCCCT	TACGAACATT	CTTTGGGCCT	CCTGGAATAC	AGGAGATGCT	GTCATTATAT	1020
AATCAACCTG	GGGTTCGAAA	TCACTGAGAC	CTGATTCAA	ATTCTGCCCT	GAAATATTGT	1080
GACTCTGGGA	ATGACAACAC	CTGGTTTGT	CTCTGTGTA	TCCCCAGCCC	CAAAGACAGC	1140
TCCTGGCCAT	ATATCAAGGT	TTCAATAAAT	ATTGCTAAA	TGAGTG		

Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

1	11	21	31	41	51	
MRILQLILLA	LATGLVGGET	RIIKGFECKP	HSQPWQAALF	EKTRLLCGAT	LIAPRWLLTA	60

AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAQT SCLISGWGST SSPQLRLPHT LRCANITIE HOKCENAYPG 180
 NITDTMVCAS VQEGGKDSQC GDGGGLVCN QSLQGIISWG QDPCAITRKP GYVTKVCKYV 240
 DWIQETMKNN

Seq ID NO: 678 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..933

10 1 11 21 31 41 51
 ATGTGCAGCA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCCTGACTGC 60
 TTCGACAAGA GTGATGAGAA GGAGTGCCTC AAGGCTAAGT CGAAATGTGG CCCGACCTTC 120
 TTCCCTCTGT CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG 180
 15 GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
 GCCCGCTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
 AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGCAGT 360
 GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTGTGTATT ACCCCAGCAT CACCTATGCC 420
 ATCATCGGCA GCTCCGTGCT TTTTGTGCTG GTGGTGGCCC TGCTGGCAGT GGTCTTGAC 480
 20 CACGAGCGGA AGCGGAACAA CCTCATGACG CTGCCCCGTC ACCGGCTGCA GCACCTGTG 540
 CTGCTGTCCC GCCTGGTGGT CCTGGACCAC CCCACCACT GCAACGTGCA CTACAACGTC 600
 AATAATGGCA TCCATATGAT GGCCAGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC 660
 CCACCTCTCT ACTCGAGGC CTGTCTGGAC CAGAGGCTCG CGTGGTATGA CCTTCCTCCA 720
 CCGCCTACT CTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCTC CTACCGCTCC 780
 25 CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCCTCTC GAGCGTGGAA 840
 GACACGAGCC ACAGCCCGGG GCAGCCTGGC CCCAGGAGG GCACTGCTGA GCCCAGGGAC 900
 TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 679 Protein sequence
 Protein Accession #: Eos sequence

30 1 11 21 31 41 51
 MCSNRCIPGP AWQCDGLPDC PDKSDEKECP KAKSKCGPTF PFCASGIHCI IGRFRCNGFE 60
 35 DCPDGSDEEN CTANPLLCST ARYHCKNGLC IDKSFICDQG NNCQDNDSE E SCESSQEPGS 120
 GQVFVTSNQ LVYYPSTIYA IIGSSVIFVL VVALLALVLH HQRKRNLMT LPVHRLQHPV 180
 LLSRLVLVDH PHHCNVTYNV NNGIQYVASQ AEQNASEVGS PPSYSEALLD QRPWWYDLPP 240
 PPYSSTESL NQADLPPYRS RSGSANSASS QAASSLLSVE DTSHSPGQPG PQEGTAEPRD 300
 SEPSQGTEEV

Seq ID NO: 680 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

45 1 11 21 31 41 51
 ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTCACCTGT CTCCATTGAA 60
 GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCGACAAT CTGTGGCTCC 120
 50 AACTATCCAC TGAGCATTTG CTTCATTGTG GTGAATGAAT TCTGCGAGCG CTTTCTCTAT 180
 TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCTGCACTG GAATGAAGAT 240
 ACCTCCACAT CTATATACCA TGCTTCAGC AGCCTCTGTT ATTTTACTCC CATCTGGGA 300
 GCAGCCATTG CTGACTCGTG GTTGGGAAA TTCAAGACAA TCATCTATCT CTCCTTGGTG 360
 TATGTGCTTG GCCATGTGAT CAAGTCTCTG GGTGCCCTAC CAATACTGGG AGGACAAGTG 420
 GTACACACAG TCCTATCATT GATCGGCCCTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC 480
 55 AAAACCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAACATGC AGAGGAACGG 540
 ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATT 600
 ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT 660
 TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACTTGTG TTGTGCAAT GGAAGCAAAA 720
 ATATACAATA AACCAACCCC TGAAGGAAAC ATAGTGGCTC AAGTTTCAA ATGTATCTGG 780
 60 TTTGCTATT CCAATCGTTT CAAGAACCGT TCTGGAGACA TTCCAAGCG ACAGCACTGG 840
 CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATTA TGATGTAAA GGCATGACC 900
 AGGGTACTAT TCCTTTATAT CCCATTGCC ATGTTCTGGG CTCTTTTGA TCAGCAGGGT 960
 TCAAGATGGA CTTTGCAGC CATCAGGATG AATAGGAATT TGGGTTTGT TGTGCTTCA 1020
 65 CCGGACCAGA TGCAGGTCTT AAATCCCTTT CTGGTCTCTA TCTTCATCCC GTTGTTCAG 1080
 TTTGTCAATT ATCGTCTGGT TCCTCAAGTG GGAATTAAC TCTCATCACT TAGGAAAATG 1140
 GCTGTTGGTA TGATCCTAGC GTGCTGGCA TTTGCACTG CGGCAGCTGT AGAGATAAAA 1200
 ATAAATGAAA TGGCCCCAGC CCACTCAGGT CCCAGGAGG TTTTCTTACA AGTCTTGAAT 1260
 CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA 1320
 70 GAGTCCATCA AATCCTTTCA GAAAACACCA CACTATTCCA AACTGCACCT GAAAACAAAA 1380
 AGCCAGGATT TTCACTTCCA CCTGAAATAT CACAATTTGT CTCTCTACAC TGAGCATTCT 1440
 GTGCAGGAGA AGAAGTGGTA CAGTCTTGTC ATTCGTGAAG ATGGGAACAG TATCTCCAGC 1500
 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGT 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 75 GAAGACTATG GTGTGCTCTG TTATAGAACT GTGCAAGAG GAGAATACCC TGCAGTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTGGGTC TTCTAGACT TGGTGCAGCA 1740
 TATCTGTTTG TTATTACTAA TAACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800
 ATTCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTTCTCTGT CACAGTCTT GAGTTTCTT ATTCTCAGG TCCTCTAGC 1920
 80 ATGAAATCTG TGCTCCAGGC AGCTTGCTA TTGACAATT CAGTGGGCCG AATTCAATTT GTTTCCTGC 2040
 CTGTTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCCG AATTCAATTT GTTTCCTGC 2040
 CTCTCTGCTG TGATCTGCTT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAG 2100
 ACAGAGGATA TCGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGGG GAACATGATC 2160
 AAACCTAGAGA CCAAGAAGAC AAAACTCTGA

Seq ID NO: 681 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
| | | | | |
MNPFQKNESK ETLFSPVSIE EVPPRPPSP KFPSPTICGS NYPLSIAFIV VNEPCERFSY 60
YGMKAVLILY FLYPLHWNED TSTSIYHAFS SLCYFTPILG AAIADSWLGG FKTIIYLSLV 120
5 YVLGHVIXSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QPEEKHAEER 180
TRYFSVYFYS INAGSLISTP ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVFPAMGSK 240
IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT 300
RVLFYLIPLP MPWALLDQOG SRWTLQAIM NRNLGPFVLQ PDQMQLVNPV LVLFIIFLFD 360
FVIYRLYSKC GINFSLLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN 420
10 LADDEVKVTV VGNENNSLLI ESIXSFQKTP HYSKLHLKTK SQDPHFHLKY HNLSTLYTEHS 480
VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
EDYGVSAYRT VQGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600
IPANKMSIAW QLFQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAALW LTIAGVNIIV 660
15 LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYYYVPVK TEDMRGPADK HIPHIQENMI 720
KLETKKTKL

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51
| | | | | |
TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
CGCGATAGAA AGGTGTTCGC TTGCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT 120
25 ACTGTAGATG CCTCCCAAT CCTTGGTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180
CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGAGT ACAAGATGAT TCTGTGTGTT CGAAATGACT TAAAGATGGG 360
AAAAGGGAAA GTGGCTGCC AGTGCTCTCA TGCTGTGTT TCAGCCTACA AGCAGATTCA 420
30 AAGAAGAAAT CCTGAAATGC TCAACCAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAA TGCTGGGACT 540
GACTGTAAAT TTAATTCAG ATGCTGGACG TACTCAGAT GCACCAGGCT CTCAACTGT 600
CCTAGGATG GTGGCCAGAC CAGCAGACCT AATTGACAA GTCACTGGTC ACCTAAACT 660
35 TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTT AGCCTGTCA 720
GATTCTAACA ACAAAGCTG AATTTCTTCA CCCAACTTAA ATGTCTCTGA GATGAAAATA 780
AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

1 11 21 31 41 51
| | | | | |
MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
DSGEYKMLV VRNDLMKMG KVAACQSHAA VSAYKQIQR NEPEMLKQWEY CGQPKVUVKA 120
45 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPGLADLID KVTGHLKLY

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

1 11 21 31 41 51
| | | | | |
CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60
TCAGATGCTC CTGGTGTTCG TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120
55 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
ATTCCGAGAG TTGCGGAAC CCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG 240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300
AGTGGGCTG GATCCGCGG GCCACCTGCA CCTGCGTATC TCTCGGGCG CCCTTCCCGA 360
60 GGGGCTCCCC GAGGCTCCCC GCCTTCACCG GCGTCTGTT CCGCTGTCCC CGACGGCGTC 420
AAGGTGCTGG GACGTGACAC GACGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
GCCGCGCGTG CACCTGCGAC TGTGCGCGC GCCGTGCGAG TCGGACCAAC TGCTGGCAGA 540
ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCGG CCAGGGGGCG 600
CCGAGAGCG CGTGCGCGCA ACGGGGAGCA CTGTCCGCTC GGGCCCGGGG GTTGCTGCCG 660
65 TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCGGATTGGG TGCTGTGCGC 720
ACGGGAGGTG CAAGTGACCA TGTGTCATCG GCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC 840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900
GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCTC 960
70 GGTCTCTCCA CTGTGCACCT GCGCGGGGGA GCGACCTCA GTTGTCTGTC CCTGTGGAAT 1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
TTATTATTAT TTAATTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
ACTGTGTATT TATTTAAAC TCTGTGATA AAAATAAAGC TGTCTGAAC GTTAAAAAAA 1200
AAAA

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

1 11 21 31 41 51
| | | | | |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS FPGPSELHSED SRFRELRKRY 60
80 EDLLTRLRAN QSWEDSNTDL VPAPAVRILT FEVRLGSGGH LHLRISRAL PEGLPASRL 120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPFSQSDQLL AESSSARPOL 180
ELHLRPQAAR GRRRARARNG DDCPLPGPRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240
85 IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCPASYN PMVLIQKTDI GVSILQYDDL 300
LAKDCHCI

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60
      TGCTGTGTGC TGTGTGCTGC CTGCCTGGCA GCCTGGCCCT GCGCTGCCT CAGGAGGCGG 120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTATCTCT 180
10     ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240
      TCTTTGGCCT ACCTATAACT GGAATGTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
      CCAGATGTGG AGTGCCAGAT GTTGCAAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
      CTTCCAAAGT GGTCACTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTC 480
15     GGAAAGTTGT ATGGGGAAT GCTGACATCA TGATTGGCTT TCGCGAGGA GCTCATGGGG 540
      ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG 600
      GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
      GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCCTTGGGT ATGGGACATT 720
      CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
      AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAGAGA AGTAATTC 840
20     GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCAATCA TTCATTGGAT TGTATATCAT 900
      TGTTCACAAA TCAGAATTGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCACC 960
      CTTTTTATT GCAGTGGTT TTTGAATGTC TTCTACTCCT TTTATTGGTT AAACCTCTTT 1020
      ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTGTCA GTGCGCGTAT ATGTCAATAA 1080
25     ATGTTACATA CACAAATAAA TAAATGTTT ATTCCATGGT AAATTTA

```

Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

```

30     1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGLSLPL PQEAGGMSEL QWEQAQDYLK RPYLYDSEK NANSLEAKLK 60
      EMQKFFGLPI TGMNLSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
      PHITVRLVS KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSYPPD GPGNTLAHAF 180
35     APGTGLGDDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240
      PQNFLSQDD IKGIQKLYGK RSNRKK

```

Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGACAGGAG TGTTCAGAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
      TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120
45     TCAGCTACCG ATCTGACTA CTACAGCCCT ACGGGGGGAG CCCGCGCAGG CTACTGCTCT 180
      CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCTTACC AGTATCAGTA TCACGGCGTG 240
      AACGGTCCG CCGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
      TACCACCACT ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
      GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420
50     AGGACTATTT ATTCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
      TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAACACAG 540
      GTGAAAATCT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG 600
      ATGCCCCCGG AGCAGCTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCCGAGTCT 660
55     CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACC TCATGCCAC 720
      CTCCGACCT CCAACCACTC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGTTAC 780
      ACAAGTGCAG CCAGCTCAAT CAATTCCCAC CTGCCGCCGC CGGGCTCCTT ACAGCACCCG 840
      CTGGCGCTGG CCTCCGGAC ACTCTATTAG

```

Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRPV SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSYYSPT TGGAPHGYCS 60
65     PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
      EVTEPEVRMV NGKPKVKRKP RTIYSSPQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
      VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMA CNSPQS PAVWEPQGSS RSLSHHPAH 240
      PPTS NQSPAS SYLENSASWY TSAASSINSH LPPFGSLQHP LALASGTLY

```


It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.